

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 23, 2001, 15:28:39 ; Search time 21.53 Seconds
(without alignments)
969.093 Million cell updates/sec

Title: US-08-887-977-10
Perfect score: 365
Sequence: 1 MFSTPVKILQCOSILHITOL.....NISRQTSFADNDNASFTM 365

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0
Searched: 390729 seqs, 57163235 residues

Word size : 10
Total number of hits satisfying chosen parameters: 7

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

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17: /SID56/gcgdata/geneseq/geneseq/AA1996.DAT.*
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20: /SID56/gcgdata/geneseq/geneseq/AA1999.DAT.*
21: /SID56/gcgdata/geneseq/geneseq/AA2000.DAT.*
22: /SID56/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	365	100.0	365	19	W48086 Human dendritic ce
2	264	72.3	365	21	Y97077 Primate (human) ch
3	10	2.7	360	17	R99274 Chemokine receptor
4	10	2.7	360	21	B07498 A human CCR4 chemo
5	10	2.7	469	21	Y92934 Human G-protein co
6	10	2.7	476	21	Y92932 Rat G-protein coup
7	10	2.7	476	21	Y92933 Rat G-protein coup

ALIGNMENTS

RESULT 1
W48086
ID W48086 standard; Protein; 365 AA.
XX
AC W48086;
XX
DT 11-JUN-1998 (first entry)
XX
DE Human dendritic cell chemokine receptor.
XX
KW Human; thymus expressed chemokine; TECK; MIP-3alpha; MIP-3beta;
KW receptor; dendritic cell; macrophage; inflammation; asthma.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 193
FT /note= "encoded by CAN"
XX
PN W09801557-A2.
XX
PD 15-JAN-1998.
XX
PF 02-JUL-1997; 97WO-US10819.
XX
PR 04-JUN-1997; 97US-0048593.
PR 05-JUL-1996; 96US-0675814.
PR 11-OCT-1996; 96US-0028329.
XX
(SCHE) SCHERING CORP.
XX
PI Gish KC, Schall TJ, Vicari A, Wang W, Zlotnik A;
XX
XX WPI; 1998-101054/09.
DR N-PSDB; V15418.
XX
XX Novel chemokines, e.g. thymus expressed chemokine - used for
PT treating inflammatory conditions including asthma.
XX
PS Claim 3; Page 94-95; 202pp; English.
XX
XX The present sequence represents human dendritic cell chemokine receptor.
CC Antibodies which bind to the protein can be used in detecting or
CC diagnosing various immunological conditions related to expression
CC of the protein. The nucleic acid can be used for screening and
CC isolating DNA clones for the chemokines, especially from other
CC species. The chemokine can be used in the treatment of conditions
CC associated with abnormal physiology or development, including
CC inflammatory conditions such as asthma.
XX
SQ Sequence 365 AA;

Query Match 100.0%; Score 365; DB 19; Length 365;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 365; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFSTPVKILQCOSILHITOLILRCYCPCRRSGSSPGYLYRIAYSLICVLGLGNILVVI 60
Db 1 mfstpvkllcqsilhitqlilrcycpcrrsgsspgylyriaysllcvgllgnilvvi 60

QY 61 TFAFYKARSMTDYLNLMAIADILFVLTLPFWAVSHATGAWVFSNATCKLLKGIYAINF 120
Db 61 tfafykarsmtdvylnlmaiadilfvtlpfwavshatgawvfnatckllkgiyainf 120

QY 121 NCGMLLLTCLISMDRYTAIVQATKSFRLRSRTLPKSKITICLVWGLSVIISSTFVFNOKY 180
Db 121 ncgmllltclismdrytaivdatskfrlrsrtlpkskiticlvwglsviisssstfvfnqky 180

QY 181 NTGSDVCEPKYQTVSEPIRWKLMGLLELFGFFIFLPMFMIFCYFTIVKTLVQAQNSKR 240
Db 181 ntgsdvcepkqtvsepiwrkllmgllellfgffiplmfmifcyftivktlvqaqnskr 240

QY 241 HKAIRVIAVVLVFLACQIPHNMLVLTAAANLGMNRSCQSEKLGTYTKTVEVLAFLHC 300
 Db 241 HKAIRVIAVVLVFLACQIPHNMLVLTAAANLGMNRSCQSEKLGTYTKTVEVLAFLHC 300
 QY 301 CLNPVLYAFIGQFRNYFLKILKDLWCVRKYSKSGFSCAGRYSENISROTSETADNDNA 360
 Db 301 CLNPVLYAFIGQFRNYFLKILKDLWCVRKYSKSGFSCAGRYSENISROTSETADNDNA 360
 QY 361 SSFTM 365
 Db 361 SSFTM 365

RESULT 2
 Y97077
 ID Y97077 standard; Protein; 365 AA.
 XX
 AC Y97077;
 XX
 DT 04-DEC-2000 (first entry)
 XX
 DE Primate (human) chemokine receptor CCR6.
 XX
 KW MIP-3-alpha; chemokine; CCR6 receptor; ligand; cytostatic; agonist;
 KW antagonist; anti-psoriatic; dermatological; immunosuppressive;
 KW anti-inflammatory.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 193
 FT /note= "Encoded by CAN#"
 PN WO200046248-A1.
 XX
 PD 10-AUG-2000.
 XX
 PF 02-FEB-2000; 2000WO-US00511.
 XX
 PR 03-FEB-1999; 99US-0244281.
 XX
 FA (SCHE) SCHERING CORP.
 XX
 PI Oldham ER, Homey B, Dieu-Nosjean M, Caux C, Zlotnik A;
 XX
 DR WPI: 2000-543477/49.
 DR N-PSDB; A51971.
 XX
 PT Novel methods for modulating the migration of cells within or to the
 PT skin using MIP-3-alpha or CCR6 agonists or antagonists, useful for
 PT treating skin disorders, e.g. cancer
 XX
 PS Disclosure; Page 53-54; 61pp; English.
 XX
 CC The MIP-3-alpha chemokine is expressed in inflamed skin cells. This
 CC chemokine is the ligand for the CCR6 receptor. MIP-3-alpha or CCR6
 CC agonists or antagonists can be used to modulate the migration of a cell
 CC within or to the skin of a mammal. MIP-3-alpha can be used to purify a
 CC population of cells expressing a MIP-3-alpha receptor. The methods are
 CC useful for treating a mammalian subject with a skin disease or condition,
 CC e.g. cancer, metastasis, psoriasis, atopic or contact dermatitis,
 CC systemic lupus erythematosus and lichen ruber planus, or for treating
 CC skin transplants or grafts.
 XX
 SQ Sequence 365 AA;

Query Match 72.3%; Score 264; DB 21; Length 365;
 Best Local Similarity 99.7%; Pred. No. 1.4e-251;
 Matches 364; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MFSTPVKILQCQSIHLITQLIRCYCAPCRSGSPGYLYRIAYSLICVLGLGNILVVI 60
 Db 1 MFSTPVKILQCQSIHLITQLIRCYCAPCRSGSPGYLYRIAYSLICVLGLGNILVVI 60
 QY 61 TFAYYKARSMTDVLNMAADILFVLTPFVAVSHATGAWFNSNATCKLLKGIYAINF 120
 Db 61 TFAYYKARSMTDVLNMAADILFVLTPFVAVSHATGAWFNSNATCKLLKGIYAINF 120
 QY 121 NCGMLLFTCISMDRYIAIVQATKSFRLRSRTPRSLKIICLVVWGLSVIISSTFVFNQY 180
 Db 121 NCGMLLFTCISMDRYIAIVQATKSFRLRSRTPRSLKIICLVVWGLSVIISSTFVFNQY 180
 QY 181 NTQGSVCEPKYQTVSEPIRWKLLMLGLELFGFFIPLMFIFCYTFIVKILVQONSKR 240
 Db 181 NTQGSVCEPKYQTVSEPIRWKLLMLGLELFGFFIPLMFIFCYTFIVKILVQONSKR 240
 QY 241 HKAIRVIAVVLVFLACQIPHNMLVLTAAANLGMNRSCQSEKLGTYTKTVEVLAFLHC 300
 Db 241 HKAIRVIAVVLVFLACQIPHNMLVLTAAANLGMNRSCQSEKLGTYTKTVEVLAFLHC 300
 QY 301 CLNPVLYAFIGQFRNYFLKILKDLWCVRKYSKSGFSCAGRYSENISROTSETADNDNA 360
 Db 301 CLNPVLYAFIGQFRNYFLKILKDLWCVRKYSKSGFSCAGRYSENISROTSETADNDNA 360
 QY 361 SSFTM 365
 Db 361 SSFTM 365

RESULT 3
 R99274
 ID R99274 standard; Protein; 360 AA.
 XX
 AC R99274;
 XX
 DT 09-DEC-1996 (first entry)
 XX
 DE Chemokine receptor K5.5.
 XX
 KW Chemokine receptor K5.5; MIP-1-alpha; RANTES; MCP-1; allergy;
 KW atheroma; HIV; AIDS; graft rejection; stem cell.
 XX
 OS Homo sapiens.
 XX
 PN WO9623068-A1.
 XX
 PD 01-AUG-1996.
 XX
 PF 24-JAN-1996; 96WO-GB00143.
 XX
 PR 27-JAN-1995; 95GB-0001683.
 XX
 PA (GLAX) GLAXO GROUP LTD.
 XX
 PI Power CA, Wells TNC;
 XX
 DR WPI: 1996-362692/36.
 DR N-PSDB; T35277.
 XX
 PT Chemokine receptor which binds MIP-1-alpha, RANTES and/or MCP-1 -
 PT useful in screening for agents to treat asthma, hay fever, eczema,
 PT allergies, atopic dermatitis, rhinitis or conjunctivitis.
 XX
 PS Claim 1; Fig 3; 47pp; English.
 XX
 CC Human chemokine receptor K5.5 (R99274) binds MIP-1-alpha, RANTES
 CC and/or MCP-1. Its amino acid sequence was deduced from a cDNA
 CC clone (T35277) obt'd. from a human spleen lambda gt11 cDNA
 CC library. Recombinant chemokine receptor K5.5 can be expressed
 CC in transformed host cells. It can be used to screen for agents
 CC which act as antagonists to MCP-1, MIP-1-alpha and/or RANTES.
 CC Such agents may be useful in treating allergies, atheromas and
 CC diseases mediated by viruses, such as AIDS. They can also be
 CC used to prevent graft rejection or to protect stem cells from

CC the effects of chemotherapy.

XX Sequence 360 AA;

Query Match 2.7%; Score 10; DB 17; Length 360;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 69 RSMETDVYLLN 78
|||||
Db 71 rsmtdvyl n 80

RESULT 4

ID B07498 standard; Protein; 360 AA.

XX AC B07498;

DT 20-OCT-2000 (first entry)

DE A human CCR4 chemokine receptor polypeptide.

XX KW Systemic memory T cell; CCR4; TARC; integrin dependent arrest;
KW thymus and activation-regulated chemokine; vascular receptor;
KW MDC; monokine derived chemokine; adhesion trigger; inflammation.

XX OS Homo sapiens.

XX PN WO200041724-A1.

XX PD 20-JUL-2000.

XX PF 14-JAN-2000; 2000WO-US00953.

XX PR 15-JAN-1999; 99US-0232878.

XX PA (STRD) UNIV LELAND STANFORD JUNIOR.
XX PA (LEUK-) LEUKOSITE INC.

XX PI Butcher EC, Campbell JJ, Wu L, Rottman JB;

XX DR WPI: 2000-475957/41.

XX DR N-PSDB; A58872.

XX PT Modulating the trafficking of systemic memory T cells in mammals by
PT administering a CCR4 modulating agent, useful for the treatment of
PT inflammation -

XX PS Disclosure; Page 35-36; 39pp; English.

XX CC The specification describes a method of modulating the trafficking of
CC systemic memory T cells in a mammalian host. The method comprises
CC administering a CCR4 modulating agent. It has been found that systemic
CC T cells such as express high levels of CCR4. Ligands of CCR4 such as
CC TARC (thymus and activation-regulated chemokine) and MDC (monokine
CC derived chemokine) act as an adhesion trigger and, upon CCR4 binding,
CC these cells undergo integrin dependent arrest to the appropriate
CC vascular receptors. This arrest acts to localize the cells at the
CC target site. The method modulates this triggering and CCR4 mediated
CC chemotaxis to affect the localization of T cells in targeted tissues.
CC The active agent may be a CCR4 agonist that acts to enhance T cell
CC localization. Alternatively, it may be an antagonist that blocks CCR4
CC biological activity. A CCR4 antagonist may be administered for the
CC treatment of inflammation. The present sequence represents a human CCR4.

XX Sequence 360 AA;

Query Match 2.7%; Score 10; DB 21; Length 360;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 69 RSMETDVYLLN 78
|||||
Db 71 rsmtdvyl n 80

RESULT 5

ID Y92934 standard; Protein; 469 AA.

XX AC Y92934;

XX DT 25-OCT-2000 (first entry)

XX DE Human G-protein coupled receptor clone hOT7T009 protein.

XX KW Hypotensive; G-protein coupled receptor protein; brain stem region;
KW antibody; hypertension; ligand; human.

XX OS Homo sapiens.

XX PN WO200024891-A1.

XX PD 04-MAY-2000.

XX PF 27-OCT-1999; 99WO-JP05938.

XX PR 28-OCT-1998; 98JP-0306543.

XX PR 28-JAN-1999; 99JP-0020356.

XX PA (TAKE) TAKEDA CHEM IND LTD.

XX PI Watanabe T, Matsumoto Y, Terao Y, Shintani Y;

XX DR WPI: 2000-350733/30.

XX DR N-PSDB; A11249.

XX PT G protein coupled receptor protein, antibodies to it and a method of
PT screening compounds which alter the binding of the receptor to its
PT ligands for treatment of disorders such as hypertension -

XX PS Example 2; Fig 10-12; 120pp; Japanese.

XX CC This sequence represents a novel human G-protein coupled receptor protein
CC (GCPR) designated clone hOT7T009. The coding sequence was isolated from
CC a foetal cDNA library. The protein and antibodies raised against it are
CC useful in the diagnosis, treatment and prevention of disorders associated
CC with the GCPR, such as hypertension. The protein is also used to identify
CC ligands of GCPR and compounds which affect the binding of GCPR to its
CC ligands.

XX SQ Sequence 469 AA;

Query Match 2.7%; Score 10; DB 21; Length 469;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 86 FVLTLPFWAV 95
|||||
Db 131 fvltpfwav 140

RESULT 6

ID Y92932 standard; Protein; 476 AA.

XX AC Y92932;

XX DT 25-OCT-2000 (first entry)

XX DE Rat G-protein coupled receptor clone rOT7T009C protein.

KW Hypotensive; rat; G-protein coupled receptor protein; brain stem region;
 KW antibody; hypertension; ligand.
 OS Rattus sp.

PN WO200024891-A1.

XX 04-MAY-2000.

XX 27-OCT-1999; 99WO-JP05938.

XX 28-OCT-1998; 98JP-0306543.

XX 28-JAN-1999; 99JP-0020356.

XX (TAKE) TAKEDA CHEM IND LTD.

PI Watanabe T, Matsumoto Y, Terao Y, Shintani Y;

XX WPI; 2000-350733/30.

DR N-PSDB; A11247.

XX G protein coupled receptor protein, antibodies to it and a method of

PT screening compounds which alter the binding of the receptor to its

PT ligands for treatment of disorders such as hypertension -

XX Claim 1; Fig 1-4; 120pp; Japanese.

XX This sequence represents a novel rat G-protein coupled receptor protein
 CC (GPR) designated clone rOT7T009C. The coding sequence was isolated from
 CC a brain stem region library. The protein and antibodies raised against
 CC it are useful in the diagnosis, treatment and prevention of disorders
 CC associated with the GPR, such as hypertension. The protein is also used
 CC to identify ligands of GPR and compounds which affect the binding of
 CC GPR to its ligands.

XX Sequence 476 AA;

Query Match 2.7%; Score 10; DB 21; Length 476;

Best Local Similarity 100.0%; Pred. No. 0.16;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 86 FVLTLPFWAV 95

Db 138 fvltpfwav 147

RESULT 7

Y92933

ID Y92933 standard; Protein; 476 AA.

XX AC Y92933;

DT 25-OCT-2000 (first entry)

DE Rat G-protein coupled receptor clone rOT7T009T protein.

XX Hypotensive; rat; G-protein coupled receptor protein; brain stem region;

KW antibody; hypertension; ligand.

XX Rattus sp.

PN WO200024891-A1.

XX 04-MAY-2000.

XX 27-OCT-1999; 99WO-JP05938.

XX 28-OCT-1998; 98JP-0306543.

XX 28-JAN-1999; 99JP-0020356.

XX (TAKE) TAKEDA CHEM IND LTD.

PI Watanabe T, Matsumoto Y, Terao Y, Shintani Y;

XX WPI; 2000-350733/30.

DR N-PSDB; A11248.

XX G protein coupled receptor protein, antibodies to it and a method of

PT screening compounds which alter the binding of the receptor to its

PT ligands for treatment of disorders such as hypertension -

XX Claim 2; Fig 5-8; 120pp; Japanese.

XX This sequence represents a novel rat G-protein coupled receptor protein
 CC (GPR) designated clone rOT7T009T. The coding sequence was isolated from
 CC a brain stem region library. The protein and antibodies raised against
 CC it are useful in the diagnosis, treatment and prevention of disorders
 CC associated with the GPR, such as hypertension. The protein is also used
 CC to identify ligands of GPR and compounds which affect the binding of
 CC GPR to its ligands.

XX Sequence 476 AA;

Query Match 2.7%; Score 10; DB 21; Length 476;

Best Local Similarity 100.0%; Pred. No. 0.16;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 86 FVLTLPFWAV 95

Db 138 fvltpfwav 147

Search completed: May 23, 2001, 15:36:41

Job time: 482 sec

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OM protein - protein search, using sw model

Run on: May 23, 2001, 15:30:14 ; Search time 13 Seconds
(without alignments)
539,382 Million cell updates/sec

Title: US-08-887-977-10
Perfect score: 365
Sequence: 1 MFSTPVKILCOSILHITOL.....NISQTSADNDNASSFTM 365

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 185757 seqs, 19210857 residues

Word size : 10

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : Issued Patents_AA.*

- 1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/2/iaa/PTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	10	2.7	360	4	US-08-875-573-20 Sequence 20, Appl

ALIGNMENTS

RESULT 1

US-08-875-573-20
Sequence 20, Application US/08875573
Patent No. 6150132

GENERAL INFORMATION:

APPLICANT: Wells, Timothy N.C.
APPLICANT: Power, Christine A.
TITLE OF INVENTION: A CHEMOKINE RECEPTOR ABLE TO BIND TO
TITLE OF INVENTION: MCP-1, MIP-1 ALPHA AND/OR RANTES. ITS USES
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:

ADDRESSEE: NIXON & VANDERHUYE P.C.
STREET: 1100 No. 6150132th Glebe Rd. 8th floor
CITY: Arlington
STATE: VA
COUNTRY: USA

ZIP: 22201-4741

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,573
FILING DATE: 31-OCT-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB96/00143
FILING DATE: 24-JAN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9501683.8
FILING DATE: 27-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Willson, Mary J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 1430-172
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4000
TELEFAX: 703-816-4100
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 360 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-875-573-20

Query Match 2.7%; Score 10; DB 4; Length 360;
Best Local Similarity 100.0%; Pred. No. 0.065;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 69 RSMSTDVYLLN 78
|||||
DB 71 RSMSTDVYLLN 80

Search completed: May 23, 2001, 15:36:57
Job time: 403 sec

1

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 23, 2001, 15:32:09 ; Search time 18.5 Seconds
(without alignments)
1355.885 Million cell updates/sec

Title: US-08-887-977-10
Perfect score: 365
Sequence: 1 MFSTPVKIIILCQSILHITQL.....NISROTSETADNDNASFTM 365

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 198801 seqs, 68722935 residues

Word size : 10

Total number of hits satisfying chosen parameters: 4

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : PIR_67:*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	315	86.3	369	2	JC5068	G protein-coupled
2	11	3.0	353	2	S28787	neuropeptide Y/pep
3	10	2.7	360	2	A57160	chemokine (C-C) re
4	10	2.7	383	2	S55594	G protein-coupled

ALIGNMENTS

RESULT 1
JC5068
G protein-coupled receptor CKR-L3 - human
C:Species: Homo sapiens (man)
C:Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 21-Jul-2000
C:Accession: JC5068
R:Zaballos, A.; Varona, R.; Gutierrez, J.; Lind, P.; Marquez, G.
Biochem. Biophys. Res. Commun. 227, 846-853, 1996
A:Title: Molecular cloning and RNA expression of two new human chemokine receptor-like
A:Reference number: JC5067; MUID:97040707
A:Accession: JC5068
A:Molecule type: DNA
A:Residues: 1-369 <ZAB>
A:Cross-references: EMBL:Z79784; NID:q1668737; PIDN:CAB02144.1; PID:q1668738
C:Comment: This protein belongs to the family of alpha chemokine receptors.
C:Genetics:
A:Gene: GDB:CMKBR6; STR:22; GPR29; CCR6; CKR-L3; GPR-CX4
A:Cross-references: GDB:5370639; OMIM:601835
A:Map position: 6q27-6q27
C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor; transmembrane protein
F:42-68/Domain: transmembrane #status predicted <TM1>
F:79-99/Domain: transmembrane #status predicted <TM2>
F:115-136/Domain: transmembrane #status predicted <TM3>
F:160-180/Domain: transmembrane #status predicted <TM4>
F:212-233/Domain: transmembrane #status predicted <TM5>
F:250-271/Domain: transmembrane #status predicted <TM6>
F:292-315/Domain: transmembrane #status predicted <TM7>

Query Match 86.3%; Score 315; DB 2; Length 369;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 GLGNILVITFAFYKKARSMTDVYLLNMAIADILFVLTLPFWAVSHATGAWFSNATCK 110
DB 55 GLGNILVITFAFYKKARSMTDVYLLNMAIADILFVLTLPFWAVSHATGAWFSNATCK 114
QY 111 LLKGIYAINFNCGMLLTCTISMDRYIAIVQATKSFRLRSRTLPRSKIIICLVVWGLSVIIS 170
DB 115 LLKGIYAINFNCGMLLTCTISMDRYIAIVQATKSFRLRSRTLPRSKIIICLVVWGLSVIIS 174
QY 171 SSTFVFNQKYNTOGSDVCEPKYQTVSEPIRWKLLMLGLELLFGFFIPLMFIFCYTFIVK 230
DB 175 SSTFVFNQKYNTOGSDVCEPKYQTVSEPIRWKLLMLGLELLFGFFIPLMFIFCYTFIVK 234
QY 231 TLVQAQNSKRHKAIIRVIAVVLFLACQIPHNMYLLVTAANLGMNRSCQSEKILGYTKT 290
DB 235 TLVQAQNSKRHKAIIRVIAVVLFLACQIPHNMYLLVTAANLGMNRSCQSEKILGYTKT 294
QY 291 VTEVLAFLHCLNPVLYAFIGOKPRNYFLKILKDLWCVRKYKSGFSCAGRYSENISRQ 350
DB 295 VTEVLAFLHCLNPVLYAFIGOKPRNYFLKILKDLWCVRKYKSGFSCAGRYSENISRQ 354
QY 351 TSETADNDNASFTM 365
DB 355 TSETADNDNASFTM 369

RESULT 2

S28787
neuropeptide Y/peptide YY receptor Y3 - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 26-Aug-1999
C:Accession: S28787
R:Kimland, J.; Xin, W.; Sweetnam, P.; Saijoh, K.; Nestler, E.J.; Duman, R.S.
Mol. Pharmacol. 40, 869-875, 1991
A:Title: Sequence and expression of a neuropeptide Y receptor cDNA.
A:Reference number: S28787; MUID:92100053
A:Accession: S28787
A:Molecule type: mRNA
A:Residues: 1-353 <RIM>
A:Cross-references: EMBL:M86739
C:Superfamily: vertebrate rhodopsin
C:Keywords: appetite; G protein-coupled receptor; transmembrane protein

Query Match 3.0%; Score 11; DB 2; Length 353;
Best Local Similarity 100.0%; Pred. No. 0.0019;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 85 LFVLTLPFWAV 95
DB 87 LFVLTLPFWAV 97

RESULT 3

A57160
chemokine (C-C) receptor 4 - human
N:Alternate names: C-C CKR-4
C:Species: Homo sapiens (man)
C:Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 21-Jul-2000
C:Accession: A57160

R:Power, C.A.; Meyer, A.; Nemeth, K.; Bacon, K.B.; Hoogewerf, A.J.; Proudfoot, A.E.I.; W
 J. Biol. Chem. 270, 19495-19500, 1995
 A:Title: Molecular cloning and functional expression of a novel CC chemokine receptor c
 A:Reference number: A57160; MUID:95370289
 A:Accession: A57160
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-360 <POM>
 A:Cross-references: GB:X85740; NID:g1370103; PIDN:CAA59743.1; PID:g971452
 A:Note: source clone K5-5
 C:Genetics:
 A:Gene: GDB:CMKBR4
 A:Cross-references: GDB:677463
 A:Map position: 3p21-3p21
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane prot
 F:40-65/Domain: transmembrane #status predicted <TM1>
 F:76-97/Domain: transmembrane #status predicted <TM2>
 F:112-133/Domain: transmembrane #status predicted <TM3>
 F:151-175/Domain: transmembrane #status predicted <TM4>
 F:208-226/Domain: transmembrane #status predicted <TM5>
 F:243-264/Domain: transmembrane #status predicted <TM6>
 F:291-308/Domain: transmembrane #status predicted <TM7>
 F:29-276, 110-187/Disulfide bonds: #status predicted
 F:72,350/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted
 F:145/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
 F:183,194/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted

Query Match 2.7%; Score 10; DB 2; Length 360;

Best Local Similarity 100.0%; Pred. No. 0.023;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 69 RSMYDVLN 78

Db 71 RSMYDVLN 80

RESULT 4

S55594

G protein-coupled receptor E1 - equine herpesvirus 2

C:Species: equine herpesvirus 2

C:Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 13-Aug-1999

C:Accession: S55594

R:Telford, E.A.R.; Watson, M.S.; Aird, H.C.; Perry, J.; Davison, A.J.

J. Mol. Biol. 249, 520-528, 1995

A:Title: The DNA sequence of equine herpesvirus 2.

A:Reference number: S55594; MUID:95302501

A:Accession: S55594

A:Status: preliminary; nucleic acid sequence not shown

A:Molecule type: DNA

A:Residues: 1-383 <TEL>

A:Cross-references: GB:U20824; NID:g695172; PIDN:AAC13788.1; PID:g695173

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor

Query Match 2.7%; Score 10; DB 2; Length 383;

Best Local Similarity 100.0%; Pred. No. 0.024;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 51 GLGNILVVI 60

Db 86 GLGNILVVI 95

Search completed: May 23, 2001, 15:37:19
 Job time: 310 sec

FT TRANSMEM 255 279 6 (POTENTIAL).
 FT DOMAIN 280 303 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 304 321 7 (POTENTIAL).
 FT DOMAIN 322 374 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 118 197 BY SIMILARITY.
 FT CARBOHYD 7 7 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 23 23 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 60 60 G -> A (IN REF. 4).
 FT CONFLICT 74 74 Y -> N (IN REF. 4).
 FT CONFLICT 86 86 L -> V (IN REF. 4).
 FT CONFLICT 164 164 S -> T (IN REF. 5).
 FT CONFLICT 182 182 T -> S (IN REF. 4).
 FT CONFLICT 192 192 Q -> L (IN REF. 4).
 FT CONFLICT 206 206 E -> V (IN REF. 4).
 FT CONFLICT 225 225 I -> F (IN REF. 4).
 FT CONFLICT 370 374 SSETM -> VLVHVIES (IN REF. 4).
 FT SEQUENCE 374 AA; 42494 MW; D7F963534E990BC4 CRC64;

Query Match 86.3%; Score 315; DB 1; Length 374;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 GLLGNLVITFAFYKARSMTDVLLNMAIADILFVLTLPFWAVSHATGAWFSNATCK 110
 Db 60 GLLGNLVITFAFYKARSMTDVLLNMAIADILFVLTLPFWAVSHATGAWFSNATCK 119

QY 111 LKGIYAINFCNGMLLTICISMDRYTAIVQATKSFRLSRTLPKSKICLVWGLSVIIS 170
 Db 120 LKGIYAINFCNGMLLTICISMDRYTAIVQATKSFRLSRTLPKSKICLVWGLSVIIS 179

QY 171 SFTFVNQYNTQGSVDCEPKYQTVSEPIRWKLLMLGLELFGFFIPLMFMICYTFTIVK 230
 Db 180 SFTFVNQYNTQGSVDCEPKYQTVSEPIRWKLLMLGLELFGFFIPLMFMICYTFTIVK 239

QY 231 FLVQAQNSRRKRAIRVIAVVLVFLACQIPHNNVLLVTAANLGMNRSKSEKLGITYTKT 290
 Db 240 FLVQAQNSRRKRAIRVIAVVLVFLACQIPHNNVLLVTAANLGMNRSKSEKLGITYTKT 299

QY 291 VTEVLAFHCLLPVLYAFIGQFRNYFLKLDLVCVRKRYKSSGFSAGRYSENISRQ 350
 Db 300 VTEVLAFHCLLPVLYAFIGQFRNYFLKLDLVCVRKRYKSSGFSAGRYSENISRQ 359

QY 351 TSETADNDNASFTM 365
 Db 360 TSETADNDNASFTM 374

RESULT 2
 CKR6_MOUSE STANDARD; PRT; 367 AA.
 AC 054689;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE C-C CHEMOKINE RECEPTOR TYPE 6 (C-C CKR-6) (CC-CKR-6) (CCR-6) (KY411).
 GN CCR6 OR CMKBR6.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Yanagihara S., Komura E., Yamaguchi Y.;
 RT "Mouse G protein-coupled receptor KY411.";
 RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95077268; PubMed=9862452;
 RA Varona R., Zaballos A., Gutierrez J., Martin P., Roncal F.,
 RA Albar J.P., Ardavin C., Marquez G.;
 RT "Molecular cloning, functional characterization and mRNA expression
 analysis of the murine chemokine receptor CCR6 and its specific ligand

RT MIP-3alpha.";
 RL FEBS Lett. 440:188-194(1998).
 CC -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-3-
 CC ALPHA/LARC AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE
 CC INTRACELLULAR CALCIUM IONS LEVEL.
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC
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 CC
 CC EMBL; AB009369; BAA23776.1; -
 CC EMBL; AJ222714; CAA10956.1; -
 CC MGD; MGI:1333797; Cmkbr6.
 DR InterPro: IPR000276; -
 DR Pfam: PF00001; 7tm1.1;
 DR PRINTS: PR00237; GPCRHHODPSN.
 DR PROSITE: PS00237; G-PROTEIN_RECEP_F1_1; 1.
 DR PROSITE: PS00262; G-PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 39 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 40 66 1 (POTENTIAL).
 FT DOMAIN 67 75 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 76 96 2 (POTENTIAL).
 FT DOMAIN 97 111 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 112 133 3 (POTENTIAL).
 FT DOMAIN 134 151 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 152 172 4 (POTENTIAL).
 FT DOMAIN 173 203 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 204 230 5 (POTENTIAL).
 FT DOMAIN 231 246 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 247 271 6 (POTENTIAL).
 FT DOMAIN 272 295 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 296 313 7 (POTENTIAL).
 FT DOMAIN 314 367 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 110 189 BY SIMILARITY.
 FT CARBOHYD 2 2 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 35 35 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 367 AA; 42102 MW; 6A309AF833B1117E CRC64;

Query Match 7.1%; Score 26; DB 1; Length 367;
 Best Local Similarity 100.0%; Pred. No. 5e-18;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 293 EVLAFHCLLPVLYAFIGQFRNYF 318
 Db 294 EVLAFHCLLPVLYAFIGQFRNYF 319

RESULT 3
 CCR4_SHEEP STANDARD; PRT; 192 AA.
 ID CCR4_SHEEP AC Q28553;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE C-X-C CHEMOKINE RECEPTOR TYPE 4 (CXC-R4) (CCR-4) (SDF-1 RECEPTOR)
 DE (STROMAL CELL-DERIVED FACTOR 1 RECEPTOR) (FUSIN) (LEUKOCYTE-DERIVED
 DE SEVEN TRANSMEMBRANE DOMAIN RECEPTOR) (LESTR) (FRAGMENT).
 GN CXC4 OR LESTR.
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Ovis.
 OX NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE FROM N.A.

RC TISSUE-Hypothalamus;
RA Dyer C.J., Matteri R.L., Keisler D.H.;
RT "Development of an ovine Y3 cDNA and expression of the Y3 receptor
RL mRNA in the ovine hypothalamus and pituitary.";
RL Abstr. Soc. Neurosci. 21:1890-1890(1995)
CC CC
CC -1- FUNCTION: RECEPTOR FOR THE C-X-C CHEMOKINE SDF-1. TRANSDUCES A
CC SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -1- CAUTION: WAS ORIGINALLY THOUGHT TO BE A RECEPTOR FOR NEUROPEPTIDE
CC Y, TYPE 3 (NPY3-R).
CC
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CC
CC EMBL; U38942; AAA81347.1;
CC GCRDB; GCR_1581;
CC InterPro; IPR000276;
CC Pfam; PF00001; 7tm.1; 1.
CC PROSITE; PS00237; G_PROTEIN_RECEP_FL_1; 1.
CC PROSITE; PS50262; G_PROTEIN_RECEP_FL_2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein.
CC
CC FT DOMAIN 1 1
CC NON_TER <1 29
CC FT TRANSMEM 30 53
CC FT DOMAIN 54 69
CC FT TRANSMEM 70 89
CC FT DOMAIN 90 100
CC FT TRANSMEM 101 122
CC FT DOMAIN 123 144
CC FT TRANSMEM 145 165
CC FT DOMAIN 166 190
CC FT TRANSMEM 191 >192
CC FT DISULFID 99 176
CC NON_TER 192 192
CC SEQUENCE 192 AA; 22178 MW; ABBCFE303C52BD98 CRC64;

Query Match 3.0%; Score 11; DB 1; Length 192;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 85 LFVLTLPFWAV 95
|||||
Db 76 LFVLTLPFWAV 86

RESULT 4
CCR4_BOVIN STANDARD; PRT; 353 AA.
AC P25930;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE C-X-C CHEMOKINE RECEPTOR TYPE 4 (CXCR-4) (CXCR-4) (SDF-1 RECEPTOR)
DE (STROMAL CELL-DERIVED FACTOR 1 RECEPTOR) (FUSIN) (LEUKOCYTE-DERIVED
DE SEVEN TRANSMEMBRANE DOMAIN RECEPTOR) (LESTR) (LCR1).
GN CXCR4.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Locus coeruleus;
RX MEDLINE=92100053; PubMed=1661837;
RA Rimland J., Xin W., Sweetnam P., Saijoh K., Nestler E.J., Duman R.S.;

RT "Sequence and expression of a neuropeptide Y receptor cDNA.";
RL Mol. Pharmacol. 40:869-875(1991).
RN [2]
RP SHOWS THAT IT IS NOT A NPY3-R.
RX MEDLINE=94052833; PubMed=8234909;
RA Jazin E.E., Yoo H., Blomqvist G., Yee F., Weng G., Walker M.W.,
RA Salon J., Larhammar D., Wahlestedt C.R.;
RT "A proposed bovine neuropeptide Y (NPY) receptor cDNA clone, or its
RT human homologue, confers neither NPY binding sites nor NPY
RT responsiveness on transfected cells.";
RL Regul. Pept. 47:247-258(1993).
CC -1- FUNCTION: RECEPTOR FOR THE C-X-C CHEMOKINE SDF-1. TRANSDUCES A
CC SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: BRAIN, HEART, KIDNEY, LUNG AND LIVER.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -1- CAUTION: WAS ORIGINALLY (REF.1) THOUGHT TO BE A RECEPTOR FOR
CC NEUROPEPTIDE Y, TYPE 3 (NPY3-R).
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; M86739; -; NOT_ANNOTATED_CDS.
CC PIR; S28787; S28787.
CC GCRDB; GCR_0180;
CC InterPro; IPR000276;
CC InterPro; IPR001277;
CC Pfam; PF00001; 7tm.1; 1.
CC PRINTS; PR00237; GPCRHDOPS.
CC PRINTS; PR00645; LCRIORPHAN.
CC PROSITE; PS00237; G_PROTEIN_RECEP_FL_1; 1.
CC PROSITE; PS50262; G_PROTEIN_RECEP_FL_2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein.
CC
CC FT DOMAIN 1 40
CC NON_TER 1 64
CC FT TRANSMEM 41 80
CC FT DOMAIN 65 80
CC FT TRANSMEM 81 100
CC FT DOMAIN 101 111
CC FT TRANSMEM 112 133
CC FT DOMAIN 134 155
CC FT TRANSMEM 156 176
CC FT DOMAIN 177 201
CC FT TRANSMEM 202 221
CC FT DOMAIN 222 241
CC FT TRANSMEM 242 262
CC FT DOMAIN 263 286
CC FT TRANSMEM 287 306
CC FT DOMAIN 307 353
CC FT CARBOHYD 11 11
CC FT DISULFID 110 187
CC BY SIMILARITY.
CC SEQUENCE 353 AA; 39938 MW; 42FFE5BC7545505E CRC64;

Query Match 3.0%; Score 11; DB 1; Length 353;
Best Local Similarity 100.0%; Pred. No. 0.0036;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 85 LFVLTLPFWAV 95
|||||
Db 87 LFVLTLPFWAV 97

RESULT 5
CCR4_FELCA STANDARD; PRT; 353 AA.
ID CCR4_FELCA
AC P56498; P79172; O02700;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)

Matches	11: Conservative	0: Mismatches	0: Indels	0: Gaps
Qy	85	LFVLTLFPWAV	95	
Db	87	LFVLTLFPWAV	97	
RESULT	6			
CKR4_HUMAN				
ID	CKR4_HUMAN	STANDARD;	PRT;	360 AA.
AC	P51679;			
DT	01-OCT-1996	(Rel. 34, Created)		
DT	01-OCT-1996	(Rel. 34, Last sequence update)		
DT	01-OCT-2000	(Rel. 40, Last annotation update)		
DE	C-C CHEMOKINE RECEPTOR TYPE 4 (C-C CKR-4) (CCR-4) (CCRA4)			
DE	(K5-5).			
DE	CKR4 OR CMKBR4.			
GN	Homo sapiens (Human).			
OS	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RI	[1]			
RN	SEQUENCE FROM N.A.			
RP	MEDLINE=95370289; PubMed=7642634;			
RX	Power C.A., Meyer A., Nemeth K., Bacon K.B., Hoogewerf A.J.,			
RA	Proudfoot A.E.I., Wells T.N.C.;			
RT	"Molecular cloning and functional expression of a novel CC chemokine			
RT	receptor cDNA from a human basophilic cell line.";			
RL	J. Biol. Chem. 270:19495-19500(1995).			
RL	[2]			
RN	FUNCTION.			
RP	MEDLINE=97313486; PubMed=9169480;			
RX	Imai T., Baba M., Nishimura M., Kakizaki M., Takagi S., Yoshie O.;			
RA	"The T cell-directed CC chemokine TARC is a highly specific			
RT	biological ligand for CC chemokine receptor 4.";			
RL	J. Biol. Chem. 272:15036-15042(1997).			
CC	-1- FUNCTION: RECEPTOR FOR C-C TYPE CHEMOKINE. BINDS TO TARC, MIP-1-			
CC	ALPHA, RANTES, AND MCP-1. SUBSEQUENTLY TRANSDUCES A SIGNAL BY			
CC	INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.			
CC	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.			
CC	-1- TISSUE SPECIFICITY: EXPRESSED STRONGLY IN PERIPHERAL BLOOD T CELLS			
CC	BUT NOT IN B CELLS, NATURAL KILLER CELLS, MONOCYTES, OR			
CC	GRANULOCYTES.			
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.			
CC	-----			
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CC	send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; X85740; CAA59743.1; -			
DR	MIM; 604836; -			
DR	GCRRdb; GCR_2115; -			
DR	InterPro; IPR000276; -			
DR	InterPro; IPR000355; -			
DR	InterPro; IPR002239; -			
DR	Pfam; PF00001; 7tm_1; 1.			
DR	PRINTS; PR00237; GPCRHHODOPS.			
DR	PRINTS; PR00657; CCHEMOKINER.			
DR	PRINTS; PR01109; CHEMOKINER4.			
DR	PROSITE; PS00237; G_PROTEIN_RECEP_FL1; 1.			
DR	PROSITE; PS50262; G_PROTEIN_RECEP_FL2; 1.			
KW	G-protein coupled receptor; Transmembrane; Glycoprotein.			
FT	DOMAIN 1 39			
FT	TRANSMEM 40 67			
FT	DOMAIN 68 77			
FT	TRANSMEM 78 98			
FT	DOMAIN 99 111			
FT	TRANSMEM 112 133			
FT	DOMAIN 134 150			
FT	CYTOPLASMIC (POTENTIAL).			
FT	1 (POTENTIAL).			
FT	CYTOPLASMIC (POTENTIAL).			
FT	2 (POTENTIAL).			
FT	EXTRACELLULAR (POTENTIAL).			
FT	3 (POTENTIAL).			
FT	CYTOPLASMIC (POTENTIAL).			

FT	TRANSMEM	151	175	4 (POTENTIAL).
FT	DOMAIN	176	206	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	207	226	5 (POTENTIAL).
FT	DOMAIN	227	242	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	243	267	6 (POTENTIAL).
FT	DOMAIN	268	284	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	285	308	7 (POTENTIAL).
FT	DOMAIN	309	360	CYTOPLASMIC (POTENTIAL).
FT	CARBOHYD	183	183	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	194	194	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	DISULFID	110	187	BY SIMILARITY.
SO	SEQUENCE	360 AA;	41402 MW;	51EBE12AD1FAFABF CRC64;

Query Match

Best Local Similarity 2.7%; Score 10; DB 1; Length 360;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	69	RSMTDYYLLN 78
Db	71	RSMTDYYLLN 80

Search completed: May 23, 2001, 15:38:14
Job time: 110 sec

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OM protein - protein search, using sw model

Run on: May 23, 2001, 15:35:24 ; Search time 35.78 Seconds
(without alignments)
1195.665 Million cell updates/sec

Title: US-08-887-977-10
Perfect score: 365
Sequence: 1 MFSPVKIILQCSILHITQL.....NISROTSETADNDNASFTM 365

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 374700 seqs, 117207915 residues

Word size : 10

Total number of hits satisfying chosen parameters: 10

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : SPTREMBL_15.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phase.*
10: sp_plant.*
11: sp_rodent.*
12: sp_unclassified.*
13: sp_vertebrate.*
14: sp_virus.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	22	6.0	367	11 Q9R1V0	Q9R1V0 mus musculus
2	11	3.0	353	13 Q93247	Q93247 cyprinus ca
3	11	3.0	353	13 Q9PTF7	Q9PTF7 brachydanio
4	11	3.0	357	13 Q42445	Q42445 oncorhynch
5	10	2.7	360	4 Q9ULY7	Q9ULY7 homo sapien
6	10	2.7	360	4 Q9ULY6	Q9ULY6 homo sapien
7	10	2.7	383	14 Q89609	Q89609 equine herp
8	10	2.7	394	5 Q9NJS6	Q9NJS6 aplysia kur
9	10	2.7	394	5 Q9NHF3	Q9NHF3 aplysia cal
10	10	2.7	469	4 Q9NSD7	Q9NSD7 homo sapien

ALIGNMENTS

RESULT 1
Q9R1V0 PRELIMINARY; PRT; 367 AA.
AC Q9R1V0;

DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE CC CHEMOKINE LARC SPECIFIC RECEPTOR.
GN MCCR6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Tanaka Y.;
RT "Molecular Cloning of Murine Homologue of CCR6, the Specific Receptor
for CC Chemokine LARC";
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB016031; BAA82443.1; -
DR INTERPRO: IPR000190; -
DR INTERPRO: IPR000276; -
DR INTERPRO: IPR000355; -
DR PFAM: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCRHHODOPSN.
DR PRINTS: PR00635; ANGIOTENSINR.
DR PRINTS: PR00657; CCHEMOKINER.
DR PROSITE: PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
KW Receptor.
SQ SEQUENCE 367 AA; 42082 MW; 207FD98B2F7A6DD3 CRC64;

Query Match 6.0%; Score 22; DB 11; Length 367;
Best Local Similarity 100.0%; Pred. No. 5.5e-14;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 248 IAVLVFLACQIPHNNVLLVTA 269
Db 249 IAVLVFLACQIPHNNVLLVTA 270
|||||

RESULT 2
ID Q93247 PRELIMINARY; PRT; 353 AA.
AC Q93247;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE CXCR4.
OS Cyprinus carpio (Common carp).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Cyprininae; Cyprinus.
OX NCBI_TaxID=7962;
RN [1]
RP SEQUENCE FROM N.A.
RA Fujiki K., Nakao M., Shin D., Yano T.;
RT "cDNA cloning of a carp homologue of mammalian CXCR4";
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL: AB012310; BAA32797.1; -
DR INTERPRO: IPR000276; -
DR PFAM: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCRHHODOPSN.
DR PROSITE: PS00237; G_PROTEIN_RECEPTOR; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
SQ SEQUENCE 353 AA; 39633 MW; 84924BE413FB3B3F CRC64;

Query Match 3.0%; Score 11; DB 13; Length 353;
Best Local Similarity 100.0%; Pred. No. 0.0094;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 85 LFVLTLPFWAV 95
Db 84 LFVLTLPFWAV 94
|||||

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Query Match 3.0%; Score 11; DB 13; Length 357;
Best Local Similarity 100.0%; Pred. No. 0.0095;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 3
Q9PTF7 PRELIMINARY; PRT; 353 AA.
ID AC Q9PTF7
AC Q9PTF7
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE CHEMOKINE RECEPTOR CXCR4.
GN CXCR4.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Rasbora; Danio;
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Tseng S., Rollins B.J.;
RT "Chemokines and chemokine receptors in zebrafish.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF201451; AAF17561.1; -
DR INTERPRO; IPR000276; -
DR INTERPRO; IPR000355; -
DR INTERPRO; IPR001277; -
DR PFAM; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PRINTS; PR00645; LCR1ORPHANR.
DR PRINTS; PR00657; CCHEMOKINER.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; 1.
RW RECEPTOR.
SQ SEQUENCE 353 AA; 39444 MW; 410F9A7F75D631BE CRC64;

Query Match 3.0%; Score 11; DB 13; Length 353;
Best Local Similarity 100.0%; Pred. No. 0.0094;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 85 LFVLTLPFWAV 95
DB 84 LFVLTLPFWAV 94
|||||
|||||

RESULT 4
ID 042445 PRELIMINARY; PRT; 357 AA.
AC 042445
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE CXC CHEMOKINE RECEPTOR.
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE FROM N.A.
RA Daniels G.D., Charlemagne J., Secombes C.J.;
RT "Cloning and sequencing of a rainbow trout, Oncorhynchus mykiss,
RT chemokine receptor homolog.";
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; AJ001039; CAA04493.1; -
DR INTERPRO; IPR000276; -
DR PFAM; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; 1.
RW G-protein coupled receptor; transmembrane; Glycoprotein.
SQ SEQUENCE 357 AA; 39817 MW; 14EC2F01DA1222C4 CRC64;

Query Match 3.0%; Score 11; DB 13; Length 357;
Best Local Similarity 100.0%; Pred. No. 0.0095;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 85 LFVLTLPFWAV 95
DB 88 LFVLTLPFWAV 98
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|||||

RESULT 5
Q9ULY7 PRELIMINARY; PRT; 360 AA.
ID AC Q9ULY7
AC Q9ULY7
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE B-CHEMOKINE RECEPTOR CCR4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kato H., Tsuchiya N., Izumi S., Miyamasu M., Nakajima T., Kawasaki H.,
RA Hirai K., Tokunaga K.;
RT "New variations of human CC-chemokine receptors CCR3 and CCR4.";
RL Genes Immun. 1:97-104(1999).
DR EMBL; AB023889; BAA86966.1; -
DR INTERPRO; IPR000190; -
DR INTERPRO; IPR000248; -
DR INTERPRO; IPR000276; -
DR INTERPRO; IPR000355; -
DR INTERPRO; IPR001277; -
DR INTERPRO; IPR002236; -
DR INTERPRO; IPR002239; -
DR PFAM; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PRINTS; PR00241; ANGIOTENSINR.
DR PRINTS; PR00635; ANGIOTENSINR.
DR PRINTS; PR00645; LCR1ORPHANR.
DR PRINTS; PR00657; CCHEMOKINER.
DR PRINTS; PR01106; CHEMOKINER1.
DR PRINTS; PR01109; CHEMOKINER4.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
RW RECEPTOR.
FT VARIANT 130 130 V -> L.
SQ SEQUENCE 360 AA; 41388 MW; F52DA1A8D9DA7DDB CRC64;

Query Match 2.7%; Score 10; DB 4; Length 360;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 69 RSMSTDVYLLN 78
DB 71 RSMSTDVYLLN 80
|||||
|||||

RESULT 6
Q9ULY6 PRELIMINARY; PRT; 360 AA.
ID AC Q9ULY6
AC Q9ULY6
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE B-CHEMOKINE RECEPTOR CCR4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kato H., Tsuchiya N., Izumi S., Miyamasu M., Nakajima T., Kawasaki H.,

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RA Hirai K., Tokunaga K.;
RT "New variations of human CC-chemokine receptors CCR3 and CCR4.";
RL Genes Immun. 1:97-104(1999).
DR EMBL: AB023891; BAA86968.1; -
DR INTERPRO: IPR000190; -
DR INTERPRO: IPR000248; -
DR INTERPRO: IPR000276; -
DR INTERPRO: IPR000355; -
DR INTERPRO: IPR001277; -
DR INTERPRO: IPR002236; -
DR INTERPRO: IPR002239; -
DR PFAM: PF00001; 7tm.1; 1.
DR PRINTS: PR00237; GPCRHDOPSN.
DR PRINTS: PR00241; ANGIOTENSINR.
DR PRINTS: PR00635; ANGIOTENSINR.
DR PRINTS: PR00645; LCRIORPHANR.
DR PRINTS: PR00657; CCHEMOKINER.
DR PRINTS: PR01106; CHEMOKINER1.
DR PRINTS: PR01109; CHEMOKINER4.
DR PROSITE: PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
KW Receptor.
FT VARIANT 178 178 S -> C.
SQ SEQUENCE 360 AA; 41386 MW; AAF0EA3AD1EAF6D2 CRC64;

Query Match 2.7%; Score 10; DB 4; Length 360;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 69 RSMTDVYLLN 78
Db 71 RSMTDVYLLN 80
|||||
|||||

RESULT 7
Q89609 PRELIMINARY; PRT; 383 AA.
AC Q89609;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-JUN-2000 (TReMBLrel. 14, Last annotation update)
DE G PROTEIN-COUPLED RECEPTOR.
OS Equine herpesvirus 2.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Betaherpesvirinae; Roseolovirus.
OX NCBI_TaxID=12657;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=86/67;
RX MEDLINE=95302501; PubMed=7783207;
RA Telford E.A., Watson M.S., Aird H.C., Perry J., Davison A.J.;
RT "The DNA sequence of equine herpesvirus 2.";
RL J. Mol. Biol. 249:520-528(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=86/67;
RA Telford E.A.R.;
RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL: U20824; AAC13866.1; -
DR EMBL: U20824; AAC13788.1; -
DR INTERPRO: IPR000276; -
DR PFAM: PF00001; 7tm.1; 1.
DR PRINTS: PR00237; GPCRHDOPSN.
SQ SEQUENCE 383 AA; 43667 MW; 0C65C53EAF539F72 CRC64;

Query Match 2.7%; Score 10; DB 14; Length 383;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 GLLGNILWVI 60
Db 86 GLLGNILWVI 95
|||||
|||||

RESULT 8
Q9NJS6 PRELIMINARY; PRT; 394 AA.
ID Q9NJS6
AC Q9NJS6;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
DE OCTOPAMINE RECEPTOR.
OS Aplysia kurodai (Kuroda's sea hare).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Opisthobranchia; Anaspidea;
OC Aplysiidae; Aplysia.
OX NCBI_TaxID=6501;
RN [1]
RP SEQUENCE FROM N.A.
RA Chang D.J., Li X.C., Kim H.K., Kim U.S., Cho N.J., Lo X., Weiss K.R.,
RA Kandel E.R., Kaang B.K.;
RT "Activation of a heterologously expressed octopamine receptor coupled
RT only to adenylyl cyclase produces all the features of presynaptic
RT facilitation in Aplysia sensory neurons.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:1829-1834(2000).
DR EMBL: AF117654; AAF28802.1; -
KW Receptor.
SQ SEQUENCE 394 AA; 44423 MW; 8C7FE47EC686B0F4 CRC64;

Query Match 2.7%; Score 10; DB 5; Length 394;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 129 CISMDRYIAI 138
Db 131 CISMDRYIAI 140
|||||
|||||

RESULT 9
Q9NHF3 PRELIMINARY; PRT; 394 AA.
ID Q9NHF3
AC Q9NHF3;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
DE OCTOPAMINE RECEPTOR.
GN APOA.
OS Aplysia californica (California sea hare).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Opisthobranchia; Anaspidea;
OC Aplysiidae; Aplysia.
OX NCBI_TaxID=6500;
RN [1]
RP SEQUENCE FROM N.A.
RA Chang D.J., Li X.C., Kim H.K., Kim U.S., Cho N.J., Lo X., Weiss K.R.,
RA Kandel E.R., Kaang B.K.;
RT "Activation of a heterologously expressed octopamine receptor coupled
RT only to adenylyl cyclase produces all the features of presynaptic
RT facilitation in Aplysia sensory neurons.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:1829-1834(2000).
DR EMBL: AF222978; AAF37686.1; -
KW Receptor.
SQ SEQUENCE 394 AA; 44334 MW; 1204086FEB6CD599 CRC64;

Query Match 2.7%; Score 10; DB 5; Length 394;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 129 CISMDRYIAI 138
Db 131 CISMDRYIAI 140
|||||
|||||

RESULT 10
Q9NSD7

```

ID Q9NSD7 PRELIMINARY; PRT; 469 AA.
AC Q9NSD7;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)
DE G-PROTEIN COUPLED RECEPTOR SALPR.
GN SALPR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Matsumoto M., Kamohara M., Sugimoto T., Hidaka K., Takasaki J.,
RA Saito T., Okada M., Yamaguchi T., Furuichi K.;
RT "The novel G-protein coupled receptor SALPR shares sequence similarity
RT with somatostatin and angiotensin receptors."
RL Gene 248:183-189(2000).
DR EMBL; D88437; BAA93001.1; -.
KW Receptor; G-protein coupled receptor.
SQ SEQUENCE 469 AA; 51123 MW; 932E7B3001689F7B CRC64;

Query Match      2.7%; Score 10; DB 4; Length 469;
Best Local Similarity 100.0%; Pred.No. 0.13;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 86 FVLTLFWAV 95
Db 131 FVLTLFWAV 140
|||||

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Search completed: May 23, 2001, 15:37:59
Job time: 155 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 23, 2001, 15:21:43 ; Search time 184.73 Seconds

(without alignments)
112.946 Million cell updates/sec

Title: US-08-887-977-10

Perfect score: 1894

Sequence: 1 MFSTPVKILLCOSILHITQL.....NISROTSETADNDNASSFTM 365

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 390729 seqs, 57163235 residues

Total number of hits satisfying chosen parameters: 390729

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A.Geneseq_0401:*

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- 22: /SID56/gcgdata/geneseq/geneseqp/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1894	100.0	365	19	W48086 Human dendritic ce
2	1888	99.7	365	21	Y97077 Primate (human) ch
3	683	36.1	378	21	Y90629 Human G protein-co
4	682	36.0	378	19	W48724 Human V31 seven tr
5	682	36.0	378	21	B21688 Human 7TM recepto
6	682	36.0	378	21	B21699 Human 7TM recepto
7	682	36.0	378	22	B50859 Human CCR7. Homo
8	680	35.9	378	15	R53744 Putative seven tra
9	678.5	35.8	410	15	R53744 Putative seven tra
10	678.5	35.8	410	19	W48723 Polypeptide sequen
11	678.5	35.8	410	21	B21687 Genomic clone of 7

12	677	35.7	358	15	R53745
13	677	35.7	358	21	B21689
14	675	35.6	378	21	Y90663
15	668.5	35.3	359	15	R53747
16	668.5	35.3	359	19	W48728
17	668.5	35.3	359	21	B21691
18	663	35.0	378	15	R54079
19	663	35.0	378	19	W56164
20	663	35.0	378	19	W53622
21	662	35.0	350	13	R27791
22	662	35.0	350	16	R68811
23	662	35.0	350	16	R80756
24	662	35.0	350	16	R80951
25	662	35.0	350	17	B09989
26	662	35.0	1060	16	R70123
27	654	34.5	355	13	R28272
28	654	34.5	355	16	R80950
29	643.5	34.0	361	20	W97348
30	636.5	33.6	358	16	R80952
31	629.5	33.2	355	14	R33420
32	629.5	33.2	355	17	B09980
33	629.5	33.2	360	13	R28273
34	629.5	33.2	360	16	R80758
35	629.5	33.2	1064	16	R70124
36	623.5	32.9	351	20	Y23825
37	615.5	32.5	360	16	R80953
38	610.5	32.2	360	21	B07498
39	607.5	32.1	360	17	R99274
40	605.5	32.0	358	13	R28274
41	600.5	31.7	312	15	R48717
42	600.5	31.6	312	17	W02689
43	598.5	31.4	342	20	W97784
44	594.5	31.4	342	20	W97785
45	593.5	31.3	357	21	B19605

ALIGNMENTS

RESULT 1	
W48086	W48086 standard; Protein: 365 AA.
XX	
AC	W48086;
XX	
DT	11-JUN-1998 (first entry)
XX	
DE	Human dendritic cell chemokine receptor.
XX	
KW	Human: thymus expressed chemokine; TECK; MIP-3alpha; MIP-3beta;
KW	receptor; dendritic cell; macrophage; inflammation; asthma.
XX	
OS	Homo sapiens.
XX	
FH	Key
FT	Misc-difference 193
FT	/note= "encoded by CAN"
XX	
PN	W09801557-A2.
XX	
PD	15-JAN-1998.
XX	
PF	02-JUL-1997; 97WO-0510819.
XX	
PR	04-JUN-1997; 97US-0048593.
PR	05-JUL-1996; 96US-0675814.
PR	11-OCT-1996; 96US-0028329.
XX	
PA	(SCHE) SCHERING CORP.
XX	
PI	Gish KC, Schall TJ, Vicari A, Wang W, Zlotnik A;
XX	
DR	WPI; 1998-101054/09.

Partial sequence o
Human 7TM recepto
Human mutant G pro
Seven transmembran
Murine V31 seven t
Epstein Barr virus
G-protein coupled
Epstein Barr virus
Interleukin-8 rece
Interleukin-8 rece
Interleukin 8 rece
Recombinant high a
Human IL-8 recepto
IL8-R type 1-GBP 1
Sequence in a high
Recombinant high a
An Epstein-Barr vi
Recombinant high a
Human IL-8 recepto
Human IL-8 recepto
Sequence in a low
Interleukin 8 rece
IL8-R type 2-GBP 1
A7 times membrane
Recombinant high a
A human CCR4 chemo
Chemokine receptor
Sequence in a low
G-protein coupled
G-protein coupled
African green monk
pig-tailed macaque
Human CC chemokine

DR N-PSDB; V15418.
XX
XX Novel chemokines, e.g. thymus expressed chemokine - used for
PT treating inflammatory conditions including asthma.
XX
XX
PS Claim 3; Page 94-95; 202pp; English.
XX
XX The present sequence represents human dendritic cell chemokine receptor.
CC Antibodies which bind to the protein can be used in detecting or
CC diagnosing various immunological conditions related to expression
CC of the protein. The nucleic acid can be used for screening and
CC isolating DNA clones for the chemokines, especially from other
CC species. The chemokine can be used in the treatment of conditions
CC associated with abnormal physiology or development, including
CC inflammatory conditions such as asthma.
XX
XX Sequence 365 AA;
SQ

Query Match 100.0%; Score 1894; DB 19; Length 365;
Best Local Similarity 100.0%; Pred. No. 1.2e-209;
Matches 365; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MESTPVKIIICOSILHITQILRLRCYCAPCRSSGSPGYIRIAYSLICVGLGNILVI 60
DB 1 mstpvkiiicqslhltqilrlrcycapcrssgspgyiriyasli cvlgllgnllvli 60
QY 61 TFAFKKARSMTDVYLLNMAIADILFVLTLPFAVSHATGAWFNSATCKLKGIYAINF 120
DB 61 tfaifykkarsmtdvyl lmaiaadilfvltlpf wavshatgawfnsatckllkgyiainf 120
QY 121 NCGMLLTCISMDRYAIVQATKSFRLSRKTLPRSKIIICLVWGLSVIISSTFVFNOKY 180
DB 121 ncgmlltcismdryaivqatksf rlsrtp rskiiiclvwglsviisstfvfnoky 180
QY 181 NTQGSDVCEPKYQVSEPIRKMLMLGELLFGEFIPLMFMFCFTFYKTVLQVQNSKR 240
DB 181 ntqgsdvcepk yqvsepirkmlmlgellfg efiplmfmfcftfyk tvlvqvnskr 240
QY 241 HKAIRVIIVAVLVFLACQIPHNMLVLTAAANLGKMNRSQSEKILGYTKVTEVLAFLHC 300
DB 241 hkaivriiavvlvflacq iphnmvlvlt aaanlgkmnrsqseki lgytkvtevlaflhc 300
QY 301 CLNPVLYAFIGKERNYFLKILKDLKMCVRRKYSKSGFCAGRYSENISROTSETADNDNA 360
DB 301 clnpvlyafigkfn yflkilkdlkwc vrrkyssgfcagrysenisrqtsetadndna 360
QY 361 SSFTM 365
DB 361 ssftm 365

RESULT 2
Y97077
ID Y97077 standard; Protein; 365 AA.
XX
XX Y97077;
AC
XX 04-DEC-2000 (first entry)
DT
XX
XX Primate (human) chemokine receptor CCR6.
DE
XX
XX MIP-3-alpha; chemokine; CCR6 receptor; ligand; cytostatic; agonist;
KW antagonist; anti-psoriatic; dermatological; immunosuppressive;
XX anti-inflammatory.
XX
XX Homo sapiens.
XX
XX
XX Key location/Qualifiers
FH Misc-difference 193 /note= "Encoded by CAN#"
FT
XX
XX WO200046248-A1.
PN

XX
XX 10-AUG-2000.
PD
XX
XX 02-FEB-2000; 2000WO-US00511.
PF
XX
XX 03-FEB-1999; 99US-0244281.
PR
XX
XX (SCHE) SCHERING CORP.
PA
XX
XX Oldham ER, Honey B, Dleu-Nosjean M, Caux C, Zlotnik A;
DR WPI. 2000-543477/49.
XX N-PSDB; A51971.
XX
XX Novel methods for modulating the migration of cells within or to the
PT skin using MIP-3-alpha or CCR6 agonists or antagonists, useful for
PT treating skin disorders, e.g. cancer
XX
XX
PS Disclosure; Page 53-54; 61pp; English.
XX
XX The MIP-3-alpha chemokine is expressed in inflamed skin cells. This
CC chemokine is the ligand for the CCR6 receptor. MIP-3-alpha or CCR6
CC agonists or antagonists can be used to modulate the migration of a cell
CC within or to the skin of a mammal. MIP-3-alpha can be used to purify a
CC population of cells expressing a MIP-3-alpha receptor. The methods are
CC useful for treating a mammalian subject with a skin disease or condition,
CC e.g. cancer, metastasis, psoriasis, atopic or contact dermatitis,
CC systemic lupus erythematosus and lichen ruber planus, or for treating
CC skin transplants or grafts.
XX
XX Sequence 365 AA;
SQ

Query Match 99.7%; Score 1888; DB 21; Length 365;
Best Local Similarity 99.7%; Pred. No. 5.8e-209;
Matches 364; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MESTPVKIIICOSILHITQILRLRCYCAPCRSSGSPGYIRIAYSLICVGLGNILVI 60
DB 1 mstpvkiiicqslhltqilrlrcycapcrssgspgyiriyasli cvlgllgnllvli 60
QY 61 TFAFKKARSMTDVYLLNMAIADILFVLTLPFAVSHATGAWFNSATCKLKGIYAINF 120
DB 61 tfaifykkarsmtdvyl lmaiaadilfvltlpf wavshatgawfnsatckllkgyiainf 120
QY 121 NCGMLLTCISMDRYAIVQATKSFRLSRKTLPRSKIIICLVWGLSVIISSTFVFNOKY 180
DB 121 ncgmlltcismdryaivqatksf rlsrtp rskiiiclvwglsviisstfvfnoky 180
QY 181 NTQGSDVCEPKYQVSEPIRKMLMLGELLFGEFIPLMFMFCFTFYKTVLQVQNSKR 240
DB 181 ntqgsdvcepk yqvsepirkmlmlgellfg efiplmfmfcftfyk tvlvqvnskr 240
QY 241 HKAIRVIIVAVLVFLACQIPHNMLVLTAAANLGKMNRSQSEKILGYTKVTEVLAFLHC 300
DB 241 hkaivriiavvlvflacq iphnmvlvlt aaanlgkmnrsqseki lgytkvtevlaflhc 300
QY 301 CLNPVLYAFIGKERNYFLKILKDLKMCVRRKYSKSGFCAGRYSENISROTSETADNDNA 360
DB 301 clnpvlyafigkfn yflkilkdlkwc vrrkyssgfcagrysenisrqtsetadndna 360
QY 361 SSFTM 365
DB 361 ssftm 365

RESULT 3
Y90629
ID Y90629 standard; Protein; 378 AA.
XX
XX Y90629;
AC
XX
XX 21-AUG-2000 (first entry)
DT

XX Human G protein-coupled receptor EB11.
 DE G protein-coupled receptor; GPCR; constitutively active;
 XX intracellular loop 3; transmembrane domain 6; drug screening;
 KW agonist; antagonist.
 KW
 XX Homo sapiens.
 OS
 XX W0200022129-A1.
 PN
 XX 20-APR-2000.
 PD
 XX 12-OCT-1999; 99WO-0523938.
 PF
 XX 13-OCT-1998; 98US-0170496.
 PR
 XX (AREN-) ARENA PHARM INC.
 PA
 XX Behan DP, Chalmers DT, Liaw CW;
 PI
 XX WPI: 2000-329165/28.
 DR
 XX N-PSDB; A30632.
 DR
 XX Non-endogenous constitutively activated human G protein-coupled
 PT receptors, useful for identifying agonists for use as pharmaceutical
 PT agents.
 PT
 XX Example 1; Page 158-159; 341pp; English.
 PS
 XX The invention relates to constitutively active, non-endogenous versions
 CC of endogenous human orphan G protein-coupled receptors (GPCRs, Y90643-
 CC Y90677 and Y90683-Y90687), and to DNA encoding them (A30709-A30743 and
 CC A30775-A30779). The mutant proteins of the invention contain a
 CC mutation in a portion of the protein comprising intracellular loop 3
 CC (IC3) and transmembrane domain 6 (TM6). A non-endogenous amino acid, X,
 CC is substituted for an endogenous residue in IC3 at a position 16 amino
 CC acids N-terminal of an endogenous proline in TM6 to form a sequence
 CC X-(AA)15-Pro. The endogenous amino acid is selected from Lys, His, Arg or
 CC Ala, and is preferably Lys. When the endogenous residue at this position
 CC is Lys, this residue is replaced by His, Arg or preferably Ala. The 15
 CC amino acid stretch between the substituted amino acid and the Pro may be
 CC endogenous, non-endogenous, or a mixture of endogenous and non-endogenous
 CC residues. The constitutively active GPCRs are useful for identifying
 CC antagonists, agonists and partial agonists for use as pharmaceutical
 CC agents. The mutant proteins are also useful in research settings for
 CC elucidating the roles of the receptors in normal and diseased conditions.
 CC Antagonists for a particular GPCR are useful for treating diseases and
 CC disorders associated with that receptor. Because the novel mutant GPCRs
 CC are constitutively active, they can be used directly for screening of
 CC compounds without the need for endogenous ligands. The present
 CC sequence represents a human wild-type GPCR referred to in an
 CC exemplification of the invention.
 XX
 SQ Sequence 378 AA;

Query Match 36.1%; Score 683; DB 21; Length 378;
 Best Local Similarity 39.4%; Pred. No. 4.3e-70;
 Matches 149; Conservative 78; Mismatches 115; Indels 36; Gaps 8;
 QY 5 PVKIIICQSTLITLITLCYCVP-----CRSG--SSPGYLYR 41
 Db 6 pmksvlvavllvfvq---clcxdevtdddygdnttdvtylfeslcskdkvnrnfkwlfp 62
 QY 42 IAYSLLICVLGLGNILVITFAFYKARSMRTDYLNNMAIADILFVLTPFWAVSHATCA 101
 Db 63 imysliicfcvllnglvlyfyfkrktmdtyllnlavadihlfltlptways-aaks 121
 QY 102 WFPSNATCKLLKGIYAFNCGMMLLLCISMDRYIAIVQATKSFRLSRTLPKSKICLV 161
 Db 122 wvfqvhcklilaflykmsffgsmllilicisidryavaiqvagsahrhrarvilliskscvg 181

QY 162 VWGLSVIISSTFVN--QKYNTOGSDVCEPKYQTVSEPIRWKLLMLGLLELLFGFFIPLM 219
 Db 182 iwilatvlsipellysdlgrssseqamrc-----slitehveafitigvqgmvgflvpll 237
 QY 220 FMIEFCYTFIVKTLVQAGNSKRHKAIRVIIAVLVFLACQIPHN-MVLLVTAANLGMNRS 278
 Db 238 amscfylviirtllqarnfcrnkaikvllavvvvflvqfpyngvvlaqtvanfnitsst 297
 QY 279 CQSEKLIQYTKVTVEFLAFLLHCCINPVLVYAFIGOKFRNYFLKILDLWCVRKYKSSGFS 338
 Db 298 celskqlniaydvtyslacrvccvpflyafigvfkfndlflkfdkgclsgseqlrwws 357
 QY 339 C--AGRYSENISROTSET 354
 Db 358 crhrrssmsveaetttt 375
 RESULT 4
 W48724
 ID W48724 standard; Protein: 378 AA.
 XX
 AC W48724;
 XX
 DT 25-SEP-1998 (first entry)
 XX
 DE Human V31 seven transmembrane receptor.
 XX
 KW V28; placenta; seven transmembrane receptor; 7TM; signal transduction;
 KW immunology; inflammation; V31.
 XX
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Domain 58..86 "Transmembrane domain 1"
 FT Domain 96..119 /note="Transmembrane domain 2"
 FT Domain 131..152 /note="Transmembrane domain 3"
 FT Domain 171..196 /note="Transmembrane domain 4"
 FT Domain 219..247 /note="Transmembrane domain 5"
 FT Domain 264..285 /note="Transmembrane domain 6"
 FT Domain 306..331 /note="Transmembrane domain 7"
 FT
 XX US5759804-A.
 PN
 XX 02-JUN-1998.
 PD
 XX 17-NOV-1993; 93US-0153848.
 PF
 XX 17-NOV-1992; 92US-0977452.
 PR
 XX (ICOS-) ICOS CORP.
 PA
 XX Godiska R, Gray PW, Schweickart VL;
 PI
 XX WPI: 1998-332132/29.
 DR
 XX N-PSDB; V18347.
 DR
 XX DNA encoding V28 seven transmembrane receptor polypeptide - useful
 PT for producing recombinant polypeptide and anti-V28 antibodies, and
 PT in screening assays for V28 agonists and antagonists
 XX
 PS Example 3; Columns 39-42; 56pp; English.
 XX
 CC The present sequence represents the V31 seven transmembrane (7TM)
 CC receptor encoded by the V31 cDNA (V18347). The invention claims for
 CC a full length V28 genomic DNA (V18343) and the V28 protein it
 CC encodes (W48722). V28 and V31 proteins are 7TM receptors which


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Db 358 crhrssmsveaetttt 375
RESULT 8
ID R53744 standard; Protein; 378 AA.
XX AC R53744;
XX DT 02-FEB-1995 (first entry)
XX DE Putative seven transmembrane receptor (V31).
XX KW Primer; seven transmembrane receptor; receptor; amplification; PCR;
XX KW polymerase chain reaction.
XX OS Homo sapiens.
XX PN WO9412635-A.
XX PD 09-JUN-1994.
XX PF 17-NOV-1993; 93WO-US11153.
XX PR 17-NOV-1992; 92US-0977452.
XX PA (ICOS-) ICOS CORP.
XX PI Godiska R, Gray PW, Schweickart VL;
XX DR WPI; 1994-200264/24.
XX DR N-PSDB; Q66160.
XX PT DNA encoding seven transmembrane receptors - used to develop
XX PT prods. for use as therapeutic or diagnostic agents for conditions
XX PT involving the receptors.
XX PS Claim 1; Page 52-53; 100pp; English.
XX CC A human cDNA encoding the seven transmembrane receptor V31 was
XX CC isolated by first amplifying a partial cDNA clone from a human
XX CC tonsil cDNA library using two primers (Q66154, Q66155). The resulting
XX CC amplified products were probed using two radioactively labelled
XX CC sequences (Q66156, Q66157). A hybridising band was isolated from the
XX CC gel and cloned. The resulting clone was named pV31-5'end (Q66158). A
XX CC full length cDNA clone was isolated from a peripheral blood
XX CC mononuclear cell library using V31 specific primers (Q66159, Q66152).
XX CC Clone PBMC75 was isolated and the V31 cDNA insert in the clone was
XX CC designated cDNA V31-B (Q66160).
XX SQ Sequence 378 AA;

Query Match 35.9%; Score 680; DB 15; Length 378;
Best Local Similarity 39.4%; Pred. No. 9.5e-70;
Matches 149; Conservative 79; Mismatches 114; Indels 36; Gaps 8;

QY 5 PVKILCSILHITQILRCYC-----APCRSG--SSPGYLYR 41
DB 6 pmksvlvavllvifqv---clcqdevtdddyignttdvtytlfscskkdvrfkawflp 62
QY 42 IAYSILICVLGLGNLIVTFAYFKKARSMTDVYLLNMAIADILFVLTLPFWAVSHATGA 101
DB 63 imyslicfvllnglvivtyfyfkrkcmtdtylinlavadiifltpfways-aaks 121
QY 102 WVFNSNATCKLKGIAINFCNMGMLITCISMDRYTAIVQATKSFRLSRRTLPRSKITCLV 161
DB 122 wvfghfcklifaiykmsffgmllilcisdryvaivqavsaahrarvlliskscvg 181
QY 162 VWGLSVIISSSTFVN--QKYNTQSDVCEPKYQTVSEPIRWKLLMLGLELLEGFTIPLM 219
DB 182 iwilatvisipellysdlqrssseqamrc-----slitehveafitlqvagmvigfivp11 237

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QY 220 FMIFCYTTFIVKTLVQAOQNSKRHKAIIRVIAVVLVFLACQIPHNMYLL-VTAANLGKMNRS 278
DB 238 amscylviirtilqarnfernkalkvliavvvfivqlpyngvvlqgtvanfnitst 297
QY 279 COSEKLIgyTKTVEVLAFLHCLNPNVLYAFETGOKERNVFLKILKDLWCVRKYSKSGFS 338
DB 298 celskqinlaydvtyslacvrcvnpfilyafgkvfrndlfkfdgiclsqeqrlqwss 357
QY 339 C--AGRYSENISET 354
DB 358 crhrssmsveaetttt 375

RESULT 9
R53743
ID R53743 standard; Protein; 410 AA.
XX AC R53743;
XX DT 02-FEB-1995 (first entry)
XX DE Putative seven transmembrane receptor (V31).
XX KW Primer; seven transmembrane receptor; receptor; amplification; PCR;
XX KW polymerase chain reaction.
XX OS Homo sapiens.
XX PN WO9412635-A.
XX PD 09-JUN-1994.
XX PF 17-NOV-1993; 93WO-US11153.
XX PR 17-NOV-1992; 92US-0977452.
XX PA (ICOS-) ICOS CORP.
XX PI Godiska R, Gray PW, Schweickart VL;
XX DR WPI; 1994-200264/24.
XX DR N-PSDB; Q66153.
XX PT DNA encoding seven transmembrane receptors - used to develop
XX PT prods. for use as therapeutic or diagnostic agents for conditions
XX PT involving the receptors.
XX PS Example 2; Page 46-48; 100pp; English.
XX CC Two primers (Q66148, Q66149) were used to amplify human genomic DNA
XX CC purified from leukocytes. Approximately 1000 clones were isolated
XX CC after the initial amplification reaction and probed with sequences
XX CC specific for seven transmembrane receptors IL8RI, AT2K and R20.
XX CC Clones which did not hybridise were then chosen for sequence
XX CC analysis. Three new clones were identified that appeared to encode
XX CC seven transmembrane receptor segments. Two more primers (Q66151,
XX CC Q66152) were used to isolate a full length version of one of these
XX CC clones, one of which was designated V31 and encoded this
XX CC polypeptide.
XX SQ Sequence 410 AA;

Query Match 35.8%; Score 678.5; DB 15; Length 410;
Best Local Similarity 40.7%; Pred. No. 1.6e-69;
Matches 149; Conservative 78; Mismatches 120; Indels 19; Gaps 8;

QY 2 FSTPVKILCS-----LLHITOLILRCYCACPGRSG--SSPGYLYRIAYSLICVLGLL 53
DB 48 fpdp-kvclcqdevtdddyignttdvtytlfscskkdvrfkawflpimysilicfvll 106
QY 54 GNILVITFAYFKKARSMTDVYLLNMAIADILFVLTLPFWAVSHATGAWFNSNATCKLKL 113

```

Db 107 gnglvltiyfkrklmttdtllnlavadihlitlpfways-aakswvfgvhfcklif 165
 QY 114 GIYAINENCGMLLTCTISMDRYIAIVQATKSPRLRSRTLPRSKIIICLVVWGLSVIISST 173
 Db 166 aiykmsffsgmllilcisdryvaivqavsaahrarvlllkslcscvgiwiatiatsipe 225
 QY 174 FVFN--QKYNTOGSDVCEPKYQTVSEPIRWKLLMLGLELFGFFIPLMPMIFCYTFIVKT 231
 Db 226 llysdldgrsseqamrc-----slitehveafitigvaqmvigflvpllamscfylviirt 281
 QY 232 LVQAQNSKRHKAIIRVITAVLVFLACQIPHN--WVLLVTAANLGKMNRSQSEKLIQYTKT 290
 Db 282 llqarnfernkaiikaivavvvfivfipyngvvlaqtvanfnitsstcelskqlniayd 341
 QY 291 VTEVLAFLHCLNPVLYAFIGOKPRNYFLKILKDLWCVRKRYKSSGFSC--AGRYSENIS 348
 Db 342 vtsylacvrccvnpflyafigvknfndlkfkdldgicseqqlrqwsscrhrrssmsve 401
 QY 349 RQTSET 354
 Db 402 aetttt 407

RESULT 10

W48723
 ID W48723 standard; Protein; 410 AA.

AC W48723;

XX W48723;

DT 25-SEP-1998 (first entry)

XX Polypeptide sequence encoded by the human V31 genomic DNA.

XX V28; placenta; seven transmembrane receptor; 7TW; signal transduction;

XX Immunology; inflammation; V31.

XX Homo sapiens.

XX US5759804-A.

XX 02-JUN-1998.

XX 17-NOV-1993; 93US-0153848.

XX 17-NOV-1992; 92US-0977452.

XX (ICOS-) ICOS CORP.

XX Godiska R, Gray PW, Schweickart VL;

XX WPI; 1998-332132/29.

XX N-PSDB; V18345.

XX DNA encoding V28 seven transmembrane receptor polypeptide - useful

XX for producing recombinant polypeptide and anti-V28 antibodies, and

XX in screening assays for V28 agonists and antagonists

XX Example 2; Columns 31-34; 56pp; English.

XX The present sequence represents the deduced polypeptide sequence encoded

XX by the V31 genomic DNA (V18345) which was isolated from a human placenta

XX genomic library. The invention claims for a full length V28 genomic DNA

XX (V18343) and the V28 (W48722) protein it encodes. V28 and V31 (W48723)

XX proteins are seven transmembrane (7TW) receptors which are probably

XX involved in signal transduction. The invention also claims that cells

XX transformed with V28 DNA can be used to produce the recombinant

XX polypeptide, to produce anti-V28 antibodies or in screening assays for

XX V28 agonists or antagonists. The antibodies, agonists and antagonists

XX could then be used to modulate V28 receptor-ligand binding, for e.g. in

XX immunological and/or inflammatory events in vivo.

XX Sequence 410 AA;

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

Query Match 35.8%; Score 678.5; DB 19; Length 410;
 Best Local Similarity 40.7%; Pred. No. 1-6e-69;
 Matches 149; Conservative 78; Mismatches 120; Indels 19; Gaps 8;
 QY 2 FSTPVKIILOS-----ILHTQILRCYCPCRRSG--SSPGYLYRIAYSILICVLGLL 53
 Db 48 fsp-kvclcqdevtdddyigdnnttdytlfesleskdvrfkawflpmylsilcfvll 106
 QY 54 GNILVVITFAYKARSMFTDVLNMAADILFVLTLPFWAVSHATGAWFSNATCKLLK 113
 Db 107 gnglvltiyfkrklmttdtllnlavadihlitlpfways-aakswvfgvhfcklif 165
 QY 114 GIYAINENCGMLLTCTISMDRYIAIVQATKSPRLRSRTLPRSKIIICLVVWGLSVIISST 173
 Db 166 aiykmsffsgmllilcisdryvaivqavsaahrarvlllkslcscvgiwiatiatsipe 225
 QY 174 FVFN--QKYNTOGSDVCEPKYQTVSEPIRWKLLMLGLELFGFFIPLMPMIFCYTFIVKT 231
 Db 226 llysdldgrsseqamrc-----slitehveafitigvaqmvigflvpllamscfylviirt 281
 QY 232 LVQAQNSKRHKAIIRVITAVLVFLACQIPHN--WVLLVTAANLGKMNRSQSEKLIQYTKT 290
 Db 282 llqarnfernkaiikaivavvvfivfipyngvvlaqtvanfnitsstcelskqlniayd 341
 QY 291 VTEVLAFLHCLNPVLYAFIGOKPRNYFLKILKDLWCVRKRYKSSGFSC--AGRYSENIS 348
 Db 342 vtsylacvrccvnpflyafigvknfndlkfkdldgicseqqlrqwsscrhrrssmsve 401
 QY 349 RQTSET 354
 Db 402 aetttt 407

RESULT 11

B21687

ID B21687 standard; Protein; 410 AA.

AC B21687;

XX B21687;

DT 26-JAN-2001 (first entry)

XX Genomic clone of 7TW receptor V31 protein.

DE Seven transmembrane receptor; 7TW; heptahelical; serpentine;

XX G-protein-coupled; V28; V31; V112; R20; R2; R12; RM3; gene therapy;

XX cancer.

XX Homo sapiens.

OS US6107475-A.

XX 22-AUG-2000.

XX 26-APR-1999; 99US-0299843.

XX 17-MAY-1994; 94US-0245242.

XX 01-JUN-1998; 98US-0088337.

XX 17-NOV-1992; 92US-0977452.

XX 17-NOV-1993; 93US-0153848.

XX (ICOS-) ICOS CORP.

XX Schweickart VL, Gray PW, Godiska R;

XX WPI; 2000-571335/53.

XX N-PSDB; A90600.

XX Polynucleotide encoding seven transmembrane receptors, antibody

XX specific to the receptor, agonist and antagonist of the receptor useful

XX for treating inflammation in a mammal

XX Example 3; Columns 33-36; 61pp; English.

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX The present sequence is a novel seven transmembrane (7TM) receptors
 CC (also known as heptahelical, serpentine or G-protein-coupled receptors).
 CC The coding sequence for the present sequence may be used for gene
 CC therapy for diseases such as cancer.
 XX Sequence 410 AA;

Query Match 35.8%; Score 678.5; DB 21; Length 410;
 Best Local Similarity 40.7%; Pred. No. 1.6e-69;
 Matches 149; Conservative 78; Mismatches 120; Indels 19; Gaps 8;

QY 2 FETPVKILQCS-----ILHITQLILRCYCPCRRSG--SSPGYLRYIAYSLICVLGLL 53
 Db 48 fsp-kvclcqdevtdydgndttvdytlfeslcskdkvnrkafwflpimysliicfvgl 106

QY 54 GNILVITFAFYKARSMTDVLLNMAIADILFVLFPWAVSHATGAWFNSNATCKLLK 113
 Db 107 gnglvltviyfrkrlkmttdtynlnlavadilfltltpfways-aakswvfgvhfcklif 165

QY 114 GIYAINFCGMILLTICISMDRYIAIVQATKSPRLRSRTLPKSKIIICLVWGLSVIISST 173
 Db 166 alykmsffgmlilicisidryvaivqavsahrarvllisclscvgiilatvlsipe 225

QY 174 FVEN--QKNTQGSVDCEPKYQTVSEPIRWKLLMLGLELFLGFFIPLMFIFCYTFIVKT 231
 Db 226 llysdqlrsseqamrc-----slitcheveafitigvaqmvigflvplamsfcylviirt 281

QY 232 LVOAQNKRHKRAIRVIAVVLVFLACQIPHNVLLVTAANLGMNRSQSEKLGITYTKT 290
 Db 282 lllqarnfernkakvliavvvvfiqvglyngvvlqvtvanfnitscelskqnlaiyd 341

QY 291 VTEVLAFLHCLLPVLYAFIGQKERNYFLKLDLCVCRKYSKSGFSC--AGRYSENIS 348
 Db 342 vtyslacvrccvnpflyafigvknrdlflkldgclsgelqrqwsccrhhrrssmsve 401

QY 349 ROTSET 354
 Db 402 aetttt 407

RESULT 12
 R53745
 ID R53745 standard; Protein; 358 AA.
 XX
 AC R53745;
 XX
 XX 02-FEB-1995 (first entry)
 XX
 DE Partial sequence of seven transmembrane receptor (V31).
 XX
 KW Primer; seven transmembrane receptor; receptor; amplification; PCR;
 XX polymerase chain reaction.
 OS Homo sapiens.
 XX
 PN W09412635-A.
 XX
 PD 09-JUN-1994.
 XX
 XX 17-NOV-1993; 93WO-US111153.
 XX
 PR 17-NOV-1992; 92US-0977452.
 XX
 FA (ICOS-) ICOS CORP.
 XX
 XX Godiska R, Gray PW, Schweickart VL;
 XX
 XX WPI; 1994-200264/24.
 DR N-PSDB; Q66162.
 XX
 PT DNA encoding seven transmembrane receptors - used to develop

prods. for use as therapeutic or diagnostic agents for conditions
 PT involving the receptors.
 XX
 PS Example 3; Page 56-57; 100pp; English.
 XX

Two primers (Q66148, Q66149) were used to amplify human genomic DNA
 CC purified from leukocytes. Approximately 1000 clones were isolated
 CC after the initial amplification reaction and probed with sequences
 CC specific for seven transmembrane receptors IL8R1, AT2R and R20.
 CC Clones which did not hybridise were then chosen for sequence
 CC analysis. Three new clones were identified that appeared to encode
 CC seven transmembrane receptor segments. Two more primers (Q66151,
 CC Q66152) were used to isolate a full length version of one of these
 CC clones designated V31 (See Q66153). This is the sequence encoded
 CC by exon 3 of the V31 genomic clone
 XX Sequence 358 AA;
 SQ

Query Match 35.7%; Score 677; DB 15; Length 358;
 Best Local Similarity 44.0%; Pred. No. 1.9e-69;
 Matches 140; Conservative 70; Mismatches 98; Indels 10; Gaps 5;

QY 42 TAYSILICVGLGNILVITFAFYKARSMTDVLLNMAIADILFVLFPWAVSHATGA 101
 Db 43 lmyslicfvglnglvltviyfrkrlkmttdtynlnlavadilfltltpfways-aaks 101

QY 102 WVFENATCKLLGIYAINFCGMILLTICISMDRYIAIVQATKSPRLRSRTLPKSKIIICLV 161
 Db 102 wvfgvhfcklifafikmsffgmlilicisidryvaivqavsahrarvllisclscvg 161

QY 162 VWGLSVIISSTSSVFVN--QKNTQGSVDCEPKYQTVSEPIRWKLLMLGLELFLGFFIPLM 219
 Db 162 llysdqlrsseqamrc-----slitcheveafitigvaqmvigflvpl 217

QY 220 FMICYTTFIVTKLVOAQNKRHKRAIRVIAVVLVFLACQIPHNVLLVTAANLGMNRS 278
 Db 218 amscfylviirtllqarnfernkakvliavvvvfiqvglyngvvlqvtvanfnitsst 277

QY 279 COSEKLGITYTKVTEVLAFLHCLLPVLYAFIGQKERNYFLKLDLCVCRKYSKSGFS 338
 Db 278 celskqnlaiydvtyslacvrccvnpflyafigvknrdlflkldgclsgelqrqws 337

QY 339 C--AGRYSENISROTSET 354
 Db 338 crhhrrssmsveaetttt 355

RESULT 13
 B21689
 ID B21689 standard; Protein; 358 AA.
 XX
 AC B21689;
 XX
 XX 26-JAN-2001 (first entry)
 XX
 DE Human 7TM receptor V31-B cDNA clone exon 1 protein.
 XX
 KW Seven transmembrane receptor; 7TM; heptahelical; serpentine;
 KW G-protein-coupled; V28; V31; V112; R20; R2; R12; RM3; gene therapy;
 KW cancer.
 XX
 OS Homo sapiens.
 XX
 PN US6107475-A.
 XX
 PD 22-AUG-2000.
 XX
 PF 26-APR-1999; 99US-0299843.
 XX
 PR 17-MAY-1994; 94US-0245242.
 PR 01-JUN-1998; 98US-0088337.
 PR 17-NOV-1992; 92US-0977452.


```

PR 17-NOV-1993; 93US-0153848.
XX (ICOS-) ICOS CORP.
PA Schweickart VL, Gray PW, Godiska R;
XX WPI; 2000-571335/53.
DR N-PSDB; A91709.
XX Polynucleotide encoding seven transmembrane receptors, antibody
PT specific to the receptor, agonist and antagonist of the receptor useful
PT for treating inflammation in a mammal
XX Example 3; Columns 49-52; 61pp; English.
XX The present sequence is a novel seven transmembrane (7TM) receptors
CC (also known as heptahelical, serpentine or G-protein-coupled receptors).
CC The coding sequence for the present sequence may be used for gene
CC therapy for diseases such as cancer.
XX Sequence 358 AA;

Query Match 35.7%; Score 677; DB 21; Length 358;
Best Local Similarity 44.08; Pred. No. 1.9e-69;
Matches 140; Conservative 70; Mismatches 98; Indels 10; Gaps 5;

QY 42 IAYSLICVLGILGNILVITFAFYKARSMTDVLLNMAIADILFVLTPFWAVSHATGA 101
DB 43 Imsyilcfvllnglvgvltiyfkrktmtctylnlavadihlflplfways-aaks 101

QY 102 WVFNSATCKLLGKIYAINFCGMLLLTCISMDRYAIVQATKSFRLSRTPRSKIICLV 161
DB 102 wvfghvcklifaikmsffsgmlllclisidryvaivqavsaahrarvllskscvg 161

QY 162 VWGLSVIISSTFFVN--QKYNTOGSDVCEPKYQTVSEPIRKLMLGLLELFGFFIPLM 219
DB 162 iwlatvisipellysdlsrsseqamrc---slitehveafitqvaqmvigflvpll 217

QY 220 FMIFCYFTIVKTLVQAKNSRKHAIKRVIIAVLVFLACQIPHN--MVLVTAANLGMNRS 278
DB 218 amsfcyliivrtllqarnfermkakvliavvvfivqlpyngvvlgtvanfnitst 277

QY 279 COSEKLIQYTKVTEVLAFLHCLLPVLYAFIGQKFRNYFLKILKDLWCVRKRYKSSGFS 338
DB 278 celskqlniaydvtyslacvrcvnpflyafigvkrndlkfklclsgqlrqlwss 337

QY 339 C--AGRYSENISROTSET 354
DB 338 crhrrssmsveaetttt 355

RESULT 14
Y90663
ID Y90663 standard; Protein; 378 AA.
XX Y90663;
AC Y90663;
XX 21-AUG-2000 (first entry)
DE Human mutant G protein-coupled receptor EB11 (I262K).
XX G protein-coupled receptor; GPCR; constitutively active;
KW intracellular loop 3; transmembrane domain 6; drug screening;
KW agonist; antagonist; mutant; mutein.
XX Homo sapiens.
OS Synthetic.
XX W020002129-A1.
PN 20-APR-2000.
PD
XX

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PF 12-OCT-1999; 99WO-US23938.
XX 13-OCT-1998; 98US-0170496.
XX (AREN-) ARENA PHARM INC.
XX Behan DP, Chalmers DT, Liaw CW;
PI WPI; 2000-329165/28.
DR N-PSDB; A30729.
XX Non-endogenous constitutively activated human G protein-coupled
PT receptors, useful for identifying agonists for use as pharmaceutical
PT agents
XX Example 2; Page 259-260; 341pp; English.
XX The invention relates to constitutively active, non-endogenous versions
CC of endogenous human orphan G protein-coupled receptors (GPCRs, Y90643-
CC Y90677 and Y90683-Y90687), and to DNA encoding them (A30709-A30743 and
CC A30775-A30779). The mutant proteins of the invention contain a
CC mutation in a portion of the protein comprising intracellular loop 3
CC (IC3) and transmembrane domain 6 (TM6). A non-endogenous amino acid, X,
CC is substituted for an endogenous residue in IC3 at a position 16 amino
CC acids N-terminal of an endogenous proline in TM6 to form a sequence
CC X-(AA)15-Pro. The endogenous amino acid is selected from Lys, His, Arg or
CC Ala, and is preferably Lys. When the endogenous residue at this position
CC is Lys, this residue is replaced by His, Arg or preferably Ala. The 15
CC amino acid stretch between the substituted amino acid and the Pro may be
CC endogenous, non-endogenous, or a mixture of endogenous and non-endogenous
CC residues. The constitutively active GPCRs are useful for identifying
CC antagonists, agonists and partial agonists for use as pharmaceutical
CC agents. The mutant proteins are also useful in research settings for
CC elucidating the roles of the receptors in normal and diseased conditions.
CC Antagonists for a particular GPCR are useful for treating diseases and
CC disorders associated with that receptor. Because the novel mutant GPCRs
CC are constitutively active, they can be used directly for screening of
CC compounds without the need for endogenous ligands. Sequences Y90643-
CC Y90677 and Y90683-Y90687 the mutant human GPCRs of the invention.
XX Sequence 378 AA;

Query Match 35.6%; Score 675; DB 21; Length 378;
Best Local Similarity 39.2%; Pred. No. 3.6e-69;
Matches 148; Conservative 79; Mismatches 115; Indels 36; Gaps 8;

QY 5 PVKIIQCQSILHITQILRCYC-----clqdevtdyigdnntvdtlfselcskdvrfkafwlp 62
DB 6 pmskvlvvalvifqv---clqdevtdyigdnntvdtlfselcskdvrfkafwlp 62

QY 42 IAYSLICVLGILGNILVITFAFYKARSMTDVLLNMAIADILFVLTPFWAVSHATGA 101
DB 63 Imsyilcfvllnglvgvltiyfkrktmtctylnlavadihlflplfways-aaks 121

QY 102 WVFNSATCKLLGKIYAINFCGMLLLTCISMDRYAIVQATKSFRLSRTPRSKIICLV 161
DB 122 wvfghvcklifaikmsffsgmlllclisidryvaivqavsaahrarvllskscvg 181

QY 162 VWGLSVIISSTFFVN--QKYNTOGSDVCEPKYQTVSEPIRKLMLGLLELFGFFIPLM 219
DB 182 iwlatvisipellysdlsrsseqamrc---slitehveafitqvaqmvigflvpll 237

QY 220 FMIFCYFTIVKTLVQAKNSRKHAIKRVIIAVLVFLACQIPHN--MVLVTAANLGMNRS 278
DB 238 amsfcyliivrtllqarnfermkakvliavvvfivqlpyngvvlgtvanfnitst 297

QY 279 COSEKLIQYTKVTEVLAFLHCLLPVLYAFIGQKFRNYFLKILKDLWCVRKRYKSSGFS 338
DB 298 celskqlniaydvtyslacvrcvnpflyafigvkrndlkfklclsgqlrqlwss 357

QY 339 C--AGRYSENISROTSET 354
DB 339 C--AGRYSENISROTSET 354

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OM protein - protein search, using sw model

Run on: May 23, 2001, 15:23:13 ; Search time 95.91 seconds
(without alignments)
73.110 Million cell updates/sec

Title: US-08-887-977-10
Perfect score: 1894
Sequence: 1 MFSTPVKILQCSILHITQL.....NISROTSETADNDASSFTM 365

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 185757 seqs, 19210857 residues

Total number of hits satisfying chosen parameters: 185757

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: /cgn2_6/ptodata/2/iaa/5A_COMB.pep: *
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep: *
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	682	36.0	378	1 US-08-153-848-15	Sequence 15, Appl
2	682	36.0	378	3 US-09-299-843A-15	Sequence 15, Appl
3	682	36.0	378	3 US-09-299-843A-66	Sequence 66, Appl
4	682	36.0	378	4 US-09-251-545-1	Sequence 1, Appl
5	682	36.0	378	5 PCT-US93-11153-15	Sequence 15, Appl
6	678.5	35.8	410	1 US-08-153-848-7	Sequence 7, Appl
7	678.5	35.8	410	3 US-09-299-843A-7	Sequence 7, Appl
8	678.5	35.8	410	5 PCT-US93-11153-7	Sequence 7, Appl
9	677	35.7	358	1 US-08-153-848-19	Sequence 19, Appl
10	677	35.7	358	3 US-09-299-843A-19	Sequence 19, Appl
11	677	35.7	358	5 PCT-US93-11153-19	Sequence 19, Appl
12	668.5	35.3	359	1 US-08-153-848-24	Sequence 24, Appl
13	668.5	35.3	359	3 US-09-299-843A-24	Sequence 24, Appl
14	668.5	35.3	359	5 PCT-US93-11153-24	Sequence 24, Appl
15	663	35.0	378	1 US-08-383-750-2	Sequence 2, Appl
16	663	35.0	378	1 US-08-383-751A-2	Sequence 2, Appl
17	663	35.0	378	3 US-08-352-678-2	Sequence 2, Appl
18	663	35.0	378	5 PCT-US93-09636-2	Sequence 2, Appl
19	662	35.0	350	1 US-08-202-056-1	Sequence 1, Appl
20	662	35.0	350	1 US-08-076-093A-2	Sequence 2, Appl
21	662	35.0	350	1 US-08-450-393A-7	Sequence 7, Appl
22	662	35.0	350	1 US-08-410-453A-1	Sequence 1, Appl
23	662	35.0	350	1 US-08-701-265-2	Sequence 2, Appl
24	662	35.0	350	1 US-08-410-454A-1	Sequence 1, Appl
25	662	35.0	350	2 US-08-284-586-2	Sequence 2, Appl
26	662	35.0	350	2 US-08-410-456A-1	Sequence 1, Appl
27	662	35.0	350	2 US-08-805-478-2	Sequence 2, Appl

28	662	35.0	350	2 US-08-802-627A-2	Sequence 2, Appl
29	662	35.0	350	2 US-08-801-238-2	Sequence 2, Appl
30	662	35.0	350	2 US-08-801-228-2	Sequence 2, Appl
31	662	35.0	350	3 US-09-104-296-2	Sequence 2, Appl
32	662	35.0	350	4 US-08-446-669-7	Sequence 7, Appl
33	662	35.0	350	5 PCT-US95-00476-7	Sequence 7, Appl
34	643.5	34.0	361	2 US-08-902-294-2	Sequence 2, Appl
35	643.5	34.0	361	3 US-09-178-637-2	Sequence 2, Appl
36	629.5	33.2	355	1 US-07-759-568-1	Sequence 1, Appl
37	629.5	33.2	355	1 US-08-450-393A-8	Sequence 8, Appl
38	629.5	33.2	355	2 US-08-390-000A-5	Sequence 5, Appl
39	629.5	33.2	355	4 US-08-446-669-8	Sequence 8, Appl
40	629.5	33.2	355	5 PCT-US95-00476-8	Sequence 8, Appl
41	629.5	33.2	360	1 US-08-202-056-7	Sequence 7, Appl
42	610.5	32.2	360	4 US-08-875-573-20	Sequence 20, Appl
43	600.5	31.7	312	1 US-08-118-270-38	Sequence 38, Appl
44	600.5	31.7	312	5 PCT-US93-08528-38	Sequence 2, Appl
45	580.5	30.6	342	2 US-08-742-011-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-08-153-848-15
: Sequence 15, Application US/08153848
: Patent No. 5759804
: GENERAL INFORMATION:
: APPLICANT: Godiska, Ronald
: APPLICANT: Gray, Patrick W.
: APPLICANT: Schweikart, Vicki L.
: TITLE OF INVENTION: No. 5759804el Seven Transmembrane Receptors
: NUMBER OF SEQUENCES: 64
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
: ADDRESSEE: Bicknell
: STREET: 6300 Sears Tower, 233 South Wacker Drive
: CITY: Chicago
: STATE: Illinois
: COUNTRY: USA
: ZIP: 60606
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION NUMBER: US/08/153,848
: APPLICATION NUMBER: 514
: FILING DATE: 17-NOV-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/977,452
: FILING DATE: 17-NOV-1992
: ATTORNEY/AGENT INFORMATION:
: NAME: No. 5759804and, Greta E.
: REGISTRATION NUMBER: 35,302
: REFERENCE/DOCKET NUMBER: 31794
: TELEPHONE: (312) 474-6300
: TELEFAX: (312) 474-0448
: TELEX: 25-3856
: INFORMATION FOR SEQ ID NO: 15:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 378 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
US-08-153-848-15

Query Match 36.0%; Score 682; DB 1; Length 378;
Best Local Similarity 39.4%; Pred. No. 4.9e-56;
Matches 149; Conservative 79; Mismatches 114; Indels 36; Gaps 8;

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; TELEA:
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 378 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
us-09-299-843A-15

Query Match      36.0%; Score 682; DB 3; Length 378;
Best Local Similarity 39.4%; Pred. No. 4.9e-56;
Matches 149; Conservative 79; Mismatches 114; Indels 36; Gaps

Qy      5 PVKILCOSILHITOLILRCYC-----APCRRSG--SSPGYLIR 41
Db      6 PMKSVLVALLVIFOV---CLCQDEVTDDYIGDNTVDYTLFESLCKKDVNRKANFLP 62

Qy      42 IAYSLLICVLGLNLGVITTFAYFKKARSMTDVLNNAIAIDILFVLTLTPWAVSHATGA 107
Db      63 IMYSIICFVGLLNGCLVVLTYIYFKRLKLTMDTYLLNLAVADILFLLTLPWAVS-AAKS 121

Qy      102 WVFNSWATCKLKGIVAINFNGCMLLLTTCISMDRYIAIVQAKSPFLKRSRTLPKSKIICLV 161
Db      122 WVFVGHFCKLFIAYIKMGFFSGMLLLLCISIDRYVAIVQAVSAUHRHARVLLISKLSCVG 188

Qy      162 VWGLSVIISSTTFVN--QKNTQGSODVCEPKYQTVSEPIRWKLLMLGLLELLFGFFPLM 211
Db      182 IWLATVSLIPELAYSDIQRSSQEARC---SLITEHVEAFITIQVAQWVIGFLVPLL 233

Qy      220 EMIFCYTFTIVTLVQAQSKRHKAIKRVIIAVVFLACIQPHN-VLLVATAANLGMKNR 279
Db      238 AMSFCYLVIIKTLQARNFERNKAIKVIAVVVVFIFQLPVGVLVLAQTVANFNITST 299

Qy      279 CQSEKLGICTKTVEVLAFLHCCLNPVLIYAFITGOKFRNYFLKILKLDLWCVRKKYKSGFS 335
Db      298 CELSKQLNIADVITYSLACVRCVNPFIYAFIGYKFRNDLFKFLKDLGLCLSQEQLQWSS 355

Qy      339 C--AGRYSENISROTSET 354
Db      358 CRHIRSSMSVEAEVTTT 375

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STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/299,843A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/088,337
FILING DATE: 01-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/153,848
FILING DATE: 17-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Jill E. Uhl
REGISTRATION NUMBER: 43,213
REFERENCE/DOCKET NUMBER: 27866/32059B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448

RESULT 3
US-09-299-843A-66
Sequence 66, Application US/09299843A
Patent No. 6107475
GENERAL INFORMATION:
APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schweikart, Vicki L.
TITLE OF INVENTION: No. 6107475el Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/299,843A
FILING DATE: 01-JUN-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/088,337
FILING DATE: 01-JUN-1998

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; FILE REFERENCE: P50753
; CURRENT APPLICATION NUMBER: US/09/251,545
; CURRENT FILING DATE: 1999-02-17
; EARLIER APPLICATION NUMBER: 60/074,883
; EARLIER FILING DATE: 1998-02-17
; NUMBER OF SEQ ID NOS: 2

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; REFERENCE/DOCKET NUMBER: 31794
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 378 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US93-11153-15

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Query Match 36.0%; Score 682; DB 5; Length 378;
Best Local Similarity 39.4%; Pred. No. 4.9e-56;
Matches 149; Conservative 79; Mismatches 114; Indels 36; Gaps 8;

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QY 5 PVKIIICOSILHITQILRCYC-----CLCQDEVTDDYIGDNTTVDYTLFESLCSKDKVRNFKAWFLP 41
DB 6 PMKSVLVVALLVIFQV---CLCQDEVTDDYIGDNTTVDYTLFESLCSKDKVRNFKAWFLP 62
QY 42 TAYSLICVLGLNLIVITFAFYKARSMTDVLNMAIADILFVLTLPFWAVSHATGA 101
DB 63 IMYSICIFVGLNGLVLTIFYFKRLKMTDTYLLNLAVALDILFLLTLPFWAYS-AAKS 121
QY 102 WYFSNATCKLGIYAINCNGMLLTCTISMDRYIAIVQATKSFRLRSRTLPRSKIIICLV 161
DB 122 WYGVHFKLIPAIYKMSFFSGMLLCLISIDRYIAIVQAVSAHRARVLLSKUSCVG 181
QY 162 WGLSVIISSTFVN--QKYNTOGSDVCEPKYQTVSEPIRWKLLMLGLELFFGLFFIPLM 219
DB 182 IWILATVLSIPPELLYDLQRSSEQAMRC---SLITEHVEAFITIQVAMVIGFLVPLL 237
QY 220 PMFYCYTIVTLVQAQNSKRKAIRVIAVLVFLACQIPHN--MVLVTAANLGMKNRS 278
DB 238 AMSFCYLIIIRTLQAQNFERNKAIRVIAVVVVFVFPQYNGVLAQTVANFNITST 297
QY 279 COSEKLGIVTKVTEVLAFLHCLNPLVYAFIGOKFRNYFLKILKDLWCVRKYSKSGFS 338
DB 298 CELSKQLNIAYDVTYSLACVRCVNPFLYAFIGVKFRNDFLKFLKDLGLCSQEQOLROWSS 357
QY 339 C--AGRYSENISRTSET 354
DB 358 CRHRRSSMSVEAETTT 375

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RESULT 6
US-08-153-848-7
; Sequence 7, Application US/08153848
; Patent No. 5759804
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schweikart, Vicki L.
; TITLE OF INVENTION: No. 5759804el Seven Transmembrane Receptors
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/153.848
; FILING DATE:

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; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/977,452
; FILING DATE: 17-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5759804and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31794
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 410 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-153-848-7
; Query Match 35.8%; Score 678.5; DB 1; Length 410;
; Best Local Similarity 40.7%; Pred. No. 1.1e-55;
; Matches 149; Conservative 78; Mismatches 120; Indels 19; Gaps 8;
QY 2 FSTPVKIIICQS-----ILHITQILRCYCPCRRSG--SSPGYLYRIAYSLICVLGLL 53
DB 48 FPSP-KVCLCQDEVTDDYIGDNTTVDYTLFESLCSKDKVRNFKAWFLPIMYSIICFVGLL 106
QY 54 GNILVITFAFYKARSMTDVLNMAIADILFVLTLPFWAVSHATGAWVFNATCKLKLK 113
DB 107 GNGLVLTIFYFKRLKMTDTYLLNLAVALDILFLLTLPFWAYS-AAKSWVFGVHCKLIF 165
QY 114 GIYAINCNGMLLTCTISMDRYIAIVQATKSFRLRSRTLPRSKIIICLVVGLSVIISST 173
DB 166 AIYKMSFFSGMLLCLISIDRYIAIVQAVSAHRARVLLSKUSCVGIIWILATVLSIPE 225
QY 174 FVFN--QKYNTOGSDVCEPKYQTVSEPIRWKLLMLGLELFFGLFFIPLMFIYFYVKT 231
DB 226 LLYSDQRSSEQAMRC---SLITEHVEAFITIQVAMVIGFLVPLAMSFCLYVIIRT 281
QY 232 LVQAQNSKRKAIRVIAVLVFLACQIPHN--MVLVTAANLGMKNRSQSEKLGITYKT 290
DB 282 LQAQNFERNKAIRVIAVVVVFVFPQYNGVLAQTVANFNITSTCELSKQLNIAYD 341
QY 291 VTEVLAFLHCLNPLVYAFIGOKFRNYFLKILKDLWCVRKYSKSGFSC--AGRYSENIS 348
DB 342 VTYSLACVRCVNPFLYAFIGVKFRNDFLKFLKDLGLCSQEQOLROWSSCRHRRSSMSVE 401
QY 349 RQTSSET 354
DB 402 AETTTT 407

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RESULT 7
US-08-299-843A-7
; Sequence 7, Application US/09299843A
; Patent No. 6107475
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schweikart, Vicki L.
; TITLE OF INVENTION: No. 6107475el Seven Transmembrane Receptors
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:

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[illegible]

Search completed: May 23, 2001, 15:30:04
Job time: 411 sec

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RESULT 15
US-08-383-750-2
; Sequence 2, Application US/08383750
; Patent No. 5744301
; GENERAL INFORMATION:
; APPLICANT: Birkenbach, Mark
; APPLICANT: Kleff, Elliot
; TITLE OF INVENTION: Epstein Barr Virus Induced Genes
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, N.W.,
; CITY: Suite 600
; STATE: Washington
; COUNTRY: D.C.
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/383,750
; FILING DATE: Herewith
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Fox, Samuel, L.
; REGISTRATION NUMBER: 30,353
; REFERENCE/DOCKET NUMBER: 0627.3300001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 378 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

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Query Match 35.0%; Score 663; DB 1; Length 378;
Best Local Similarity 39.2%; Pred. No. 2.9e-54;
Matches 148; Conservative 78; Mismatches 116; Indels 36; Gaps 8;

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	1670	88.2	369	2	JC5068	G protein-coupled lymphocyte-specific
2	682	36.0	378	2	B55735	G protein-coupled
3	682	36.0	378	2	A55735	interleukin-8 rece
4	665	35.1	350	2	A39445	G protein-coupled
5	663	35.0	378	2	A45680	interleukin-8 rece
6	654	34.5	355	2	JQ1231	G protein-coupled
7	636.5	33.6	358	2	A53752	interleukin-8 rece
8	629.5	33.2	360	2	A53611	interleukin-8 rece
9	610.5	32.2	360	2	A57160	chemokine (C-C) re
10	593	31.3	356	2	A42096	interleukin-8 rece
11	580.5	30.6	359	2	A48921	interleukin-8 rece
12	574.5	30.3	360	2	JC4587	chemokine (C-C) re
13	571.5	30.2	359	2	I49341	MIP-1 alpha recept
14	564.5	29.8	354	2	A23669	interleukin-8 rece
15	547.5	28.9	355	2	A45177	chemokine (C-C) re
16	545	28.8	360	2	JC2443	chemokine (C-C) re
17	538	28.4	354	2	I58186	probable G protein
18	536.5	28.3	374	2	I38450	chemokine (C-C) re
19	532.5	28.1	367	2	JE0349	chemokine (C-C) re
20	531	28.0	355	2	G02436	interferon-inducib
21	527.5	27.9	352	2	A43113	chemokine (C-C) re
22	518	27.3	355	2	JC5067	G protein-coupled
23	512	27.0	355	2	JC4304	orphan G protein-c
24	504.5	26.6	355	2	I49339	macrophage inflamm
25	503	26.5	383	2	S55594	G protein-coupled
26	502.5	26.5	350	2	JN0621	G protein-coupled
27	496.5	26.2	352	2	A45747	neuropeptide Y/pep
28	492.5	26.0	352	2	G00048	fusin (LESTRA) - c
29	489	25.8	359	2	S15403	angiotensin II rec

1000

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being predicted and is derived by analysis of the total score distribution.

Db	364	ASSETM	369
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C;Keywords: G protein-coupled receptor

0v 339 C--AGPVSNTSROTSET 354

R/Anhuja, S.K.; Shetty, A.; Tiliary, H.L.; Murphny, P.M.
J. Biol. Chem. 269, 26381-26389, 1994

C; Keywords: G protein-coupled receptor; transmembrane protein

Query Match 35.0%; Score 663; DB 2; Length 378;
Best Local Similarity 39.2%; Pred. No. 2.6e-48;
Matches 148; Conservative 78; Mismatches 116; Indels 36; Gaps 8;

QY 5 PVKILQCSLHITQLILRCYC-----CLCQDEVTDDYIGDNTVDYTLFESLCSKKDVRNFKAWFLP 62
Db 6 PMKSVLVALLVIRQV---CLCQDEVTDDYIGDNTVDYTLFESLCSKKDVRNFKAWFLP 62

QY 42 IAYSLICVLGLLGNILVVITAFYKKARSMTDVYLLNMAIDILFVLPLPFWAVSHATGA 101
Db 63 IMYSIIICFVGLLGNLGVLLTYIFKRLKTMDTYLLNLAVADILFLLTLPFWAYS-AAKS 121

QY 102 WFFSNATCKLLKGIYAINFCNGMLLTICISMDRYTAIVQATKSPRLRSRTILPRSKIIICLV 161
Db 122 WVFQHFCKLFAIYKNSFFSGMLLLLCISIDRVAIVQAVSAHRHARVLLISLSCVG 181

QY 162 VWGLSVIISSSTVFVN--QKYNTOGSDYCEPKYQTVSEPIRWKLLMLGLELLFGFFPLM 219
Db 182 SAILATVLSIPELLYSDLQRSSEQAMRC----SLITEHVEAFITIOVAQMWIGFLVPLL 237

QY 220 FMICYFTIVKTLVQAKNSKHKRAIRVIAVVLFLACQIPH-NMVLVLTAAANLGMNRS 278
Db 238 AMSECYLVIIRTLQARNFERNKAIVIAVWVIFVQLPNGVLAQTVANFNITSST 297

QY 279 COSEKLLGYTKTVEVLAFLHCLNPVLAFTIGOKFRNVELKILKLCWCRKKYKSSGFS 338
Db 298 CELSKQINIAVDVYSLACVRCNCVNFYAFIGYKFRNDIFKLFKDLGCLSQEQLQWMSG 357

QY 339 C--AGRYSENISROTSET 354
Db 358 CRHIRSSMSVEAETTTT 375

RESULT 6
JQ1231
interleukin-8 receptor - rabbit
C; Species: Oryctolagus cuniculus (domestic rabbit)
C; Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 05-Nov-1999
C; Accession: JQ1231; A46483
R; Beckmann, M.P.; Munger, W.E.; Kozlosky, C.; VandenBos, T.; Price, V.; Lyman, S.; Ge-
Biochem. Biophys. Res. Commun. 179, 784-789, 1991
A; Title: Molecular characterization of the interleukin-8 receptor.
A; Reference number: JQ1231; MUID: 91378994
A; Accession: JQ1231
A; Molecule type: DNA
A; Residues: 1-355 <BBC>
A; Cross-references: GB:M74240; NID:g165438; PIDN:AAA31375.1; PID:g165439
R; Lee, J.; Kuang, W.J.; Rice, G.C.; Wood, W.I.
J. Immunol. 148, 1261-1264, 1992
A; Title: Characterization of complementary DNA clones encoding the rabbit IL-8 receptor
A; Reference number: A46483; MUID:92148149
A; Accession: A46483
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-355 <LEE>
A; Cross-references: GB:M82873; NID:g165440; PIDN:AAA31376.1; PID:g165441
A; Experimental source: neutrophils
A; Note: sequence extracted from NCBI backbone (NCBI:81526, NCBI:81530)
C; Superfamily: vertebrate rhodopsin
C; Keywords: G protein-coupled receptor; transmembrane protein

Query Match 34.5%; Score 654; DB 2; Length 355;
Best Local Similarity 41.2%; Pred. No. 1.4e-47;
Matches 135; Conservative 65; Mismatches 106; Indels 22; Gaps 7;

QY 38 YLRIAYSLICVLGLLGNILVVITAFYKKARSMTDVYLLNMAIDILFVLTPFWAVSH 97
Db 45 YVWVIVLAVFLSLGNSLVMVLVILYSRNSRNTVDVYLLNMAIDLALTMPITWAVSK 104

QY 98 ATGAWFNSNATCKLLKGIYAINFNCGLMLLTCTISMDRYIAIQAATSKFRLRSRTLPKSKI 157
 Db 105 EKG-WIFGTPCKVSLVKEVNFYSGILLACISVDYLAIVAHATRLTQKRHLV---KF 160
 QY 158 ICLVWGLSVLISSSTVFVNQKYN-TQSDVCEPKYQTVS-EPKRWKLLMGLLELFGFF 215
 Db 161 ICLGTAWSLILSLPFLFRQVFNSSNPVC---YEDLGHNTAKRWMLRILPHPTFGFI 217
 QY 216 IPLMFIMFYCTEIVTKLVAQNSKRKAIRVIAVVLVLAQOIPHNMLLV-TAANLKG 274
 Db 218 LPLVWMLFCYGTFLTLFQAHGQKRRAMRVFAVAVLLELLWLPXNVILLADTLMRTHV 277
 QY 275 MNRSCQSEKLIQYTKTVTEVLAFLHCLNPVLYAFTGQFRNYFLKILKDLQMCVRRKYKS 334
 Db 278 IQETQCRNDIDRALDATEILGLHSCNLPYIYAFIQGNFGLKMLAARGLSKEFLT 337
 QY 335 SGFSCAGRYSENISQTSSTADNDNASS 362
 Db 338 R-----HRTSYTSSTNVPS 353
 RESULT 7
 A53752
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
 C:Accession: A53752
 R:Prado, G.N.; Thomas, K.M.; Suzuki, H.; LaRosa, G.J.; Wilkinson, N.; Folco, E.; Navarro
 J. Biol. Chem. 269, 12391-12394, 1994
 A:Title: Molecular characterization of a novel rabbit interleukin-8 receptor isotype.
 A:Reference number: A53752; MUID:94230294
 A:Accession: A53752
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-358 <PRA>
 A:Cross-references: GB:L24445; NID:9437661; PIDN:AAA31378.1; PID:9437662
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 33.6%; Score 636.5; DB 2; Length 358;
 Best Local Similarity 42.7%; Pred. No. 4.2e-46;
 Matches 140; Conservative 59; Mismatches 116; Indels 13; Gaps 9;

QY 27 APCR-RSGSPGYLYRIAYSILCVLGLNLTWITFAFYKKARSMTDVYLLNMAIADIL 85
 Db 35 APCRSESLNYSYVLLIYILVFLSLGNSLVMLVILYRSCTCSVDYLLNLAIDL 94
 QY 86 FVLTLPTWAVSHATGAWFNSNATCKLLKGIYAINFNCGLMLLTCTISMDRYIAIQAATSKF 145
 Db 95 FATTLPWAASKVHG-WTFTGTPCKRWSLVKEVNFYSGILLACISVDRYLAIVHATRTM 153
 QY 146 RLRSRTLPKSKIICLVWGLSVLISSSTVFV-NQYNTQSGDVCEPKYQTV-SEPIRWKL 203
 Db 154 -IQKRHL--VFPCLSMGMVSLILSLPILFLFRNAIFPPNPPVPC---YEDMGNSTAKRM 207
 QY 204 LMLGLELLELFGFFIPLMFIMFYCTFIVTKLVAQNSKRKAIRVIAVVLVLAQOIPHN 263
 Db 208 VLRLPQTFEGFILPLVLMFCYVFLRLFLQAHGQKRRAMRVFAVAVLIFLLCWLPYNL 267
 QY 264 VLLV-TAANLGMNRSQSEKLIQYTKTVTEVLAFLHCLNPVLYAFIQGNFNYFLKIL 322
 Db 268 VLLDITLMTQVIOETCERRNDIDRALDATEILGLHSCNLPYIYAFIQGNFNYFLKIL 327
 QY 323 KDLWCVRKY--KSSGFSCAGRYSENIS 348
 Db 328 AAHLISKEFLAKESRPSFVASSSGNTS 355

RESULT 8
 A53611
 C:Species: Homo sapiens (man)

C:Date: 07-Oct-1994 #sequence_revision 12-Apr-1996 #text_change 05-Nov-1999
 C:Accession: I37898; I38712; A53611; A39446
 R:Ahuja, S.K.; Shetty, A.; Tiffany, H.L.; Murphy, P.M.
 J. Biol. Chem. 269, 26381-26389, 1994
 A:Title: Comparison of the genomic organization and promoter function for human inter
 A:Reference number: I37898; MUID:95014476
 A:Accession: I37898
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-360 <RES>
 A:Cross-references: EMBL:U11801; NID:9511801; PIDN:AAB60656.1; PID:9511803
 A:Accession: I38712
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-15 <RES2>
 A:Cross-references: EMBL:U11872; NID:9511808; PIDN:AAA64380.1; PID:9511809; EMBL:U118
 I1876; NID:9511816; PID:9511817; EMBL:U11877; NID:9511818; PID:9511819; EMBL:U11878;
 R:Sprenger, H.; Lloyd, A.R.; Lautens, L.L.; Bonner, T.I.; Kelvin, D.J.
 J. Biol. Chem. 269, 11065-11072, 1994
 A:Title: Structure, genomic organization, and expression of the human interleukin-8 r
 A:Reference number: A53611; MUID:94209273
 A:Accession: A53611
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 6-360 <SPR>
 A:Cross-references: GB:M99412; GB:L19593
 R:Murphy, P.M.; Tiffany, H.L.
 Science 253, 1280-1283, 1991
 A:Title: Cloning of complementary DNA encoding a functional human interleukin-8 recep
 A:Reference number: A39446; MUID:91368200
 A:Accession: A39446
 A:Status: preliminary; nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 6-360 <MUR>
 A:Cross-references: GB:M73969
 C:Comment: This receptor, unlike IL8RA, binds several peptides besides interleukin-8,
 C:Genetics:
 A:Gene: GDB:IL8RB; IL8RA
 A:Cross-references: GDB:127868; OMIM:146928
 A:Map position: 2q35-2q35
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 33.2%; Score 629.5; DB 2; Length 360;
 Best Local Similarity 43.4%; Pred. No. 1.6e-45;
 Matches 132; Conservative 56; Mismatches 97; Indels 19; Gaps 8;

QY 27 APCR-RSGSPGYLYRIAYSILCVLGLNLTWITFAFYKKARSMTDVYLLNMAIADIL 85
 Db 37 APCPESELEINKYFVVIYALVFLSLGNSLVMLVILYRSVGRSVDYLLNLAIDL 96
 QY 86 FVLTLPTWAVSHATGAWFNSNATCKLLKGIYAINFNCGLMLLTCTISMDRYIAIQAATSKF 145
 Db 97 FALTLPWAASKVNG-WIFGTFCKVSVLSLKEVNFYSGILLACISVDRYLAIVHAT--- 152
 QY 146 RLRSRTLPKSKIICLVWGLSVLISSSTVFVNQK-YNTQSGDVCEPKYQTV-SEPI 199
 Db 153 ----RTLTQRYLVKFCILSWGLSLLLALPVLFRFRVYSSNVSPAC---YEDMGNTA 205
 QY 200 RWKLLMLGLELLELFGFFIPLMFIMFYCTFIVTKLVAQNSKRKAIRVIAVVLVLAQOIPHN 259
 Db 206 NWRMLLRILPQSGFIVPPLLIMLFCYGTFLRTLFAHMGQKRRAMRVFAVAVLIFLLCW 265
 QY 260 PHNMLLV-TAANLGMNRSQSEKLIQYTKTVTEVLAFLHCLNPVLYAFIQGNFNYF 318
 Db 266 PYNLVLADITLMTQVIOETCERRNHIDRALDATEILGLHSCNLPYIYAFIQGNFNYF 325
 QY 319 LKIL 322
 Db 326 LKIL 329

submitted to the EMBL Data Library, February 1994

A;Description: Molecular cloning of the rat IL8 receptor.

A;Reference number: S42096

A;Accession: S42096

A>Status: preliminary

A:Molecule type: mRNA

A;Residues: 1-356 <GOB>

A;Cross-references: EMBL:X77797

C;Superfamily: vertebrate rhodopsin

C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 31.3%; Score 593; DB 2; Length 356;
Best Local Similarity 39.3%; Pred. No. 1.9e-42;
Matches 129; Conservative 64; Mismatches 119; Indels 16; Gaps

QY 27 APCRRSSPG-VLYRIAYSLICVLGLGNILVITAFYFKKARSMTDVYLNLMAIADIL 85
||| : | : | : | : ||| : : | : ||||| : ||| :
Db 36 APCPSANLDINRYAVVIYVLVTLLSLVGNSLVMLVILYNRSTCSVTDVYLLNLAIDLF 95

QY 86 FVLTLPPWAYSHATGAWVESNATCKLLKGIYAINFCMGLLLTCISMDRYIAIVQATXSF 145
||| ||| : | : | : | : ||| : ||| : ||| : ||| : ||| : ||| :
Db 96 FAULTPWAASKVNG-WIFGSFQVFSEFLQETFTYSVLLCLACISMDRYLIAIVHATSTL 154

QY 146 RLRSRTLPRSKIICLVWVLSIISSSTFFVENKYNTQGSD-VCEPKYQTV-SEPIRWKL 203
:: : | : | : | : ||| : | : | : | : ||| : : : : : ||| :
Db 155 -IQKRHL--VKFCVITHWFLSVLSVIPFILRTVTVANSTVVC---YENIGNTSKRWV 208

QY 204 LMLGLELLEFGFIPLMFICYTFIVKTLVQAOSKRHKRAIRVIIAAVLVFLACIPHNM 263
: : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 209 VLRILPTQYGFLLPLLIMLFCYGTFLTRLFKAHWGQKHARMRVFAVVLVELLCWLPLYNI 268

QY 264 VLLV-TAANLGKNMRSCOEKLLGYTKTVTVEVLAFHLCCLNPNVLYAFIQGRNFYKIL 322
|| : : : : : : : : : : : : | : | : | : | : | : | : | : | : | : | :
Db 269 VLFTDLMTKLIKETCRQNEI--NKASEILGLFHLSCNPITPIYAFIQGRFHGLLKIM 325

QY 323 KDLWCVRKKY-KSSGFSCAGRYSENIS 348
: : : : : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 326 ANYGLYSKEFLAKREGSPFVGSSANTS 353

RESULT 11
A48921
interleukin-8 receptor type B - mouse
N;Alternate names: G-protein coupled receptor Gpcrl6
C;Species: Mus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 05-Nov-1999
R;Accession: A48921; A53677; I49348; I54421; H48909; I53774
C;Cerretti, D.P.; Nelson, N.; Koslosky, C.J.; Morrissey, P.J.; Copeland, N.A.
Genomics 18, 410-413, 1993
A;Title: The murine homologue of the human interleukin-8 receptor type B ma
A;Reference number: A48921; MUID:94117014
A;Accession: A48921
A:Molecule type: DNA
A;Residues: 1-359 <SUZ>
A;Cross-references: GB:L26367; NID:g435093; PIDN:AAA39305.1; PID:g435094
R;Suzuki, H.; Prado, G.N.; Wilkinson, N.; Navarro, J.
J. Biol. Chem. 269, 18263-18266, 1994
A;Bio1. The N terminus of interleukin-8 (IL-8) receptor confers high affin
A;Reference number: A53677; MUID:94308043
A;Accession: A53677
A;Status: nucleic acid sequence not shown; not compared with conceptual tra
A:Molecule type: DNA
A;Residues: 1-359 <SUZ>
A;Cross-references: GB:L26549
A;Note: sequence extracted from NCBI backbone (NCBIP:I49812)
R;Lee, J.; Cacalano, G.; Camerato, T.; Toy, K.; Moore, M.W.; Wood, W.I.
J. Immunol. 155, 2158-2164, 1995
A;Title: Chemokine binding and activities mediated by the mouse IL-8 recepto
A;Reference number: I49348; MUID:95363183
A;Accession: I49348
A;Status: preliminary
A:Molecule type: DNA
A;Reference number: translated from GB/EMBL/DDBJ

Matches 110; Conservative 67; Mismatches 113; Indels 5; Gaps 3;

QY 25 YCAPCR--RSGSPGYLRIAYSLICVLGNILVITFAFYKKARSMTDVYLLNMAIA 82
 Db 24 WAPCEKRIEELGSLWLPPLSLVIFLIGLGNMAMVLLIKYKLOIMTNVILFNLAIS 83
 QY 83 DILFVLTPFWAVSHATGAWFNSATCKLLKGIYAINFCNGLMLLTFCISMDRYIAIVQAT 142
 Db 84 DLLFELTPFWHYVLLWNEGFGHYMKMLSGFYLLALYSEIFFIILLTIDRYLAIVHAV 143
 QY 143 KSFRLRSRTLPKSKILCLVWGLSVIISSTFVNQKNTQSDVCEPKYQTVSEPIRWK 202
 Db 144 --FALRAETVTFATITTSITWGLAGLAALPEFIFHESQDSFGFESCPRYPE-GEEDSWK 200
 QY 203 LLMGLLELFGFFIFLPMFIFCYTIVKTLVQAQNSKRHKAIRVIAVVLVFLACIAPHN 262
 Db 201 RFHALRMNIFGLALPLLVAVICYSGLIKTLRCPCPKKKHKAIRLIPVVMIVFIFWTPYN 260
 QY 263 MVLVTAANLGMNRSQSEKLGITKTVTEVLAFLHCLNPNVLYAFIQGKFRNY 317
 Db 261 LVLLFSAFHSTFLETSCEQSKHLDLMAQVTEVIATHCVCNPNVYAFVGERFRKH 315

RESULT 14
 A23669
 Interleukin-8 receptor, high affinity - rabbit
 N:Alternate names: fMLP receptor
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C>Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 05-Nov-1999
 C:Accession: A23669
 R:Thomas, K.M.; Pyun, H.Y.; Navarro, J.
 J. Biol. Chem. 265, 20061-20064, 1990
 A:Title: Molecular cloning of the fMet-Leu-Phe receptor from neutrophils.
 A:Reference number: A23669; MUID:91056034
 A:Accession: A23669
 A:Molecule type: mRNA
 A:Residues: 1-354 <THO>
 A:Cross-references: GB:M58021; GB:J05705; NID:g165442; PIDN:AAA31377.1; PID:g165443
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: G protein-coupled receptor; glycoprotein; membrane protein; neutrophil

Query Match 29.8%; Score 564.5; DB 2; Length 354;
 Best Local Similarity 37.7%; Pred. No. 4.6e-40;
 Matches 126; Conservative 65; Mismatches 108; Indels 35; Gaps 9;

QY 38 YLYRIAYSLICVLGNILVITFAFYKKARSMTDVYLLNMAIADILFVLTPFWAVSH 97
 Db 45 YVWVYIYALVFLSLGNSLVMLVILYSRSNRSVTDVYLLNLAMA-----PAPCPDH 96
 QY 98 A----TCGAWV-FSNATCKLLKGIYAINFCNGLMLLTFCISMDRYIAIVQATKSFRLRSRT 151
 Db 97 AYLGKQKRLDFTPLCKVSVLKEVNFYSGLILLACISVDRIYLAIVOSTRTLTQKRHL 156
 QY 152 LPRSKIIICLVWGLSVIISSTFVNQKYN-TQGSVCEPKYQTVS-EPIRWKLLMLGLE 209
 Db 157 V---KFCILGIWALSLLSLPFLERQVSPNNSPVC---YEDLGHNTAKCMVLRILP 210
 QY 210 LLFGFFFLPMFIFCYTIVKTLVQAQNSKRHKAIRVIAVVLVFLACIAPHNMLLV-T 268
 Db 211 HTFGFIPLLVLMFCYGTTLTFLQAHMGQKRAMRVFAVVLIFLCLWLPYNLVLLADT 270
 QY 269 AANLGMNRSQSEKLGITKTVTEVLAFLHCLNPNVLYAFIQGKFRNYFLKILKLCWV 328
 Db 271 LMRTHVIOETCORRNELDRALDATEILGLHSLNPIIYAFITQCNFRNGFLKMLAARGLI 330
 QY 329 RRYKSSGFSAGRYSENISROTSETADNDNASS 362
 Db 331 SKEFLTR-----HRTVSTSSSTNVPS 352

RESULT 15
 A45177

chemokine (C-C) receptor 1 - human
 N:Alternate names: C-C CKR-1; macrophage inflammatory protein-1-alpha receptor
 C:Species: Homo sapiens (man)
 C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 13-Aug-1999
 C:Accession: A45177; I55671
 R:Neote, K.; DiGregorio, D.; Mak, J.Y.; Horuk, R.; Schall, T.J.
 Cell 72, 415-425, 1993
 A:Title: Molecular cloning, functional expression, and signaling characteristics of a
 A:Reference number: A45177; MUID:93161416
 A:Accession: A45177
 A>Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-355 <NEO>
 A:Cross-references: GB:L10918; NID:g292416; PIDN:AAA36543.1; PID:g292417
 A:Experimental source: HL60 cells
 A>Note: sequence extracted from NCBI backbone (NCBIP:124876)
 R:Gao, J.
 J. Exp. Med. 177, 1421-1427, 1993
 A:Title: Structure and functional expression of the human macrophage inflammatory 1 a
 A:Reference number: I55671; MUID:93240122
 A:Accession: I55671
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-355 <RES>
 A:Cross-references: GB:L10918; NID:g292416; PIDN:AAA36543.1; PID:g292417
 C:Genetics:
 A:Gene: GDB:CMKBR1; CMKR-1
 A:Cross-references: GDB:138446; OMIM:601159
 A:Map position: 3p21-3p21
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: disulfide bond; G protein-coupled receptor; glycoprotein; phosphoprotein;
 F:36-60/Domain: transmembrane #status predicted <TM1>
 F:71-91/Domain: transmembrane #status predicted <TM2>
 F:108-129/Domain: transmembrane #status predicted <TM3>
 F:147-171/Domain: transmembrane #status predicted <TM4>
 F:205-223/Domain: transmembrane #status predicted <TM5>
 F:240-264/Domain: transmembrane #status predicted <TM6>
 F:288-305/Domain: transmembrane #status predicted <TM7>
 F:5/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:24-273,106-183/Disulfide bonds: #status predicted
 F:345/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted

Query Match 28.9%; Score 547.5; DB 2; Length 355;
 Best Local Similarity 36.4%; Pred. No. 1.2e-38;
 Matches 120; Conservative 69; Mismatches 116; Indels 25; Gaps 10;

QY 44 YSLICVLGNILVITFAFYKKARSMTDVYLLNMAIADILFVLTPFWAVSHATGAWV 103
 Db 41 YSLVFVIGLVGNILVVLVLYVQYKRLKNTSIYLLNLALISDLLFLTPFWIDYKLDQDV 100
 QY 104 FSNATCKLLKGIYAINFCNGLMLLTFCISMDRYIAIVQATKSFRLRSRTLPKSKILVW 163
 Db 101 FGDAMCKILSGFYTYGLYSEIFFIILLTIDRYLAIVHAV--FALRAETVTFGVTISI 158
 QY 164 GLSVIISSTFVNQKNTQSDVCEPKYQTVS-----EPIR-WKLLMLGLEL-LFGFFI 216
 Db 159 ALAILASMPGLYFSK---TQ---WEFTHHTCSLHFHESLREWKLFQ-ALKNLFLGLV 210
 QY 217 PLFMFIPCYTIVKTLVQAQNSKRHKAIRVIAVVLVFLACIAPHNMLLVTAANLGMN 276
 Db 211 PLLVMIICTYGIKILLRRPNEKSKAVRLIFVIMIIFFLFTWTPYNTILISVQDFLFT 270
 QY 277 RSCQSEKLGITKTVTEVLAFLHCLNPNVLYAFIQGKFRNYFLKILKDLWCVR---RKYK 333
 Db 271 HECEQSRHLDLAVQVTEVIATHCVCNPNVYAFVGERFRKY----LQLPFRRVAVHLVK 326
 QY 334 SSGFSCAGRYSENISROTSETADNDNASS 363
 Db 327 WLPFLSVDRIL-ERVSTSPSTGEHLSAGE 355

Search completed: May 23, 2001, 15:31:57
Job time: 504 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 23, 2001, 15:25:29 ; Search time 62.39 Seconds
(without alignments)
200.405 Million cell updates/sec

Title: US-08-887-977-10

Perfect score: 1894

Sequence: 1 MFSTPVKILQCSILHITQL.....NISQTSADNDNASPTM 365

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1670	88.2	374	1	CCR6_HUMAN
2	1375.5	72.6	367	1	CCR6_MOUSE
3	682	36.0	378	1	CCR7_HUMAN
4	682	36.0	378	1	CCR7_MOUSE
5	666.5	35.2	350	1	IL8A_PANTR
6	663.5	35.0	350	1	IL8A_GORGO
7	662	35.0	350	1	IL8A_HUMAN
8	654	34.5	355	1	IL8A_RABIT
9	645	34.1	356	1	IL8B_CANFA
10	644.5	34.0	360	1	IL8B_BOVIN
11	636.5	33.6	358	1	IL8B_RABIT
12	631.5	33.3	353	1	IL8B_PANTR
13	629.5	33.2	353	1	IL8B_MACMU
14	629.5	33.2	360	1	IL8B_HUMAN
15	623.5	32.9	353	1	IL8B_GORGO
16	613.5	32.4	369	1	CCR9_MOUSE
17	610.5	32.2	360	1	CCR4_HUMAN
18	610	32.2	349	1	IL8A_RAT
19	604.5	31.9	359	1	IL8B_RAT
20	598.5	31.6	342	1	BONZ_CERAE
21	595.5	31.4	343	1	BONZ_MACMU
22	594.5	31.4	342	1	BONZ_MACNE
23	593.5	31.3	357	1	CCR9_HUMAN
24	580.5	30.6	342	1	BONZ_HUMAN
25	580.5	30.6	359	1	IL8B_MOUSE
26	574.5	30.3	360	1	CCR4_MOUSE
27	571.5	30.2	359	1	CCR3_MOUSE
28	565.5	29.9	359	1	CCR3_RAT
29	558	29.5	358	1	CCR3_CAVPO
30	551	29.1	354	1	CCR5_RAT
31	548.5	29.0	373	1	CCR2_RAT
32	547.5	28.9	355	1	CCR1_HUMAN
33	546.5	28.9	352	1	CCR5_CERTO

34	546	28.8	373	1	CCR2_MOUSE	P51683 mus musculu
35	539.5	28.5	368	1	CCR3_HUMAN	P49682 homo sapien
36	538	28.4	354	1	C3X1_RAT	P35411 rattus norv
37	537.5	28.4	352	1	CCR5_CERAE	P56493 cercopithec
38	537.5	28.4	352	1	CCR5_MACMU	P79436 macaca mula
39	536.5	28.3	352	1	CCR5_PAPHA	P56441 papio hamad
40	536.5	28.3	374	1	CCR2_HUMAN	P41597 homo sapien
41	534	28.2	354	1	CCR5_MOUSE	P51682 mus musculu
42	533.5	28.2	352	1	CCR5_PYGNE	O97882 pygathrix n
43	532.5	28.1	352	1	CCR5_PYGBI	O97880 pygathrix b
44	532.5	28.1	352	1	CCR5_TRAFR	O97878 trachypithe
45	532.5	28.1	352	1	CCR5_TRAPH	O97879 trachypithe

ALIGNMENTS

RESULT 1

ID	CCR6_HUMAN	STANDARD:	PRT;	374 AA.
AC	P51684; Q92846; P78553;			
DT	01-OCT-1996 (Rel. 34, Created)			
DT	15-JUL-1998 (Rel. 36, Last sequence update)			
DT	01-OCT-2000 (Rel. 40, Last annotation update)			
DE	C-C CHEMOKINE RECEPTOR TYPE 6 (C-C CCR-6) (CCR-6) (LARC RECEPTOR) (GPR-CY4) (GPCRY4) (CHEMOKINE RECEPTOR-LIKE 3) (CCR-L3) (DRY6).			
DE	CCR6 OR CMKBR6 OR STRL22 OR GPR29 OR CCR13.			
GN	Homo sapiens (Human).			
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A. AND FUNCTION.			
RX	MEDLINE=97313465; PubMed=9169459;			
RA	Baba M., Imai T., Nishimura M., Kakizaki M., Takagi S., Hieshima K.,			
RA	Nomiyama H., Yoshie O.;			
RT	"Identification of CCR6, the specific receptor for a novel			
RT	lymphocyte-directed CC chemokine LARC.";			
RL	J. Biol. Chem. 272:14893-14898(1997).			
[2]				
RN	SEQUENCE FROM N.A.			
RP	SEQUENCE FROM N.A.			
RA	Lautens L.L., Modi W., Bonner T.I.;			
RL	Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.			
[3]				
RN	SEQUENCE FROM N.A.			
RP	MEDLINE=97040707; PubMed=8886020;			
RX	Zaballos A., Varona R., Gutierrez J., Lind P., Marquez G.;			
RA	"Molecular cloning and RNA expression of two new human chemokine			
RT	receptor-like genes.";			
RL	Biochem. Biophys. Res. Commun. 227:846-853(1996).			
[4]				
RN	SEQUENCE FROM N.A.			
RP	SEQUENCE FROM N.A.			
RA	McCoy R., Perlmutter D.H.;			
RL	Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.			
[5]				
RN	SEQUENCE FROM N.A.			
RP	MEDLINE=97224503; PubMed=9070937;			
RA	Liao F., Lee H.-H., Farber J.M.;			
RT	"Cloning of STRL22, a new human gene encoding a G-protein-coupled			
RT	receptor related to chemokine receptors and located on chromosome			
RT	6q27.";			
RL	Genomics 40:175-180(1997).			
CC	-1- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-3-			
CC	ALPHA/LARC AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE			
CC	INTRACELLULAR CALCIUM IONS LEVEL.			
CC	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.			
CC	-1- TISSUE SPECIFICITY: SPLEEN, LYMPH NODES, APPENDIX, AND FETAL			
CC	NATURAL KILLER CELLS, MONOCYTES, OR GRANULOCYTES.			
CC	-1- INDUCTION: INTERLEUKIN-2.			
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.			
CC	-1- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-6 IS THE INITIATOR.			

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DR EMBL; U45984; AAB62714.1; -
 DR EMBL; 279784; CAB02144.1; ALT_INIT.
 DR EMBL; U60000; AAB06949.1; -
 DR EMBL; U68030; AAC51124.1; -
 DR EMBL; U68032; AAC51125.1; -
 DR HSSP; P34996; 1DDD.
 DR GCRDB; GCR_1037; -
 DR GCRDB; GCR_1075; -
 DR GCRDB; GCR_1906; -
 DR GCRDB; GCR_1919; -
 DR GCRDB; GCR_1941; -
 DR GCRDB; GCR_2110; -
 DR MIM; 601835; -
 DR InterPro; IPR000276; -
 DR Pfam; PF00001; 7tm1.1; 1.
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PROSITE; PS00237; G-PROTEIN_RECEP_FL_1; 1.
 DR PROSITE; PS0262; G-PROTEIN_RECEP_FL_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 47
 FT TRANSMEM 48 74
 FT DOMAIN 75 83
 FT TRANSMEM 84 104
 FT DOMAIN 105 119
 FT TRANSMEM 120 141
 FT DOMAIN 142 159
 FT TRANSMEM 160 180
 FT DOMAIN 181 211
 FT TRANSMEM 212 238
 FT DOMAIN 239 254
 FT TRANSMEM 255 279
 FT DOMAIN 280 303
 FT TRANSMEM 304 321
 FT DOMAIN 322 374
 FT DISULFID 118 197
 FT CARBOHYD 7 7
 FT CONFLICT 23 23 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CONFLICT 60 60 G -> A (IN REF. 4).
 FT CONFLICT 74 74 Y -> N (IN REF. 4).
 FT CONFLICT 86 86 L -> V (IN REF. 4).
 FT CONFLICT 164 164 S -> T (IN REF. 5).
 FT CONFLICT 182 182 T -> S (IN REF. 4).
 FT CONFLICT 192 192 Q -> L (IN REF. 4).
 FT CONFLICT 206 206 E -> V (IN REF. 4).
 FT CONFLICT 225 225 I -> F (IN REF. 4).
 FT CONFLICT 370 374 SSFTM -> VLVHVIIES (IN REF. 4).
 SQ SEQUENCE 374 AA; 42494 MW; D7F963534E990BC4 CRC64;

Query Match 88.2%; Score 1670; DB 1; Length 374;
 Best local Similarity 89.6%; Pred. No. 4.2e-99;
 Matches 328; Conservative 8; Mismatches 10; Indels 20; Gaps 2;

QY 2 ESTPVKILC--QSILHITQILRCYCPCRRSSSPGLYRYATYSICVLGLGNILVW 59
 DB 27 YSVDEMLLCISQEVRFGRFV-----PIAYSICVFGLLGNILVW 68
 QY 60 ITFAFYKARSMTDVLNMAIADILVLTLPFAVSHATCAWVFSNATCKLLKGIYAIN 119
 DB 69 ITFAFYKARSMTDVLNMAIADILVLTLPFAVSHATCAWVFSNATCKLLKGIYAIN 128
 QY 120 FNCGMLLLTCISMDRYIAIVQATKSPFLRSRTLPKRSKICLVVWGLSVIISSTFTVFNQK 179
 DB 129 FNCGMLLLTCISMDRYIAIVQATKSPFLRSRTLPKRSKICLVVWGLSVIISSTFTVFNQK 188

QY 180 YNTQSDVCEPKYQTVSEPIRWKLLMGLLELFGFFIPLMFICYTFIVKTLVQAQNSK 239
 DB 189 YNTQSDVCEPKYQTVSEPIRWKLLMGLLELFGFFIPLMFICYTFIVKTLVQAQNSK 248
 QY 240 RHKAIRVITAVLVFLACQIPHNMLLVTAANLGKNNRSCQSEKLGITYKTVTEVLAFLH 299
 DB 249 RHKAIRVITAVLVFLACQIPHNMLLVTAANLGKNNRSCQSEKLGITYKTVTEVLAFLH 308
 QY 300 CCLNPVLYAFIGOKFERNYELKILKDLWCVRRYKYSKSGSCAGRYSENISQTSQTDNDN 359
 DB 309 CCLNPVLYAFIGOKFERNYELKILKDLWCVRRYKYSKSGSCAGRYSENISQTSQTDNDN 368
 QY 360 ASSFTM 365
 DB 369 ASSFTM 374

RESULT 2
 CKR6_MOUSE
 ID CKR6_MOUSE STANDARD; PRT: 367 AA.
 AC 054689;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE C-C CHEMOKINE RECEPTOR TYPE 6 (C-C CKR-6) (CC-CKR-6) (CCR-6) (KY411).
 GN CCR6 OR CMKBR6.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Yanagihara S., Komura E., Yamauchi Y.;
 RT "Mouse G protein-coupled receptor KY411.";
 RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-99077268; PubMed-9862452;
 RA Varona R., Zaballios A., Gutierrez J., Martin P., Roncal F.,
 RA Albar J.P., Ardavin C., Marquez G.;
 RT "Molecular cloning, functional characterization and mRNA expression
 RT analysis of the murine chemokine receptor CCR6 and its specific ligand
 RT MIP-3alpha.";
 RL FEBS Lett. 440:188-194(1998).
 CC -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-3-
 CC ALPHA/LARC AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE
 CC INTRACELLULAR CALCIUM IONS LEVEL.
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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DR EMBL; AB009369; BAA23776.1; -
 DR EMBL; AJ222714; CAA10956.1; -
 DR MGD; MGI:1333797; Cmkbr6.
 DR InterPro; IPR000276; -
 DR Pfam; PF00001; 7tm1.1; 1.
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PROSITE; PS00237; G-PROTEIN_RECEP_FL_1; 1.
 DR PROSITE; PS0262; G-PROTEIN_RECEP_FL_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 39
 FT TRANSMEM 40 66
 FT DOMAIN 67 75
 FT TRANSMEM 76 96
 FT DOMAIN 97 111
 FT EXTRACELLULAR (POTENTIAL).
 FT CYTOPLASMIC (POTENTIAL).
 FT EXTRACELLULAR (POTENTIAL).

Db 63 IMYSIIICVGLGNGWLVITIIYFKRLKMTDTYLLNLAVALADILFLTLFPWYS-AAKS 121
 Qy 102 WYFSNATCKLLKGIYAINFCMGLLTTCISMDRYIAIVQATKFRSLRSTLPKSIICLV 161
 Db 122 WYGVHFKLFIAYIKMSFSGMLLLCISIDRYAIVQASVHRHRRVLLSKLSCVG 181
 Qy 162 VNGLSVIISSTVFVN--QKYNQSGDVCPEPKYQTVSEPIRWKLLMLGLLELFGFFIPLM 219
 Db 182 IWLATVLSIPELLYSDLRSSSEQAMR-----SLITEHVEAFITIQVAQWVGFLVPLL 237
 Qy 220 FMIFCYTFIVKTLVQAOQNSKRHKAIRVIAVLFVFLACQIPHN-VWLLVTAANLGNKMS 278
 Db 238 AMSFCYLVIIIRTLQARNFERNKAIRVIAVVFVIFVQLPYNGVLAQTVANFNITSST 297
 Qy 279 COSEKLGIVTKTVTEVLAFLHCCNPVLVAFIGOKFRNYELKILKDLWCVRKYSKSGFS 338
 Db 298 CELSQNLNAYDVITYSLACVRCVNFVLYAFIGVGRNDLFLKDLGCLGSLQSLROWSS 357
 Qy 339 C-AGRYSENISROTSET 354
 Db 358 CRHRRSSMSVEAETTT 375

RESULT 4
 ID CKR7_MOUSE STANDARD; PRT; 378 AA.
 AC P47774;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE C-C CHEMOKINE RECEPTOR TYPE 7 PRECURSOR (C-C CKR-7) (CCR-7)
 DE (MIP-3 BETA RECEPTOR) (EBV-INDUCED G PROTEIN-COUPLED RECEPTOR 1)
 DE (EB1).
 GN CKR7 OR CMKBR7 OR EB1 OR EB1H.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-B6/CBA; TISSUE=Thymus;
 RX MEDLINE=95154835; PubMed=7851893;
 RA Schweickart V.L., Raport C.J., Godiska R., Byers M.G., Eddy R.L. Jr.,
 RA Shows T.B., Gray P.W.;
 RT "Cloning of human and mouse EB1, a lymphoid-specific
 RT G-protein-coupled receptor encoded on human chromosome 17q12-q21.2.";
 RL Genomics 23:643-650(1994).
 CC -!- FUNCTION: RECEPTOR FOR THE MIP-3-BETA CHEMOKINE. PROBABLE MEDIATOR
 CC OF EBV EFFECTS ON B LYMPHOCYTES OR OF NORMAL LYMPHOCYTE FUNCTIONS.
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 CC -----
 DR EMBL; L31580; AAA74232.1;
 DR MGD; MGI:103011; Cmkbr7.
 DR InterPro; IPR000276;
 DR InterPro; IPR001718;
 DR Pfam; PF00001; 7cm1; 1.
 DR PRINTS; PR00237; GPCRHHODOPS.N.
 DR PRINTS; PR00641; CHEMOKINER7.
 DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL1; 1.
 DR PROSITE; PS00262; G-PROTEIN RECEPTOR FL2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 24 POTENTIAL.
 FT CHAIN 25 378 C-C CHEMOKINE RECEPTOR TYPE 7.

FT DOMAIN 25 59
 FT TRANSSEM 60 86
 FT DOMAIN 87 95
 FT TRANSSEM 96 116
 FT TRANSSEM 117 130
 FT TRANSSEM 131 152
 FT TRANSSEM 153 170
 FT TRANSSEM 171 191
 FT TRANSSEM 192 219
 FT TRANSSEM 220 247
 FT TRANSSEM 248 263
 FT TRANSSEM 264 289
 FT TRANSSEM 290 313
 FT TRANSSEM 314 331
 FT TRANSSEM 332 378
 FT CARBOHYD 36 36
 FT DISULFID 129 210
 SQ SEQUENCE 378 AA; 42941 MW; ACBIA422CF54AA54 CRC64;

Query Match 36.0%; Score 682; DB 1; Length 378;
 Best Local Similarity 38.8%; Pred. No. 9.9e-37;
 Matches 145; Conservative 76; Mismatches 123; Indels 30; Gaps 6;
 Qy 5 PVKIIQCSTLHITQLILRCYC-----APCRSG--SSPGYLYR 41
 Db 6 PRKNVVLVALLVIFQV---CFQDEVTDDYIGENTTVDTLVESVCFKKDVRNFKAWFLP 62
 Qy 42 IAYSLICVLGGLGNILVVITFAFYKARSMTDVLNNMAIDILFVLTLPWYVSHATGA 101
 Db 63 LMYSVIGFVGLGNGVLVITFYFKRLKMTDTYLLNLAVALADILFLTLFPWYSEAK-S 121
 Qy 102 WYFSNATCKLLKGIYAINFCMGLLTTCISMDRYIAIVQATKFRSLRSTLPKSIICLV 161
 Db 122 WYGVHFKLFIAYIKMSFSGMLLLCISIDRYAIVQASVHRHRRVLLSKLSCVG 181
 Qy 162 VNGLSVIISSTVFVNQKYNQSGDVCPEPKYQTVSEPIRWKLLMLGLLELFGFFIPLMFM 221
 Db 182 IWLATVLSIPELLYSGLKNSGEDTL--RCSLYSAQVEALITTIQVAQWVGFLVPMLAM 239
 Qy 222 IFCTYTFIVKTLVQAOQNSKRHKAIRVIAVLFVFLACQIPHN-VWLLVTAANLGNKMSRQ 280
 Db 240 SFCYLVIIIRTLQARNFERNKAIRVIAVVFVIFVQLPYNGVLAQTVANFNITSNCSCE 299
 Qy 281 SEKLGIVTKTVTEVLAFLHCCNPVLVAFIGOKFRNYELKILKDLWCVRKYSKSGFS 340
 Db 300 TSKQNLNAYDVITYSLASVRCVNFVLYAFIGVGRNDLFLKDLGCLGSLQSLROWSSCR 359
 Qy 341 GRYSENISROTSET 354
 Db 360 HVRNASVMEAEET 373

RESULT 5
 ID IL8A_PANTR STANDARD; PRT; 350 AA.
 AC P55920;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DE HIGH AFFINITY INTERLEUKIN-8 RECEPTOR A (IL-8R A) (IL-8 RECEPTOR TYPE
 DE 1) (CXCR-1) (CDW128).
 GN IL8RA OR CXCR1.
 OS Pan troglodytes (Chimpanzee).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
 OX NCBI_TaxID=9598;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96175151; PubMed=9110929;
 RA Alvarez V., Coto E., Setien F., Gonzalez S., Gonzalez-Roces S.,
 RA Lopez-Larrea C.;
 RT "Characterization of interleukin-8 receptors in non-human primates.";

FT TRANSMEM 286 308 7 (POTENTIAL),
 FT DOMAIN 309 350 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 3 3 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 16 16 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT DISULFID 110 187 BY SIMILARITY.
 SQ SEQUENCE 350 AA; 39790 MW; DB99591CD6C10757 CRC64;
 Query Match 35.0%; Score 663.5; DB 1; Length 350;
 Best Local Similarity 41.2%; Pred. No. 1.4e-35;
 Matches 140; Conservative 66; Mismatches 111; Indels 23; Caps 8;
 QY 27 APCR-BSGSSPGYLYRAYSLICVLGLGLNGLVITFAFYKKARSMYDVLNNAIADIL 85
 DB 28 SPCRLTETLNKVVIIITTAALFLLSLGSLVNLVLYSRGGRSVYDVLNLLALADLL 87
 QY 86 FVLTLPFAVSHATGAWFNSATCKLKGIAYNFNGCMILLTICISMDRYTAIVQAKSF 145
 DB 88 FALTLPWAASKYNG-WIFGTFLCKVSVLLKEVNFYSGLILLACISVDYRLAIVHATFTL 146
 QY 146 RLRSTPLPRSKICLVVWGLSVIISSTFVNOKYN-TQSDVCEPKYQTV-SEPIRWKL 203
 DB 147 TOKRHLY--KFVCLGCGWGLSMILSPFLFRQAYHPNNSPVC---YEVLGNDTAKWRM 200
 QY 204 LMLGLELLEFFFLPMFIFCYTFIVKTLVQAKSKRHKRAIRVIAVFLVFLACQIPHM 263
 DB 201 VLRLPHTFGFVPLRVMLFCYGTUFLPKAHMGOKHRAMRVIFAVVFLFLCWLPLYNL 260
 QY 264 VLIV-TAANLGNKRNRCQSEKLGTYKTVTFLAFLHCLNPLVYAFIGOKFRNYFLKIL 322
 DB 261 VLLADFLMTQVIOESCERNVNSLADATEILGFLHCLNPLIYAFIGQFRNGFLKIL 320
 QY 323 KDLWCVRKYKSGFGSCAGRYSENISQRTSETADNDNASS 362
 DB 321 AMHGLVSKFEFLAR-----HRVTSYTSSSVNVSS 348
 RESULT 7
 IL8A_HUMAN
 ID IL8A_HUMAN STANDARD; PRT; 350 AA.
 AC P25024;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE HIGH AFFINITY INTERLEUKIN-8 RECEPTOR A (IL-8R A) (IL-8 RECEPTOR TYPE
 DE 1) (CXCR-1) (CDW128A).
 GN IL8RA OR CXCR1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91368199; PubMed=1840701;
 RA Holmes W.E., Lee J., Kuang W.-J., Rice G.C., Wood W.I.;
 RT "Structure and functional expression of a human interleukin-8
 RT receptor".
 RL Science 253:1278-1280(1991).
 RN [2]
 RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
 RX MEDLINE=93205012; PubMed=8384312;
 RA Cerretti D.P., Kozlosky C.J., Vanden Bos T., Nelson N., Gearing D.P.,
 RA Beckmann M.P.;
 RT "Molecular characterization of receptors for human interleukin-8,
 RT GRO/melanoma growth-stimulatory activity and neutrophil activating
 RT peptide-2".
 RL Mol. Immunol. 30:359-367(1993).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93252387; PubMed=8486366;
 RA Mollereau C., Passage E., Mattei M.-G., Vassart G., Parmentier M.;
 RT "The high-affinity interleukin 8 receptor gene (IL8RA) maps to the
 RT 2q33-q36 region of the human genome: cloning of a pseudogene

(IL8RBP) for the low-affinity receptor.";
 Genomics 16:248-251(1993).
 [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=95014476; PubMed=7929358;
 RA Ahuja S.K., Shetty A., Tiffany H.L., Murphy P.M.;
 RT "Comparison of the genomic organization and promoter function for
 RT human interleukin-8 receptors A and B".
 J. Biol. Chem. 269:26381-26389(1994).
 [5]
 RP CHARACTERIZATION.
 RX MEDLINE=92355587; PubMed=1379593;
 RA Lee J., Horuk R., Rice G.C., Bennett G.L., Camerato T., Wood W.I.;
 RT "Characterization of two high affinity human interleukin-8
 RT receptors".
 J. Biol. Chem. 267:16283-16287(1992).
 [6]
 RP STRUCTURE BY NMR OF 9-29 IN COMPLEX WITH IL-8.
 RX MEDLINE=99148123; PubMed=10368283;
 RA Skelton N.J., Quan C., Reilly D., Lowman H.;
 RT "Structure of a CXC chemokine-receptor fragment in complex with
 RT interleukin-8".
 Structure 7:157-168(1999).
 CC -!- FUNCTION: RECEPTOR TO INTERLEUKIN-8, WHICH IS A POWERFUL
 CC NEUTROPHILS CHEMOTACTIC FACTOR. BINDING OF IL-8 TO THE RECEPTOR
 CC CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA A
 CC G-PROTEIN THAT ACTIVATES A PHOSPHATIDYLINOSITOL-CALCIUM SECOND
 CC MESSENGER SYSTEM. THIS RECEPTOR BINDS TO IL-8 WITH A HIGH AFFINITY
 CC AND TO MSGA (GRO) WITH A LOW AFFINITY.
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -!- DATABASE: NAME=PROW; NOTE=CD guide CDW128a entry;
 CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cdw128a.htm".
 CC -----
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 CC -----
 CC EMBL; L19591; AAB59436.1; -
 CC EMBL; L19592; AAA59160.1; -
 CC EMBL; M68932; AAA59159.1; -
 CC EMBL; X65858; CAA46688.1; -
 CC EMBL; U11870; AAA64378.1; -
 CC PIR; A39445; A39445.
 CC PDB; 1ILP; 23-DEC-98.
 CC PDB; 1ILQ; 23-DEC-98.
 CC GCRDb; GCR_0175; -
 CC GCRDb; GCR_0696; -
 CC GCRDb; GCR_1832; -
 CC GCRDb; GCR_1833; -
 CC GCRDb; GCR_2052; -
 CC MIM; 146929; -
 CC InterPro; IPR000174; -
 CC InterPro; IPR000276; -
 CC InterPro; IPR001355; -
 CC Pfam; PF00001; 7tm_1; 1.
 CC PRINTS; PR00237; GPCRHHODOPSN.
 CC PRINTS; PR00427; INTRLEUKIN8R.
 CC PRINTS; PR00572; INTRLEUKIN8R.
 CC PROSITE; PS00237; G_PROTEIN_RECEPT_F1_1; 1.
 CC PROSITE; PS00262; G_PROTEIN_RECEPT_F1_2; 1.
 CC G-protein coupled receptor; Transmembrane; Glycoprotein;
 CC Chemotaxis; Polymorphism; 3D-structure.
 FT DOMAIN 1 39 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 40 66 1 (POTENTIAL).
 FT DOMAIN 67 75 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 76 96 2 (POTENTIAL).
 FT DOMAIN 97 111 EXTRACELLULAR (POTENTIAL).

OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RA SEQUENCE FROM N.A.
 RA Li Y., Feng J., Templeton J.W.;
 RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: RECEPTOR TO INTERLEUKIN-8, WHICH IS A POWERFUL
 CC NEUTROPHILS CHEMOTACTIC FACTOR. BINDING OF IL-8 TO THE RECEPTOR
 CC CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA A
 CC G-PROTEIN THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND
 CC MESSENGER SYSTEM. THIS RECEPTOR BINDS TO IL-8 WITH A HIGH AFFINITY
 CC AND TO GRO/MGSA AND NAP-2 ALSO WITH A HIGH AFFINITY (BY
 CC SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC
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 CC EMBL; U19947; AAA84996.1;
 CC GCRDB; GCR_1224;
 CC InterPro; IPR000174;
 CC InterPro; IPR000276;
 CC Pfam; PF00001; 7tm.1; 1.
 CC PRINTS; PR00237; GPCRHHODOPS.
 CC PRINTS; PR00427; INTRLEUKIN8.
 CC PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 CC PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
 CC G-protein coupled receptor; Transmembrane; Glycoprotein;
 CC Chemotaxis.
 CC DOMAIN 1 48 EXTRACELLULAR (POTENTIAL).
 CC TRANSSEM 49 75 1 (POTENTIAL).
 CC DOMAIN 76 84 2 (POTENTIAL).
 CC TRANSSEM 85 105 2 (POTENTIAL).
 CC DOMAIN 106 120 EXTRACELLULAR (POTENTIAL).
 CC TRANSSEM 121 142 3 (POTENTIAL).
 CC DOMAIN 143 163 3 (POTENTIAL).
 CC TRANSSEM 164 183 4 (POTENTIAL).
 CC DOMAIN 184 208 EXTRACELLULAR (POTENTIAL).
 CC TRANSSEM 209 231 5 (POTENTIAL).
 CC DOMAIN 232 251 6 (POTENTIAL).
 CC TRANSSEM 252 273 6 (POTENTIAL).
 CC DOMAIN 274 294 7 (POTENTIAL).
 CC TRANSSEM 295 315 7 (POTENTIAL).
 CC DOMAIN 316 360 7 (POTENTIAL).
 CC TRANSSEM 360 406 7 (POTENTIAL).
 CC DISULFID 10 10 N-LINKED (GLCNAC...) (POTENTIAL).
 CC CARBOHYD 24 24 N-LINKED (GLCNAC...) (POTENTIAL).
 CC SEQUENCE 360 AA; 40625 MW; 9A7F70C982A632D1 CRC64;
 SQ
 Query Match 34.0%; Score 644.5; DB 1; Length 360;
 Best Local Similarity 42.8%; Pred. No. 2.2e-34;
 Matches 142; Conservative 57; Mismatches 112; Indels 21; Gaps 9;
 QY 27 APCRRSSSPG-YLYRTAIVSLVGLGNILVITFAFYKKARSMTDYLNNMAIADIL 85
 DB 37 SPCEISTETLNKAVVVIDALVFLLSLLGNSLVMLVILYSRIGRSVTDYLLNLAADLL 96
 QY 86 FVLTLFWANSHATGAWVFSNATKLLKGIYAINFCGMLLTCTISMDRYIAIVQATKSF 145
 DB 97 FAMLPLIWTASKAG-WVFGTPLCKVWSLLKEVNFYSGILLACISMDRYLAIVHAT--- 152
 QY 146 RLRSRTLPSS---KILLVWGLSVILSSSTFVFNQKYNTOGSD-VCEPKYQTV-SEPI 199
 DB 153 ----RLTQTKWHVVKFICGLWALSVAIPLPIFIREAYQPPYSDLVC---YEDLGANTT 205
 QY 200 RWKLLMLGLELFGFFIPLMEMIFCYTFIVKTLVQAQNSKRHKAIKRVIAVVLVFLACQI 259

DB 206 KWRIMRVLPQTFGFLPLLVMLFCYGTFLTLFSAQMGHKKRAMRVFAVVLVFLCWL 265
 QY 260 PHNMVLLV-TAANLGKMRSCSEKLYGTVTVTVEVLAFLHCLLPVLYVAFTGQKFRNYF 318
 DB 266 PYNLVLIADTLMRHVIAETCORRNDIGRALDATEILFLHSCLNPLIYVFIGQKFRHGL 325
 QY 319 LKILKDLWCVRKY--KSSGFCAGRYSGNIS 348
 DB 326 LKIMAIHGLISKEFLAKDGRFSFVSSSGNIS 357
 RESULT 11
 IL8B_RABIT STANDARD; PRT; 358 AA.
 ID IL8B_RABIT
 AC P35344;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE HIGH AFFINITY INTERLEUKIN-8 RECEPTOR B (IL-8R B) (CXCR-2) (GRO/MGSA
 DE RECEPTOR).
 GN IL8RB OR CXCR2.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ALBINO; TISSUE=Blood;
 RX MEDLINE=94230294; PubMed=8175642;
 RA Prado G.N., Thomas K.M., Suzuki H., Larosa G.J., Wilkinson N.C.,
 RA Folco E., Navarro J.;
 RT "Molecular characterization of a novel rabbit interleukin-8 receptor
 RT isotype".
 RL J. Biol. Chem. 269:12391-12394(1994).
 CC -1- FUNCTION: RECEPTOR TO INTERLEUKIN-8, WHICH IS A POWERFUL
 CC NEUTROPHILS CHEMOTACTIC FACTOR. BINDING OF IL-8 TO THE RECEPTOR
 CC CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA A
 CC G-PROTEIN THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND
 CC MESSENGER SYSTEM. THE AFFINITY OF THIS RECEPTOR IS IL-8 >> NAP-2 >
 CC MGSA (GRO).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: EXPRESSED PREFERENTIALLY IN NEUTROPHILS.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC
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 CC
 CC EMBL; L24445; AAA31378.1;
 CC PIR; A53752; A53752.
 CC GCRDB; GCR_0861;
 CC InterPro; IPR000057;
 CC InterPro; IPR000174;
 CC InterPro; IPR000276;
 CC Pfam; PF00001; 7tm.1; 1.
 CC PRINTS; PR00237; GPCRHHODOPS.
 CC PRINTS; PR00427; INTRLEUKIN8.
 CC PRINTS; PR00573; INTRLEUKIN8R.
 CC PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 CC PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
 CC G-protein coupled receptor; Transmembrane; Glycoprotein;
 CC Chemotaxis.
 CC DOMAIN 1 46 EXTRACELLULAR (POTENTIAL).
 CC TRANSSEM 47 73 1 (POTENTIAL).
 CC DOMAIN 74 82 2 (POTENTIAL).
 CC TRANSSEM 83 103 2 (POTENTIAL).
 CC DOMAIN 104 118 3 (POTENTIAL).
 CC TRANSSEM 119 140 3 (POTENTIAL).

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FT DOMAIN 141 161 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 162 181 4 (POTENTIAL).
FT DOMAIN 182 206 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 207 229 5 (POTENTIAL).
FT DOMAIN 230 249 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 250 271 6 (POTENTIAL).
FT DOMAIN 272 292 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 293 313 7 (POTENTIAL).
FT DOMAIN 314 358 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 8 8 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 20 20 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 117 194 BY SIMILARITY.
SQ SEQUENCE 358 AA; 40632 MW; 6899716944D6126A CRC64;

Query Match 33.6%; Score 636.5; DB 1; Length 358;
Best Local Similarity 42.7%; Pred. No. 7.1e-34;
Matches 140; Conservative 59; Mismatches 116; Indels 13; Gaps 9;

QY 27 APCR-RSGSPGYLYRIAYSLICVLGLGNILVITFAFYKARSMTDVYLLNMAIADIL 85
Db 35 APCRSLETSYVLLITVILFLLSLGNSLVMLVILYSRSTCSVTDVYLLNMAIADIL 94
QY 86 FVLTPFWAVSHATGAWFVSNATCKLLKGIYAINFCGMLLLTCISMDRYIAIVQATKSF 145
Db 95 FATTLPIWAASKVHG-WTEGTPLCVKVSLVKEVNFYSGILLACISVDRLAIVHATRM 153
QY 146 RLRSFTPLRSKICLVVGLSVIISSTFVF-NQNTQGSVDCEPKYQTV-SEPIRWKL 203
Db 154 -::KRRHL--VKFICLSMWGVSILSLPILLFRNAIPPPNSPPVC---YEDMGNSTAKWRM 207
QY 204 LMLGLELFGFFIPLMFIMFYCTFIVKTLVQAQNSKRHRKAIIRVIAVVLVFLACQIPHNH 263
Db 208 VLRILPQTEGFIPLVLMVLCYVFTLRTLFAHMGQKHRAVRVFAVVLFLCWLPLN 267
QY 264 VLLV-TAANLGMNRSQSEKLGITYKTVTEVLAFHCLLNPLVYAFIGQKFRNYFKIL 322
Db 268 VLLTDTLMTHTVIOETCERRNDIDRALDATEILGFLHCLNPLIYAFIGQKFRNYGLKIL 327
QY 323 KDLWCVRKY--KSGFCAGRYSENI 348
Db 328 AAHLISKEFLAKESRPSVASSGNTS 355

RESULT 12
IL8B_PANTR.
ID IL8B_PANTR STANDARD; PRT; 353 AA.
AC Q28807;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE HIGH AFFINITY INTERLEUKIN-8 RECEPTOR B (IL-8R B) (CXCR-2) (FRAGMENT).
GN IL8RB OR CXCR2.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96175151; PubMed=9110929;
RA Alvarez V., Coto E., Setien F., Gonzalez S., Gonzalez-Roces S.,
RA Lopez-Larrea C.;
RT "Characterization of interleukin-8 receptors in non-human primates.";
RL Immunogenetics 43:261-267(1996).
CC -!- FUNCTION: RECEPTOR TO INTERLEUKIN-8, WHICH IS A POWERFUL
CC NEUTROPHILS CHEMOTACTIC FACTOR. BINDING OF IL-8 TO THE RECEPTOR
CC CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA A
CC G-PROTEIN THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND
CC MESSENGER SYSTEM. THIS RECEPTOR BINDS TO IL-8 WITH A HIGH AFFINITY
CC AND TO GRO/MGSA AND NAP-2 ALSO WITH A HIGH AFFINITY.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC -----
DR EMBL; X91113; CAA62563.1;
DR HSP; P34996; IDDD.
DR InterPro; IPR000276;
DR Pfam; PF00001; 7tm_1; 1.
DR PROSITE; PS00237; G_PROTEIN_RECF1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECF1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Chemotaxis.
FT NON_TER 1 1.
FT DOMAIN <1 45 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 46 72 1 (POTENTIAL).
FT DOMAIN 73 81 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 82 102 2 (POTENTIAL).
FT DOMAIN 103 117 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 118 139 3 (POTENTIAL).
FT DOMAIN 140 160 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 161 180 4 (POTENTIAL).
FT DOMAIN 181 205 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 206 228 5 (POTENTIAL).
FT DOMAIN 229 248 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 249 270 6 (POTENTIAL).
FT DOMAIN 271 291 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 292 312 7 (POTENTIAL).
FT DOMAIN 313 >353 CYTOPLASMIC (POTENTIAL).
FT DISULFID 116 193 BY SIMILARITY.
FT CARBOHYD 19 19 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT NON_TER 353 353
SQ SEQUENCE 353 AA; 39998 MW; E745ACD9EC10C1E2 CRC64;

Query Match 33.3%; Score 631.5; DB 1; Length 353;
Best Local Similarity 43.4%; Pred. No. 1.4e-33;
Matches 132; Conservative 56; Mismatches 97; Indels 19; Gaps 8;

QY 27 APCR-RSGSPGYLYRIAYSLICVLGLGNILVITFAFYKARSMTDVYLLNMAIADIL 85
Db 34 APCPESELEINKYFVVIIVLYVLLSLGNSLVMLVILYSRVSVDVYLLNMAIADIL 93
QY 86 FVLTPFWAVSHATGAWFVSNATCKLLKGIYAINFCGMLLLTCISMDRYIAIVQATKSF 145
Db 94 FALTPIWAASKVNG-WIFGTFLCKVSVLLKEVNFYSGILLACISVDRLAIVHAT--- 149
QY 146 RLRSFTPLRS---KIICLVVWGLSVIISSTFVFENQK-YNTQGSVDCEPKYQTV-SEPI 199
Db 150 ----RITLQKRYLVKFCISLWGLSLALPVLLFRFVYSSNVSPAC---YEDMGNTA 202
QY 200 RWKLMLELLELFGFFIPLMFIMFYCTFIVKTLVQAQNSKRHRKAIIRVIAVVLVFLACQI 259
Db 203 NWRMLRLPQSGFIVPILLMFCYGTFLRTLFKAHMGQKHRAVRVFAVVLFLCWL 262
QY 260 PHNMVLLV-TAANLGMNRSQSEKLGITYKTVTEVLAFHCLLNPLVYAFIGQKFRNYF 318
Db 263 PYNVLLADTLMTQVIOETCERRNHNIRALDADTEILGILHCLNPLIYAFIGQKFRHGL 322
QY 319 LKIL 322
Db 323 LKIL 326

RESULT 13
IL8B_MACMU
ID IL8B_MACMU STANDARD; PRT; 353 AA.
AC Q28519;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT -----
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QY	146	RLRSTLPRS----	KIICLVWVGLSVIISSTTFVNOK-YNTQSGDVCEPKYQTV-SEPI	2599
			: : : : : : : : : : : :	
Db	150	---RTLTKRKYLVKFKICLSIWGLSLALLPVLFLFRRTVYSSNVSPAC---	YEDMGNTA	3120
QY	200	RWKLLMLGLLELFGFFIPMPMEIWCYTFIVKTLVQAQNSKREKHAIRVIAVVLVFLACQI	2599	
		: : : : : : : : : : : :		
Db	203	NWRMLRLRLDSQFGFIVPLLIMLCFYGTSLTLFLRAHMGOKHRAVRVIAVVLFLCLCWL	2620	
		: : : : : : : : : : : : :		
QY	260	PHNMYLLV-TAANGKMNRSQSEKLIGYTKTVTEVLAFLHCCCLNPVLIYAFIGOKFRNYF	3188	
		: : : : : : : : : : : : :		
Db	263	PYSVLLADTLMRQTQVIOETCERRNHIDRALDATEILGILHSLCNPLIYAFIGOKFRHGL	3222	
QY	319	LKIL 322		
Db	323	LKIL 326		
RESULT	14			
IL8B_HUMAN				
ID	IL8B_HUMAN	STANDARD;	PRT;	360 AA.
AC	P25025;			
DT	01-MAY-1992 (Rel. 22, Created)			
DT	01-FEB-1996 (Rel. 33, Last sequence update)			
DT	01-OCT-2000 (Rel. 40, Last annotation update)			
DE	HIGH AFFINITY INTERLEUKIN-8 RECEPTOR B (IL-8R B) (CXCR-2) (GRO/MGSA			
DE	RECEPTOR) (IL-8 RECEPTOR TYPE 2) (CDW128B).			
GN	IL8RB OR CXCR2.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxId=9606;			
RP	SEQUENCE FROM N.A.			
RP	MEDLINE=91368200; PubMed=1891716;			
RX	Murphy P.M., Tiffany H.L.;			
RA	"Cloning of complementary DNA encoding a functional human			
RT	interleukin-8 receptor.";			
RT	Science 253:1280-1283(1991).			
RL	[2]			
RP	SEQUENCE FROM N.A. AND CHARACTERIZATION.			
RP	MEDLINE=93205012; PubMed=8384312;			
RX	Cerretti D.P., Kozlosky C.J., Vanden Bos T., Nelson N., Gearing D.P.,			
RA	Beckmann M.P.;			
RT	"Molecular characterization of receptors for human interleukin-8,			
RT	GRO/melanoma growth-stimulatory activity and neutrophil activating			
RT	peptide-2.";			
RT	Mol. Immunol. 30:359-367(1993).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RP	MEDLINE=94209273; PubMed=7512557;			
RX	Sprengher H., Lloyd A.R., Lautens L.L., Bonner T.I., Kelvin D.J.;			
RA	"Structure, genomic organization, and expression of the human			
RT	interleukin-8 receptor B gene.";			
RT	J. Biol. Chem. 269:11065-11072(1994).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RP	TISSUE=Placenta;			
RC	MEDLINE=95014476; PubMed=79293358;			
RX	Ahuja S.K., Shetty A., Tiffany H.L., Murphy P.M.;			
RA	"Comparison of the genomic organization and promoter function for			
RT	human interleukin-8 receptors A and B.";			
RT	J. Biol. Chem. 269:26381-26389(1994).			
RN	[5]			
RP	CHARACTERIZATION.			
RP	MEDLINE=92355587; PubMed=1379593;			
RX	Lee J., Horuk R., Rice G.C., Bennett G.L., Camerato T., Wood W.I.;			
RA	"Characterization of two high affinity human interleukin-8			
RT	receptors.";			
RT	J. Biol. Chem. 267:16283-16287(1992).			
CC	-!- FUNCTION: RECEPTOR TO INTERLEUKIN-8, WHICH IS A POWERFUL			
CC	NEUTROPHILS CHEMOTACTIC FACTOR. BINDING OF IL-8 TO THE RECEPTOR			
CC	CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA			

FT	DOMAIN	229	248	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	249	270	6 (POTENTIAL).
FT	DOMAIN	271	291	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	292	312	7 (POTENTIAL).
FT	DOMAIN	313	>353	CYTOPLASMIC (POTENTIAL).
FT	DISULFID	116	193	BY SIMILARITY.
FT	CARBOHYD	19	19	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	NON_TER	353	353	
SQ	SEQUENCE	353 AA;	39919 MW;	1FF04E31A7E825E4 CRC64;
Query Match 32.9%; Score 623.5; DB 1; Length 353;				
Best Local Similarity 43.1%; Pred. No. 4.6e-33;				
Matches 131; Conservative 56; Mismatches 98; Indels 19; Gaps 8;				
Qy	27	APCR-RSGSSPGYRIAYSLICVLGLNLIVITFAFYKKARSTDDVYLLNMAIADIL	85	
Db	34	SPCEPESLEINKYFVVIYVALVFLLSLLGNSLVILYISRGVRSVTDVYLLNLALADLL	93	
Qy	86	FVLTLPFWAVSHATGAWFESNATCKLLKGIYAINFCNCGMLLLTCISMDRYIAIVQATKSF	145	
Db	94	FALTLPWAASKVNG-WIFGTFLCKVWSLLKEVNFYSGILLACISVDRYLAIVHAT---	149	
Qy	146	RLRSRTLPRS----KIICLVWGLSVIISSTFVFNOK-YNTOGSDVCEPKYQTV-SEPI	199	
Db	150	---RTLQKRYLVKRFICLSINGLSLLALPVLFRRTIYPSNVSPVC---YEDMGNTA	202	
Qy	200	RWKLMLGLELFGFPIPLMFIFCYTFIVKTIVQAQNSKRHKAIIRVIAVVLVFLACQI	259	
Db	203	NWRMLRLPQSGFGFIVPLIIMLFICYGFTLRTLFKAHMGOKHRAMRVIFAVWLIFLLCWL	262	
Qy	260	PHNMYLLV-TAANLGKMRSCOSEKLGITKTVTEVLAFHLHCLNPVLYAFIGOKERNYF	318	
Db	263	PYNVLLADTLMRTQVIQETCERRNHINQALDATEILGILHSCLNPLIYAFIGOKFCHGL	322	
Qy	319	LKIL	322	
Db	323	LKIL	326	

Search completed: May 23, 2001, 15:36:16
Job time: 647 sec

Result No.	Score	Query		Length	DB	ID	Description
		Match					
1	1365.5	72.1	367	11	Q9R1V0	Q9rlv0 homo musculus	
2	613.5	32.4	360	4	Q9ULY6	Q9uly6 homo sapien	
3	610.5	32.2	360	4	Q9ULY7	Q9uly7 homo sapien	
4	599.5	31.7	343	6	Q9N0Z0	Q9n0z0 cercocebus	
5	595.5	31.4	343	6	Q9X745	Q9xr45 macaca mula	
6	593.5	31.3	369	4	Q9U0Q6	Q9u0q6 homo sapien	
7	583.5	30.8	342	6	Q9RTV6	Q9rtv6 pan troglod	
8	578.5	30.5	368	13	O42444	O42444 oncorhynchu	
9	556	29.4	360	6	O18793	O18793 macaca mula	
10	548.5	29.0	373	11	O55193	O55193 rattus norv	
11	547.5	28.9	352	6	O77776	O77776 cercocebus	
12	547	28.9	352	6	Q9RTV44	Q9rtv44 cercopithec	
13	546.5	28.9	339	6	Q9RTUS4	Q9rtus4 lemur varie	
14	545.5	28.8	339	6	Q9RTUS3	Q9rtus3 lemur catta	
15	545.5	28.8	339	6	Q9RTUQ5	Q9rtuq5 erythrocebu	
16	543.5	28.7	339	6	Q9RTUQ3	Q9rtuq3 lemur catta	
17	542.5	28.6	339	6	Q9RTUQ6	Q9rtuq6 erythrocebu	
18	542.5	28.6	352	6	Q9RTV47	Q9rtv47 cercopithec	
19	541.5	28.6	339	6	Q9RTUS6	Q9rtus6 papio cynoc	

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Db 103 WYFSDALCKLMKGTAYVNFNCMGLLACISMDRYIAIVQATKSFVRVSRRTLTHSKVICVA 162
QY 162 WGLSVIISSTFVFNQKYNQTSVDCEPKYQTVSEPIRWKLLMLGLELFGFFIPLMF 221
Db 163 VWFISIISSPTFENKYYELQDQDCEPRYSVSEPTWKLLGLGLELFGFFIPLMF 222
QY 222 IFCYTFIVKTLVQAQNSKRHKAIRVIAVVLVFLACIQIPHNWVLLVTAANLGMKNSRCSQ 281
Db 223 VFCYLFIIKTLVQAQNSKRHKAIRVIAVVLVFLACIQIPHNWVLLVTAANTGVARSCST 282
QY 282 EKLICYTIVTVEFLAFLHCLAPLVYAFIGOKFRNRYFLAKLDLWCVRRKYSKSGFSCAG 341
Db 283 EKVLATYRNAEVLAFALHCLAPLVYAFIGOKFRNRYFLAKLDLWCVRRKYSKSGFSCAG 342
QY 342 RYSEN-ISQTSSETADNONSFTM 365
Db 343 VYSEYISQTSSETVENDNASSFTM 367

RESULT 2
ID Q9ULY6 PRELIMINARY; PRT; 360 AA.
AC Q9ULY6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE B-CHEMOKINE RECEPTOR CCR4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kato H., Tsuchiya N., Izumi S., Miyamasu M., Nakajima T., Kawasaki H.,
RA Hirai K., Tokunaga K.;
RT "New variations of human CC-chemokine receptors CCR3 and CCR4.";
RL Genes Immun. 1:97-104(1999).
DR EMBL; AB023891; BAA86968.1; -
DR INTERPRO; IPR000190; -
DR INTERPRO; IPR000248; -
DR INTERPRO; IPR000276; -
DR INTERPRO; IPR000355; -
DR INTERPRO; IPR001277; -
DR INTERPRO; IPR002236; -
DR INTERPRO; IPR002239; -
DR PFAM; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PRINTS; PR00241; ANGIOTENSINR.
DR PRINTS; PR00635; ANGIOTENSINR.
DR PRINTS; PR00645; LCR1ORPHANR.
DR PRINTS; PR00657; CCHEMOKINER.
DR PRINTS; PR01106; CHEMOKINER1.
DR PROSITE; PS01109; CHEMOKINER4.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
KW Receptor.
FT VARIANT 178 178 S -> C.
SQ SEQUENCE 360 AA; 41386 MW; AAF0EA3ADIEAF6D2 CRC64;

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Query Match 32.4%; Score 613.5; DB 4; Length 360;
Best Local Similarity 38.8%; Pred. NO. 1.3e-42;
Matches 135; Conservative 61; Mismatches 115; Indels 37; Gaps 10;

QY 28 PCRRSG-SSPGYLY-RIAYSLICVLGLNGLVITFAFYKKARSMTDYYLLNMAADIL 85
Db 28 PCTKEGKAFGELFPLPYLSLVFVGLGNSVVLVLFYKRLRSMTDYYLLNLAISDL 87

QY 86 FVLTLPEWAVSHATGAWVFNATCKLLKGIYAINFNCMGLLTCISMDRYIAIVQATKSF 145
Db 86 FVSLPFWGY-YAADOWVFGGLCKMISWMYLVGVGSIFFVWMLSIDRYLAIVHAV--F 144

QY 146 RLRSRTLPKRSKIICLVWGLSVIISSTFVFNQKYNQTSVDCEPKYQTVSEPIRWKLLM 205

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Db 145 SLRARTITYGVITSLATWSAVFASLPGLFLESTSYTERNHTYCKTKYSLNS--TTWKVLS 202
QY 206 LGLEL-LFGFFIPLMFIFCYTFIVKTLVQAQNSKRHKAIRVIAVVLVFLACIQIPHNW 264
Db 203 -SLEINILGLVPLIGIMLCYCSMIIRTLQHCNKKKNAKVMIFAVVVLFGFWPTPINV 261
QY 265 LLVTAANLGMKNSRCSQSEKLGITYTKTVTEVLAFLHCLNPNVLYAFIGOKFRNRYFLKILK 324
Db 262 LFLTELVELEVLQDCTFERYLDYAQATETELAFVHCCLNPIIYFFLGEKFKFYILQLFK- 320
QY 325 LMCVRRYKSSGFSACGR-----YSENI--SRQTSSETADND 358
Db 321 -----TCRGLVLCQYCGLLQIYSADTPSSSYTQSTMDHD 355

RESULT 3
ID Q9ULY7 PRELIMINARY; PRT; 360 AA.
AC Q9ULY7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE B-CHEMOKINE RECEPTOR CCR4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kato H., Tsuchiya N., Izumi S., Miyamasu M., Nakajima T., Kawasaki H.,
RA Hirai K., Tokunaga K.;
RT "New variations of human CC-chemokine receptors CCR3 and CCR4.";
RL Genes Immun. 1:97-104(1999).
DR EMBL; AB023889; BAA86966.1; -
DR INTERPRO; IPR000190; -
DR INTERPRO; IPR000248; -
DR INTERPRO; IPR000276; -
DR INTERPRO; IPR000355; -
DR INTERPRO; IPR001277; -
DR INTERPRO; IPR002236; -
DR INTERPRO; IPR002239; -
DR PFAM; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PRINTS; PR00241; ANGIOTENSINR.
DR PRINTS; PR00635; ANGIOTENSINR.
DR PRINTS; PR00645; LCR1ORPHANR.
DR PRINTS; PR00657; CCHEMOKINER.
DR PRINTS; PR01106; CHEMOKINER1.
DR PROSITE; PS01109; CHEMOKINER4.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
KW Receptor.
FT VARIANT 130 130 V -> L.
SQ SEQUENCE 360 AA; 41388 MW; F52DA1A8D9DA7DDB CRC64;

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Query Match 32.2%; Score 610.5; DB 4; Length 360;
Best Local Similarity 38.8%; Pred. NO. 2.3e-42;
Matches 135; Conservative 61; Mismatches 115; Indels 37; Gaps 10;

QY 28 PCRRSG-SSPGYLY-RIAYSLICVLGLNGLVITFAFYKKARSMTDYYLLNMAADIL 85
Db 28 PCTKEGKAFGELFPLPYLSLVFVGLGNSVVLVLFYKRLRSMTDYYLLNLAISDL 87

QY 86 FVLTLPEWAVSHATGAWVFNATCKLLKGIYAINFNCMGLLTCISMDRYIAIVQATKSF 145
Db 86 FVSLPFWGY-YAADOWVFGGLCKMISWMYLVGVGSIFFVWMLSIDRYLAIVHAV--F 144

QY 146 RLRSRTLPKRSKIICLVWGLSVIISSTFVFNQKYNQTSVDCEPKYQTVSEPIRWKLLM 205
Db 145 SLRARTITYGVITSLATWSAVFASLPGLFLESTSYTERNHTYCKTKYSLNS--TTWKVLS 202
QY 206 LGLEL-LFGFFIPLMFIFCYTFIVKTLVQAQNSKRHKAIRVIAVVLVFLACIQIPHNW 264

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Db 203 -SLEINILGLVPLGIMLCFCYSIIITLQHCNKKNAKVMIFAVVVVFLGFWTPNIV 261
 Qy 265 LLVTAANLGMNRQSEKRLIGTKVTVEVLAFHCLNPLVYAFIQKERNYFLKLKD 324
 Db 262 LPLETIVELEVQDCTFERYLDAIOATETLAFVHCLNPLIIFLGEKFKYILQLFK- 320
 Qy 325 LMCVRRKYKSGFSCAGR-----YSNI--SROTSETADND 358
 Db 321 -----TCRGLFVQCYCGLLIQIYSADTPSSSYTQSTMDHD 355

RESULT 4
 Q9N020 PRELIMINARY; PRT; 343 AA.
 AC Q9N020
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
 DE STRL33.
 OS Cercopithecus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
 OC Cercopitheidae; Cercopithecus.
 OC NCBI_TaxID=9531;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20261727; PubMed=10799581;
 RA Pohlmann S., Lee B., Meister S., Krumbiegel M., Leslie G., Doms R.W.,
 RA Kirchhoff F.;
 RT "Simian immunodeficiency virus utilizes human and sooty mangabey but
 not rhesus macaque STRL33 for efficient entry.";
 RL J. Virol. 74:5075-5082(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Pohlmann S., Lee B., Meister S., Krumbiegel M., Leslie G., Doms R.W.,
 RA Kirchhoff F.;
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF237559; AAF68392.1;
 SQ SEQUENCE 343 AA; 39588 MW; A75B7A0751C13455 CRC64;

Query Match 31.7%; Score 599.5; DB 6; Length 343;
 Best Local Similarity 34.7%; Pred. No. 1.8e-41;
 Matches 126; Conservative 77; Mismatches 107; Indels 53; Gaps 8;
 Qy 12 OSILHITOLILRCYCPCRRSGSPGYLYRIAYSLICVLGLNGLNVLVITFAFYKKARM 71
 Db 25 QDFLQFQKVFELPC-----MYLVFVCGLVGNSLVLSIFHYHKLQSL 66
 Qy 72 TDVYLINMAIADILFVLTPFWAVSHATGAVFNSATCKLLKGIAINFCGMLLTCTIS 131
 Db 67 TDVFLVNLPLADLVFVCTLPFWAYA-GIHEWIFGVQVCKTLGIVTYNFTYMLTCTIT 125
 Qy 132 MDRIYTAIVQATKSFRLSRSTLPRSKTICLVWGLSVIISSTFVFNQKYNQTSQDVCEPK 191
 Db 126 VDRFIVVVKATKAYNQAKRWGKVICLLIWIISLVSLPQIIYGNVFNLD-KLICRYH 184
 Qy 192 YQTVSEPIRWKLLMGLLELFGFFPLMFIMFYCTTIVKTLVQAQNSKRKAIRVIAV 251
 Db 185 DEEIS-----TVLATQMTLGFLLPMLMIVCYSVIILWISLVSLPQIIYGNVFNLD-KLICRYH 238
 Qy 252 LVFLACQPHNMLVLTAAANLGMNRQSE-----KLIGYTKVTVEVLAFHCLNPLV 307
 Db 239 AVFLTQTPFNVLKLI-----RSTHWEIYAMTSFHYTIIVTEAIVLACLNPLV 289
 Qy 308 AFIGOKFRNYFLKILKDLWC-----VRRKYKSGFSCAGRYSENI SROTSETADNDNASS 362
 Db 290 AFVSLKFRKNFKWLVKDICLPYLGVSQWKS-----SEDNKTFSASHNVEATSM 340
 Qy 363 FTM 365
 Db 341 FOL 343

RESULT 6
 Q9U0Q6 PRELIMINARY; PRT; 369 AA.

RESULT 5
 Q9XT45 PRELIMINARY; PRT; 343 AA.
 AC Q9XT45
 DT 01-NOV-1999 (TREMBlrel. 12, Created)
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
 DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
 DE CHEMOKINE RECEPTOR BONZO.
 GN STRL33
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
 OC Cercopitheidae; Macaca.
 OC NCBI_TaxID=9544;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Margulies B.J., Hauer D.A., Clements J.E.;
 RT "Identification of Thirteen Rhesus Macaque Chemokine Receptors.";
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF124380; AAD31419.1;
 DR INTERPRO; IPR000248;
 DR INTERPRO; IPR000276;
 DR INTERPRO; IPR000355;
 DR INTERPRO; IPR001277;
 DR INTERPRO; IPR002235;
 DR PFAM; PF00001; 7tm.1.1;
 DR PRINTS; PR00237; GPCRHDOPSN.
 DR PRINTS; PR00241; ANGIOTENSINR.
 DR PRINTS; PR00645; LCRIORPHANR.
 DR PRINTS; PR00657; CCHEMOKINER.
 DR PRINTS; PR01105; BONZOORPHANR.
 DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
 KW Receptor.
 SQ SEQUENCE 343 AA; 39423 MW; 48DB2544949EB83F CRC64;

Query Match 31.4%; Score 595.5; DB 6; Length 343;
 Best Local Similarity 34.7%; Pred. No. 3.7e-41;
 Matches 126; Conservative 76; Mismatches 108; Indels 53; Gaps 8;
 Qy 12 OSILHITOLILRCYCPCRRSGSPGYLYRIAYSLICVLGLNGLNVLVITFAFYKKARM 71
 Db 25 QDFLQFQKVFELPC-----MYLVFVCGLVGNSLVLSIFHYHKLQSL 66
 Qy 72 TDVYLINMAIADILFVLTPFWAVSHATGAVFNSATCKLLKGIAINFCGMLLTCTIS 131
 Db 67 TDVFLVNLPLADLVFVCTLPFWAYA-GIHEWIFGVQVCKTLGIVTYNFTYMLTCTIT 125
 Qy 132 MDRIYTAIVQATKSFRLSRSTLPRSKTICLVWGLSVIISSTFVFNQKYNQTSQDVCEPK 191
 Db 126 VDRFIVVVKATKAYNQAKRWGKVICLLIWIISLVSLPQIIYGNVFNLD-KLICRYH 184
 Qy 192 YQTVSEPIRWKLLMGLLELFGFFPLMFIMFYCTTIVKTLVQAQNSKRKAIRVIAV 251
 Db 185 DEEIS-----TVLATQMTLGFLLPMLMIVCYSVIILWISLVSLPQIIYGNVFNLD-KLICRYH 238
 Qy 252 LVFLACQPHNMLVLTAAANLGMNRQSE-----KLIGYTKVTVEVLAFHCLNPLV 307
 Db 239 AVFLTQTPFNVLKLI-----RSTHWEIYAMTSFHYTIIVTEAIVLACLNPLV 289
 Qy 308 AFIGOKFRNYFLKILKDLWC-----VRRKYKSGFSCAGRYSENI SROTSETADNDNASS 362
 Db 290 AFVSLKFRKNFKWLVKDICLPYLGVSQWKS-----SEDNKTFSASHNVEATSM 340
 Qy 363 FTM 365
 Db 341 FOL 343

RESULT 6
 Q9U0Q6 PRELIMINARY; PRT; 369 AA.

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AC Q9U0Q6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE CHEMOKINE RECEPTOR CCR9 (CC CHEMOKINE RECEPTOR 9A).
GN CCR9.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Zaballos A., Gutierrez J., Varona R., Ardavin C., Marquez G.;
RT "Identification of the orphan chemokine receptor GPR-9-6 as CCR9, the
RT receptor for the chemokine TECK."
RL J. Immunol. 162:5671-5675(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA Yu C.-R., Peden K.W.C., Farber J.M.;
RT "CCR9A and CCR9B, Two Receptors for the Chemokine CCL25 (TECK/Ckbeta-
RT 15)."
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ132337; CAB43477.1; -
DR EMBL; AF145439; AAF66699.1; -
DR INTERPRO; IPR000248; -
DR INTERPRO; IPR000276; -
DR INTERPRO; IPR000355; -
DR INTERPRO; IPR001277; -
DR INTERPRO; IPR001718; -
DR PFAM; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PRINTS; PR00241; ANGIOTENSINR.
DR PRINTS; PR00641; CHEMOKINER.
DR PRINTS; PR00645; LCR1ORPHANR.
DR PRINTS; PR00657; CCHEMOKINER.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
KW Receptor.
SQ SEQUENCE 369 AA; 42015 MW; F27CEAOCFB66B44C CRC64;

Query Match 31.3%; Score 593.5; DB 4; Length 369;
Best Local Similarity 40.2%; Pred. No. 5.9e-41;
Matches 115; Conservative 64; Mismatches 104; Indels 3; Gaps 3;

QY 44 YSLICVLGILGILNIVITFAFYKARSMIDVLLNMAIADILEVLTLFPWAVSHATCAW 103
DB 55 YWLIVFVIGALNSLVILVYCTRYKVTMDMLLNIAIADILEVLTLFPWAVIA-AAQWK 113

QY 104 FSNATCKLLKGIYAINFCGMLLLTICISMDRYTAIVQATKSFRLSRTLPRSKIIICLVVW 163
DB 114 FQTEWCKVNSVMYKMFYSCVLLIMCISVDRYTAIAQAMRAHWREKRLLYSKWVCFTIW 173

QY 164 GLSVIISSTFFVFNQYNTGSDVCEPKYQTVSEPTRWKLLMLGLELLFFGFFPLPMFIF 223
DB 174 VLAALCIPEILYSQIESGIAICTMYVPS-DESKLKSAVLTLLKVLGFFLPFVVMAC 232

QY 224 CYTEIVKTLVQAQNSKRRAIRVIAVLAVLACQIPHNMVLLVTAANLCKMNRN-CQSE 282
DB 233 CYTIIHTLIQAKSKKALKKALVTILVLFVLSQPPYCNILLVQITIDAYAMFISCAVS 292

QY 283 KLIGYTKTVTEVLAFLHCCNLNPNVAFIGQKFRNYFLKILKDLWCV 328
DB 293 TNIDICFQVQTIAFPHSLNPNVLYVFGFRDLVKTLKNLGCI 338

RESULT 7
ID Q9TV16 PRELIMINARY; PRT; 342 AA.
AC Q9TV16;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE G PROTEIN-COUPLED RECEPTOR STRL33.

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OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=STRL33(BONZO);
RA Brussel A., Pretet J.L., Girard M., Butor C.;
RT "Sequences and Predicted Structures of Chimpanzee STRL33 (Bonzo) and
RT 9pL5 (BOB)."
RL AIDS Res. Hum. Retroviruses 15:0-0(1999).
DR EMBL; AF084229; AAD52041.1; -
DR INTERPRO; IPR000248; -
DR INTERPRO; IPR000276; -
DR INTERPRO; IPR000355; -
DR INTERPRO; IPR001277; -
DR INTERPRO; IPR002235; -
DR PFAM; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PRINTS; PR00241; ANGIOTENSINR.
DR PRINTS; PR00645; LCR1ORPHANR.
DR PRINTS; PR00657; CCHEMOKINER.
DR PROSITE; PS00105; BONZOORPHANR.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
KW Receptor.
SQ SEQUENCE 342 AA; 39273 MW; 5B58003797806B2A CRC64;

Query Match 30.8%; Score 583.5; DB 6; Length 342;
Best Local Similarity 34.4%; Pred. No. 3.6e-40;
Matches 125; Conservative 77; Mismatches 108; Indels 53; Gaps 8;

QY 12 QSIHLITOLILRCYCPCRRSGSPGYLYRIAYSLICVLGILNIVITFAFYKARSM 71
DB 24 QDFLOFSKVFLLPC-----MYLVFVCGLVGNSLVLVISIFYHKLQSL 65

QY 72 TDVYLLNMAIADILEVLTLFPWAVSHATCAWVFSNATCKLLKGIYAINFCGMLLLTICIS 131
DB 66 TDVFLVNLPLADLVFVCTLPFWAYA-GIHEWVFGVGMCKSLGIVTINFTYTSMLITCIT 124

QY 132 MDRIATVQATKSFRLSRTLPRSKIIICLVVWGLSVIISSTFFVFNQYNTGSDVCEPK 191
DB 125 VDREIVVYKATKAYNQAKRTMGKVTSLLIWISLVSLPQIYGNVFNLD-KLICGYH 183

QY 192 YQTVSEPTRWKLLMLGLELLFFGFFPLPMFIFCYFIVKTLVQAQNSKRRAIRVIAV 251
DB 184 DEATIS-----TVVLATQMTLGFLLPLMTMIVCYSVIKTLHAGGFGQKRSKLIFLVM 237

QY 252 LVFLACQIPHNMVLLVTAANLCKMNRN-CQSE----KLIGYTKTVTEVLAFLHCCNLNPNVLY 307
DB 238 AVFLLTQMPFNLMKLI-----RSTHWEYVYAMTSFHYTMVTEATAYLRACLNPVLY 288

QY 308 AFIGQKFRNYFLKILKDLWC-----VRRKYKSGSGFCAGRYSENISROTSETADNDNASS 362
DB 289 AFVSLKFRKFNKLVKVDIGCLGYPYLGVSQWKS-----SEDSKTSFASHHNVEATSM 339

QY 363 FTM 365
DB 340 FOL 342

RESULT 8
ID O42444 PRELIMINARY; PRT; 368 AA.
AC O42444;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE INTERLEUKIN-8-LIKE RECEPTOR.
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.

```

DR	PRINTS; PRO1106; CHEMOKINER1.
DR	PRINTS; PRO1107; CHEMOKINER2.
DR	PRINTS; PRO1110; CHEMOKINERS.
DR	PROSITE; PS00237; G_PROTEIN_RECEPTOR; UNKNOWNL1.
SQ	SEQUENCE 360 AA; 41139 MW; 4B2552BCE513FE9F CRC64;

Query Match	29.4%; Score 556; DB 6; Length 360;
Best Local Similarity	34.8%; Pred. No. 6.6e-38;
Matches 120; Conservative 67; Mismatches 130; Indels 28; Gaps	

QY	25 YCAPCRSGSP--GYLYRIAYSLICVLGLLNILVITAFYKKARSMTDYLNLMAIA 82
	: : : : : : : : : :
Db	28 YGAPCHKEDVKYGAQLPLPLYSLVFIFGVGNMLVLLIINCCLKLSLTIDYLLNLAIS 87
	: : : : : : : : : :
QY	83 DLFLVLTLPFWAYSHATGAWFSNATCKLKLGITYAINENCGMLLTCTISMDRVYAIVQAT 142
	: : : : : : : :
Db	88 DLFLTLPLWAHS--ANENWFGNAKCLTGTHIGYLGGFIFILLTIDRLAIVHAV 146
	: : : : : : : :
QY	143 KSFRLRSRTLPRSKIICLVVMGLSVLISSSTFFVNOKYNTQGSDVCPEPKYQTVSPIRWK 202
	: : : : : : : :
Db	147 --FALKARTVTFGVTSVITWLVAVPASVPGIIFTKCQEEDSVYICGPYF-----PRGMN 199
	: : : : : : : :
QY	203 LLMGLLELGGFFIPDMFIPTFTFKVLVQAQN--SKRHKAIRVIIVLVFLACQIPH 261
	: : : : : : : : : :
Db	200 NFHTIMENILGLVPLPILMVICYSGIKLTLLRCRNEKRHRVARLFTTMIVYVFLWTYP 259
	: : : : : : : : : :
QY	262 NVLLVTAAN--LGKMNRSQSEKLGYTKTVTEVLAFHLCCINPLVLYAFIGOKERNYFL 319
	: : : : : : : :
Db	260 NIVLLTNFOETGLSN--CESTRQDOQATQVTTETLGMTHCCINPLIIYAFVGKEKFRYLS 317
	: : : : : : : :
QY	320 KILKDLWCVRKYKSSGF--SCAGRYSENI----SRQTSSETADND 358
	: : : : : : : :
Db	318 MEF-----RKYTIRECKQCQPVFYREIVDGVTSTNPSTAQEE 355
	: : : : : : : :

RESULT 10	
ID .	O55193 PRELIMINARY; PRT; 373 AA.
AC	O55193;
DT	01-JUN-1998 (TrEMBLrel. 06, Created)
DT	01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DE	01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE	C-C CHEMOKINE RECEPTOR TYPE 2 (C-C CKR-2) (CCR-2) (CCR2).
OS	CMKBK2.
GN	Rattus norvegicus (Rat).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NB	NCBI_TaxId=10116;
RP	[1]
RN	SEQUENCE FROM N.A.
RC	STRAIN=SPRAGUE DAWLEY;
RX	MEDLINE=98318173; PubMed=9655467;
TX	Jiang Y., Salafiranga M.N., Adhikari S., Xia Y., Feng L., Sonntag M.K.,
RA	deGibrie C.M., Pennell N.A., Streit W.J., Harrison J.K.;
RT	"Chemokine receptor expression in cultured glia and rat experimental
RL	allergic encephalomyelitis".
RL	J. Neuroimmunol. 86:1-12(1998).
CC	-1- FUNCTION: RECEPTOR FOR THE MCP-1 (JE), MCP-3 (PIC) AND MCP-5
CC	CHEMOKINES. TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR
CC	CALCIUM IONS LEVEL (BY SIMILARITY).
CC	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
CC	-1- TISSUE SPECIFICITY: EXPRESSED IN LUNG, SPLEEN, KIDNEY, THYMUS AND
CC	MACROPHAGES.
CC	-1- INDUCTION: IN ANIMALS IN WHICH EXPERIMENTAL ALLERGIC
CC	ENCEPHALOMYELETIS (EAE) HAS BEEN INDUCED.
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
EMBL	U77349; AAC03242.1; -
DR	INTERPRO; IPRO0276; -
DR	INTERPRO; IPRO00355; -
DR	INTERPRO; IPRO02237; -
PFAM	PF00001; 7tm_1; 1.
DR	PRINTS; PR00237; GPCRHHODPSN.

DR PRINTS; PR00237; GPCRHHODPSN.
 DR PRINTS; PR00241; ANGIOTENSINR.
 DR PRINTS; PR00645; LCR1ORPHANR.
 DR PRINTS; PR00657; CCHEMOKINER.
 DR PRINTS; PR01106; CHEMOKINER1.
 DR PRINTS; PR01107; CHEMOKINER2.
 DR PRINTS; PR01108; CHEMOKINER3.
 DR PRINTS; PR01110; CHEMOKINER5.
 DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
 KW Receptor.
 FT NON_TER 1
 FT NON_TER 339
 SQ SEQUENCE 339 AA; 38678 MW; 4CF660C5648C8DC1 CRC64;

Query Match 28.8%; Score 545.5; DB 6; Length 339;
 Best Local Similarity 38.9%; Pred. No. 4.5e-37;
 Matches 119; Conservative 58; Mismatches 100; Indels 29; Gaps 9;

QY 28 PORRSGSPGYLYRIA-----YSLICVLGLGNILVVTTFAYFKKARSMTDYLINMA 80
 DB 12 PQOKID-----VKRIAAQLPLLYSLVFEIFGLVGNMLVLTLLNCKKLSMTDIYLLNLA 66
 QY 81 IADILEVLTLPFWAVSHATGAWVFSNATCKLLKGIYAINFCNGMLLLTLCISMDRYIAIVQ 140
 DB 67 ISDLLELTVPFWA-HYAAAQWDFGNTMCQLTGLYFIFGFGVFFIILITIDRYLAIVH 125
 QY 141 ATKSFRLRSRTLPKSKIIICLVVWGLSVIISSSTFFVFNOKYNTGSDVC-----EPKYQTV 195
 DB 126 AV--FALKARTVTFGVVTSVTVAVLASLPGLIIFTRSQKEGLRYTCSLHFPHSQYQF- 182
 QY 196 SEPIRWKLLMLGLELFGFFIPLMFEMIFCYTFIVKTLVQAQN-SKRHKAIRVIAVVLVF 254
 DB 183 -----WKNFQTLKMLVGLVPLINVICYSGILKTLRCRNEKKRHKAVRLIFAIMIV 237
 QY 255 LACQIPHNMLLV-TAANLGKMNRSQSEKLIQYTKTTEVLAFHCCLNPLVLYAIFGQK 313
 DB 238 FLFWAPYINVLNLTFFPEFGLN-DCSSSNGLDQAMQVTTETLGMTCCINPVVYAFVGEK 296
 QY 314 FRNYFL 319
 DB 297 FRKYIL 302

RESULT 15
 Q9TUQ5 PRELIMINARY; PRT; 339 AA.
 AC Q9TUQ5;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
 DE C-C CHEMOKINE RECEPTOR 5 (FRAGMENT).
 GN CCR5.
 OS Erythrocebus patas (Red guenon) (Hussar).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecoidea; Erythrocebus.
 OX NCBI_TaxID=9538;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
 RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
 FT "Sequences of the CCR5 genes from diverse simian and prosimian
 RT species";
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF162054; AAD47809.1; -
 DR INTERPRO; IPR000248; -
 DR INTERPRO; IPR000276; -
 DR INTERPRO; IPR000355; -
 DR INTERPRO; IPR001277; -
 DR INTERPRO; IPR002236; -
 DR INTERPRO; IPR002237; -
 DR INTERPRO; IPR002240; -

DR PFAM; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PRINTS; PR00241; ANGIOTENSINR.
 DR PRINTS; PR00645; LCR1ORPHANR.
 DR PRINTS; PR00657; CCHEMOKINER.
 DR PRINTS; PR01106; CHEMOKINER1.
 DR PRINTS; PR01107; CHEMOKINER2.
 DR PRINTS; PR01110; CHEMOKINER5.
 DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
 KW Receptor.
 FT NON_TER 1
 FT NON_TER 339
 SQ SEQUENCE 339 AA; 39048 MW; 1A2E19E3A6A5A52A CRC64;

Query Match 28.8%; Score 545.5; DB 6; Length 339;
 Best Local Similarity 36.7%; Pred. No. 4.5e-37;
 Matches 114; Conservative 65; Mismatches 109; Indels 23; Gaps 8;

QY 11 CQSILHITQLILRCYCPCRRSGSPGYLYRIAAYSLICVLGLGNILVVTTFAYFKKARS 70
 DB 13 CQKI-NVKQIAARLLPP-----YSLVFIQFVGNILVVLINCKRLKS 56
 QY 71 MTDVYLLNMAIADILFVLTLFPWAVSHATGAWVFSNATCKLLKGIYAINFCNGMLLLTLCI 130
 DB 57 MTDIYLLNLAISDLFLITVPFWA-HYAAAQWDFGNTMCQLTGLYFIFGFGFIILL 115
 QY 131 SMDRYIAIVQATKSFRLRSRTLPKSKIIICLVVWGLSVIISSSTFFVFNOKYNTGSDVC 190
 DB 116 TIDRYLAIVHAV--FALKARTVTFGVVTSVTVAVLASLPGLIIFTRSQKEGLRYTCS 172
 QY 191 KYQTVSEPIRWKLLMLGLELFGFFIPLMFEMIFCYTFIVKTLVQAQN-SKRHKAIRVIA 249
 DB 173 SHFPYSQCFWKNFQTLKIVILGLVPLLVVVICYSGILKTLRCRNEKKRHKAVRLIFT 232
 QY 250 VLVFLACQIPHNMLLV-TAANLGKMNRSQSEKLIQYTKTTEVLAFHCCLNPLVLYA 308
 DB 233 IMIVYFLFWAPYINVLNLTFFPEFGLN-NCSSSNGLDQAMQVTTETLGMTCCINPIYA 291
 QY 309 FIGOKFRNYFL 319
 DB 292 FVGEKFRNYLL 302

Search completed: May 23, 2001, 15:35:10
 Job time: 616 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 23, 2001, 15:28:24 ; Search time 184.73 Seconds
(without alignments)
11.759 Million cell updates/sec

Title: US-08-887-977-10_COPY_1_38

Perfect score: 206

Sequence: 1 MFSTPVKILQCSILHITQLILRCYCPCRRSGSPGY 38

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 390729 seqs, 57163235 residues

Total number of hits satisfying chosen parameters: 390729

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_0401.*

- 1: /SID56/gcgdata/geneseq/geneseq/AA1980.DAT.*
- 2: /SID56/gcgdata/geneseq/geneseq/AA1981.DAT.*
- 3: /SID56/gcgdata/geneseq/geneseq/AA1982.DAT.*
- 4: /SID56/gcgdata/geneseq/geneseq/AA1983.DAT.*
- 5: /SID56/gcgdata/geneseq/geneseq/AA1984.DAT.*
- 6: /SID56/gcgdata/geneseq/geneseq/AA1985.DAT.*
- 7: /SID56/gcgdata/geneseq/geneseq/AA1986.DAT.*
- 8: /SID56/gcgdata/geneseq/geneseq/AA1987.DAT.*
- 9: /SID56/gcgdata/geneseq/geneseq/AA1988.DAT.*
- 10: /SID56/gcgdata/geneseq/geneseq/AA1989.DAT.*
- 11: /SID56/gcgdata/geneseq/geneseq/AA1990.DAT.*
- 12: /SID56/gcgdata/geneseq/geneseq/AA1991.DAT.*
- 13: /SID56/gcgdata/geneseq/geneseq/AA1992.DAT.*
- 14: /SID56/gcgdata/geneseq/geneseq/AA1993.DAT.*
- 15: /SID56/gcgdata/geneseq/geneseq/AA1994.DAT.*
- 16: /SID56/gcgdata/geneseq/geneseq/AA1995.DAT.*
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- 19: /SID56/gcgdata/geneseq/geneseq/AA1998.DAT.*
- 20: /SID56/gcgdata/geneseq/geneseq/AA1999.DAT.*
- 21: /SID56/gcgdata/geneseq/geneseq/AA2000.DAT.*
- 22: /SID56/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
1	206	100.0	365	19	W48086		Human dendritic ce
2	206	100.0	365	21	Y97077		Primate (human) ch
3	56.5	27.4	292	20	Y29255		Amino acid sequenc
4	56	27.2	219	21	B43512		Human cancer assoc
5	56	27.2	361	21	B03950		Human mesenchymal
6	56	27.2	643	21	Y87347		Human signal pepti
7	56	27.2	874	21	B01431		Human TANGO 224 (f
8	55	26.7	122	12	R15123		hCG/hLH chimera, A
9	55	26.7	145	12	R15116		hCG/hLH chimera, A
10	55	26.7	145	12	R15118		hCG/hLH chimera, A
11	55	26.7	145	12	R15122		hCG/hLH chimera, A

12	55	26.7	145	12	R15124	hCG/hLH chimera, A
13	55	26.7	145	12	R15125	hCG/hLH chimera, A
14	54	26.2	106	20	Y32825	HIV chemokine gene
15	54	26.2	121	21	Y92001	Human luteinizing
16	54	26.2	122	20	Y29594	Human luteinizing
17	54	26.2	141	7	P60602	Sequence of human
18	54	26.2	141	20	W99548	hLH-beta analogue
19	54	26.2	141	20	W99547	hLH-beta analogue
20	54	26.2	141	20	W99520	Glycoprotein hormo
21	54	26.2	141	20	W99522	Glycoprotein hormo
22	54	26.2	141	20	W99523	Glycoprotein hormo
23	54	26.2	141	20	W99524	Glycoprotein hormo
24	54	26.2	141	20	W99525	Glycoprotein hormo
25	54	26.2	141	20	W99516	Glycoprotein hormo
26	54	26.2	141	20	W99517	Glycoprotein hormo
27	54	26.2	141	20	W99518	Glycoprotein hormo
28	54	26.2	141	20	W99519	Glycoprotein hormo
29	54	26.2	234	16	R86271	Single chain gonad
30	54	26.2	234	16	R86261	Partially deglycos
31	54	26.2	234	16	R86249	Single chain gonad
32	54	26.2	446	21	B43754	Human cancer assoc
33	53	25.7	62	20	Y19648	SEQ ID NO 366 from
34	53	25.7	147	19	W72404	Arabidopsis thalia
35	52.5	25.5	111	18	W21859	Leech protein caus
36	51	24.8	326	21	B18989	Amino acid sequenc
37	50	24.3	122	12	R15119	hCG/hLH chimera, A
38	50	24.3	145	12	R15106	hCG/hLH chimera, A
39	50	24.3	145	12	R15102	hCG/hLH chimera, D
40	50	24.3	218	22	B48600	Human oligodendroc
41	50	24.3	877	19	W23946	Porcine phosphoino
42	50	24.3	877	20	W90082	Porcine G-protein
43	50	24.3	877	21	Y76801	p1g p101 regulator
44	50	24.3	1480	13	R25079	Drosophila SLIT pr
45	49	23.8	141	20	W99521	Glycoprotein hormo

ALIGNMENTS

RESULT 1	
W48086	
ID W48086 standard; Protein; 365 AA.	
XX	
AC W48086;	
XX	
DT 11-JUN-1998 (first entry)	
XX	
DE Human dendritic cell chemokine receptor.	
XX	
KW Human: thymus expressed chemokine; TECK; MIP-3alpha; MIP-3beta;	
KW receptor; dendritic cell; macrophage; inflammation; asthma.	
XX	
OS Homo sapiens.	
XX	
FH Key Location/Qualifiers	
FT MISC-difference 193	
FT /note= "encoded by CAN"	
XX	
PN WO9801557-A2.	
XX	
PD 15-JAN-1998.	
XX	
PF 02-JUL-1997; 97WO-US10819.	
XX	
PR 04-JUN-1997; 97US-0048593.	
PR 05-JUL-1996; 96US-0675814.	
PR 11-OCT-1996; 96US-0028329.	
XX	
PA (SCHE) SCHERING CORP.	
XX	
PI Gish KC, Schall TJ, Vicari A, Wang W, Zlotnik A;	
XX	
DR WPI; 1998-101054/09.	

DR N-PSDB; V15418.
 XX Novel chemokines, e.g. thymus expressed chemokine - used for
 PT treating inflammatory conditions including asthma.
 XX
 PS Claim 3; Page 94-95; 202pp; English.
 XX
 CC The present sequence represents human dendritic cell chemokine receptor.
 CC Antibodies which bind to the protein can be used in detecting or
 CC diagnosing various immunological conditions related to expression
 CC of the protein. The nucleic acid can be used for screening and
 CC isolating DNA clones for the chemokines, especially from other
 CC species. The chemokine can be used in the treatment of conditions
 CC associated with abnormal physiology or development, including
 CC inflammatory conditions such as asthma.
 XX
 SQ Sequence 365 AA;

Query Match 100.0%; Score 206; DB 19; Length 365;
 Best Local Similarity 100.0%; Pred. No. 1.9e-19;
 Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFSTPVKILQCSILHITQLILRCYCPCRRSGSPGY 38
 |||||
 DB 1 mfstpvkllcqsilhitqlilrcycapcrrsgsgpy 38

RESULT 2
 Y97077
 ID Y97077 standard; Protein; 365 AA.
 AC Y97077;
 XX
 XX
 DT 04-DEC-2000 (first entry)
 XX
 DE Primate (human) chemokine receptor CCR6.
 KW MIP-3-alpha; chemokine; CCR6 receptor; ligand; cytostatic; agonist;
 KW antagonist; anti-psoriatic; dermatological; immunosuppressive;
 KW anti-inflammatory.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH Misc-difference 193
 FT /note= "Encoded by CAN#"
 XX
 PN WO200046248-A1.
 XX
 PD 10-AUG-2000.
 XX
 PF 02-FEB-2000; 2000WO-US00511.
 XX
 PR 03-FEB-1999; 99US-0244281.
 XX
 PA (SCHE) SCHERING CORP.
 XX
 XI Oldham ER, Honey B, Dieu-Nosjean M, Caux C, Zlotnik A;
 PI
 DR WPI; 2000-543477/49.
 XX
 DR N-PSDB; A51971.
 XX
 CC Novel methods for modulating the migration of cells within or to the
 PT skin using MIP-3-alpha or CCR6 agonists or antagonists, useful for
 PT treating skin disorders, e.g. cancer
 XX
 PS Disclosure; Page 53-54; 61pp; English.
 XX
 CC The MIP-3-alpha chemokine is expressed in inflamed skin cells. This
 CC chemokine is the ligand for the CCR6 receptor. MIP-3-alpha or CCR6
 CC agonists or antagonists can be used to modulate the migration of a cell
 CC within or to the skin of a mammal. MIP-3-alpha can be used to purify a

CC population of cells expressing a MIP-3-alpha receptor. The methods are
 CC useful for treating a mammalian subject with a skin disease or condition,
 CC e.g. cancer, metastasis, psoriasis, atopic or contact dermatitis,
 CC systemic lupus erythematosus and lichen ruber planus, or for treating
 CC skin transplants or grafts.
 XX
 SQ Sequence 365 AA;

Query Match 100.0%; Score 206; DB 21; Length 365;
 Best Local Similarity 100.0%; Pred. No. 1.9e-19;
 Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFSTPVKILQCSILHITQLILRCYCPCRRSGSPGY 38
 |||||
 DB 1 mfstpvkllcqsilhitqlilrcycapcrrsgsgpy 38

RESULT 3
 Y29255
 ID Y29255 standard; Protein; 292 AA.
 XX
 AC Y29255;
 XX
 DT 25-OCT-1999 (first entry)
 XX
 DE Amino acid sequence of a virulence factor encoded by ORF40238.
 XX
 KW Human pathogen; virulence polypeptide; virulence factor;
 KW pathogenic infection; Pseudomonas aeruginosa infection.
 XX
 OS Pseudomonas aeruginosa.
 XX
 PN WO9927129-A1.
 XX
 PD 03-JUN-1999.
 XX
 PF 25-NOV-1998; 98WO-US25247.
 XX
 PR 25-NOV-1997; 97US-0066517.
 XX
 PA (GEHO) GEN HOSPITAL CORP.
 XX
 XI Ausubel F, Cao H, Drenkard E, Goodman HM, Mahajan-Miklos S;
 PI Rahme LG, Tan M, Tsongalis J;
 XX
 DR WPI; 1999-357851/30.
 XX

Virulence factors useful in developing disease treatments

Disclosure; Fig 3; 228pp; English.

The present sequence represents a Pseudomonas aeruginosa polypeptide
 sequence. P. aeruginosa is an opportunistic human pathogen present in
 CC soil water and plants. The specification describes virulence polypeptides
 CC and nucleic acid sequence encoding such polypeptides. These sequences
 CC can be used to identify a compound which is capable of decreasing the
 CC expression of a pathogenic virulence factor. Compounds that inhibit
 CC the expression or activity of virulence factor polypeptides can be
 CC used to treat pathogenic infections, especially where the infection
 CC is a P. aeruginosa infection.
 CC note: the sequences given in the specification were poorly legible, and
 CC in some instances assumptions were made as to the identity of the
 CC residue; it is therefore possible that the sequence given below is
 CC not entirely correct.
 XX
 SQ Sequence 292 AA;

Query Match 27.4%; Score 56.5; DB 20; Length 292;
 Best Local Similarity 36.1%; Pred. No. 7.9;
 Matches 13; Conservative 3; Mismatches 9; Indels 11; Gaps 1;

Qy	4	TPVKIILCQSILHITQLI-----LRC-YCAPCRR	31
		: : ! :	
Db	224	tpagvflaesahmaglaevpmqgelasaissgkkkrkrcgmcaprr	271

CC (potential therapeutic agents). Ab are used to diagnose, or monitor,
CC HSPF-related diseases (in usual immunoassays), as therapeutic
CC antagonists, in competitive drug screens, and for purification of HSPF
CC from natural sources.

QY 4 TPVKIILCQSIIHITQLI-----LRC-YCAPCRR 31
|| : | |||
Db 224 tpgvfiaesalhmaglaeypmqglasaisgkkrkcrgmcaprr 271

RESULT 6
Y87347
ID Y87347 standard; Protein; 643 AA.
XX AC AC
XX XX
XX DT 11-MAY-2000 (first entry)
XX DE Human signal peptide containing protein HSPP-124 SEQ ID NO:124.
XX DE
XX KW Human; signal peptide-containing protein; HSPP; diagnosis; cancer;
KW inflammation; cardiovascular disease; anticancer; anti-inflammatory;
KW antimicrobial; nootropic; neuroprotective; cardiovascular; hepatotropic;
KW antidiabetic; gene therapy; cell proliferation; neurological disorder;
KW reproductive disorder; developmental disorder; arteriosclerosis;
KW cirrhosis; psoriasis; acquired immune deficiency syndrome; anaemia;
KW asthma; Crohn's disease; infection; Alzheimer's disease; schizophrenia;
KW Parkinson's disease; Huntington's diseases; ovulatory defect;
KW muscular dystrophy.
XX OS Homo sapiens.
XX WO200000610-A2.
XX PN
XX PD 06-JAN-2000.
XX PF 25-JUN-1999; 99WO-US14484.
XX PR 26-JUN-1998; 98US-0090762.
PR 31-JUL-1998; 98US-0094983.
PR 01-OCT-1998; 98US-0102686.
PR 11-DEC-1998; 98US-0112129.
XX PA (INCY-) INCYTE PHARM INC.
PI Lal P., Tang YT, Gorgone GA, Corley NC, Guegler KJ, Baughn MR;
PI Akerblom IE, Au-Young J, Yue H, Patterson C, Reddy R, Hillman JL;
PI Bandman O;
XX WPI: 2000-160673/14.
DR N-PSDB: Z98232.
PT New human signal peptide-containing proteins useful in treatment,
PT prevention and diagnosis of e.g. cancer, inflammation and
PT cardiovascular disease -
XX XX
XX Claim 1; Page 243-244; 327pp; English.

Z98109 to Z98242 encode Y87224 to Y87357 which represent the human
signal peptide-containing proteins HSPP-1 to HSPP-134. HSPPs have
anticancer, anti-inflammatory, antimicrobial, nootropic, hepatotropic,
neuroprotective, cardiovascular and antiasthmatic activities, and can
be used in gene therapy. HSPPs can be used to treat or prevent disorders
associated with decreased activity or function of HSPP. Antagonists of
HSPP are used to treat or prevent disorders associated with increased
activity or function of HSPP. Such diseases include cell proliferation
(including cancer), inflammation, cardiovascular, neurological,
reproductive or developmental disorders, (e.g. arteriosclerosis,
cirrhosis, psoriasis, acquired immune deficiency syndrome, anaemia,
asthma, Crohn's disease, microbial or other infections, congestive or
ischaemic heart disease, Alzheimer's, Parkinson's or Huntington's
diseases, schizophrenia, ovulatory defects, muscular dystrophy). HSPP
nucleic acids can be used for the recombinant production of HSPP, for
detecting HSPP in standard hybridisation and amplification assays (for
diagnosis and monitoring), in gene therapy, as antisense, triplex-forming
or ribozyme therapeutics, for detecting related sequences or genetic
variations, and for chromosomal mapping. HSPP are also used to raise
specific antibodies (Ab) and to screen for agonists and antagonists

RESULT
R15116

14-NOV-1991

22 LRCYAPCRRSGSSPG 37

00 86 TScrcgpcrrstscg 101

RESULT 10

13118
2 R15118 standard: protein: 145 AA

R15118:

11-FEB-1992 (first entry)

hCG/hLH chimera. A3b.

Glycoprotein hormone; immuno-castration;
immuno-contragestive; vaccine; human chorionic gonadotropin;
luteinising hormone; LH; CG.

Homo sapiens.

WO9116922-A.

14-NOV-1991

PF 07-MAY-1991; 91WO-US03162.
 XX
 PR 08-MAY-1990; 90US-0520703.
 XX
 PA (UYNE-) UNIV MED NEW JERSEY.
 XX
 PI Campbell RK, Moyle WR;
 XX

DR WPI; 1991-353528/48.
 XX

XX The sequence is an analogue of mature hCG beta subunit having
 CC residues 89, 91, 92 and 99 replaced by the corresponding
 CC residues in the human LH protein. The chimeric hormone may be
 CC useful in the treatment of infertility in men and women and the
 CC promotion of fertility in male and female animals.
 CC See R15043, R15061-R15125 and R15161-R15198.
 XX
 XX

PS Table VI; Page 65; 94pp; English.
 XX

XX The sequence is an analogue of mature hCG beta subunit having
 CC residues 89, 91, 92 and 99 replaced by the corresponding
 CC residues in the human LH protein. The chimeric hormone may be
 CC useful in the treatment of infertility in men and women and the
 CC promotion of fertility in male and female animals.
 CC See R15043, R15061-R15125 and R15161-R15198.
 XX
 XX

SQ Sequence 145 AA;

Query Match 26.7%; Score 55; DB 12; Length 145;
 Best Local Similarity 62.5%; Pred. No. 6;
 Matches 10; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 22 LRCYCPCRRSGSSPG 37
 | | | | | | | | | |
 Db 86 lscrcgpcrrsttscg 101

RESULT 11

R15122
 ID R15122 standard; Protein; 145 AA.

XX

AC R15122;

XX

DT 11-FEB-1992 (first entry)

XX hCG/hLH chimera, A7.

XX

KW Glycoprotein hormone; immuno-castration;
 KW immuno-contraceptive agents, for suppressing reproductive system
 KW luteinising hormone; LH; CG.

XX

OS Homo sapiens.

XX

PN WO9116922-A.

XX

PD 14-NOV-1991.

XX

PF 07-MAY-1991; 91WO-US03162.

XX

PR 08-MAY-1990; 90US-0520703.

XX

PA (UYNE-) UNIV MED NEW JERSEY.

XX

PI Campbell RK, Moyle WR;

XX

DR WPI; 1991-353528/48.

XX

XX New glyco-protein hormone analogues - for inducing fertility as
 PT immuno-castration agents, for suppressing reproductive system
 PT development and as immuno-contraceptive vaccines.

XX

PS Table VI; Page 65; 94pp; English.

XX

XX The sequence is an analogue of mature hCG beta subunit having
 CC residues 42, 47, 51, 77, 82, 83, 89, 91, 92 and 99 replaced by the

CC corresponding residues in the human LH protein. The chimeric
 CC hormone may be useful in the treatment of infertility in men and
 CC women and the promotion of fertility in male and female animals.
 CC See R15043, R15061-R15125 and R15161-R15198.

XX Sequence 145 AA;

Query Match 26.7%; Score 55; DB 12; Length 145;
 Best Local Similarity 62.5%; Pred. No. 6;
 Matches 10; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 22 LRCYCPCRRSGSSPG 37
 | | | | | | | | | |
 Db 86 lscrcgpcrrsttscg 101

RESULT 12

R15124

ID R15124 standard; Protein; 145 AA.

XX

AC R15124;

XX

DT 11-FEB-1992 (first entry)

XX

DE hCG/hLH chimera, A9.

XX

KW Glycoprotein hormone; immuno-castration;
 KW immuno-contraceptive agents, for suppressing reproductive system
 KW luteinising hormone; LH; CG.

XX

OS Homo sapiens.

XX

PN WO9116922-A.

XX

PD 14-NOV-1991.

XX

PF 07-MAY-1991; 91WO-US03162.

XX

PR 08-MAY-1990; 90US-0520703.

XX

PA (UYNE-) UNIV MED NEW JERSEY.

XX

PI Campbell RK, Moyle WR;

XX

DR WPI; 1991-353528/48.

XX

XX New glyco-protein hormone analogues - for inducing fertility as
 PT immuno-castration agents, for suppressing reproductive system
 PT development and as immuno-contraceptive vaccines.

XX

PS Table VI; Page 65; 94pp; English.

XX

XX The sequence is an analogue of mature hCG beta subunit having
 CC residues 2, 8, 10, 15, 77, 82, 83, 89, 91, 92 and 99 replaced by the
 CC corresponding residues in the human LH protein. The chimeric
 CC hormone may be useful in the treatment of infertility in men and
 CC women and the promotion of fertility in male and female animals.
 CC See R15043, R15061-R15125 and R15161-R15198.

XX

SQ Sequence 145 AA;

Query Match 26.7%; Score 55; DB 12; Length 145;
 Best Local Similarity 62.5%; Pred. No. 6;
 Matches 10; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 22 LRCYCPCRRSGSSPG 37
 | | | | | | | | | |
 Db 86 lscrcgpcrrsttscg 101

RESULT 13

R15125
ID R15125 standard; Protein: 145 AA.
XX AC R15125;
XX XX
DT 11-FEB-1992 (first entry)
XX DE hCG/hLH chimera, A10.
XX KW Glycoprotein hormone; immuno-castration;
KW immuno-contragestive; vaccine; human chorionic gonadotropin;
KW luteinizing hormone; LH; CG.
XX OS Homo sapiens.
XX XX WO9116922-A.
XX PN 14-NOV-1991.
XX PD 07-MAY-1991; 91WO-US03162.
XX PF 08-MAY-1990; 90US-0520703.
XX PR (UYNE-) UNIV MED NEW JERSEY.
XX PA Campbell RK, Moyle WR;
XX PI WPI; 1991-353528/48.
XX DR New glyco-protein hormone analogues - for inducing fertility as
XX PT immuno-castration agents, for suppressing reproductive system
XX PT development and as immuno-contragestive vaccines.
XX XX
XX PS Table VI; Page 65; 94pp; English.
XX XX
CC The sequence is an analogue of mature hCG beta subunit having
CC residues 42, 47, 51, 89, 91, 92 and 99 replaced by the
CC corresponding residues in the human LH protein. The chimeric
CC hormone may be useful in the treatment of infertility in men and
CC women and the promotion of fertility in male and female animals.
CC See R15043, R15061-R15125 and R15161-R15198.
XX XX
SQ Sequence 145 AA;

Query Match 26.7%; Score 55; DB 12; Length 145;
Best Local Similarity 62.5%; Pred. No. 6;
Matches 10; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 22 LRCYCPCRRSGSSPG 37
DB 86 lscrcgpcrrstscg 101

RESULT 14
Y32825
ID Y32825 standard; Protein: 106 AA.
XX AC Y32825;
XX XX
DT 09-NOV-1999 (first entry)
XX DE HIV chemokine gene product from strain p896.
XX KW HIV; AIDS; chemokine; SDF-1; gp120; glycoprotein 120; antisense;
KW long terminal repeat; vaccine; detection; entry phase.
XX OS Human immunodeficiency virus.
XX XX
XX Key Location/Qualifiers
FT Misc-difference 28
FT /label= unknown
FT Misc-difference 38

FT Misc-difference 73 /label= Unknown
FT /label= Unknown
XX WO9941355-A2.
XX 19-AUG-1999.
XX 12-FEB-1999; 99WO-US03162.
XX 13-FEB-1998; 98US-0074640.
XX (UYNV) UNIV NEW YORK STATE RES FOUND.
XX Ambrus JL, Krawczyk KA, Ludwig LB;
XX WPI; 1999-518447/43.
XX New HIV gene, encoding chemokines useful for binding to the
XX chemokine receptor on human cells during the entry phase of HIV
XX infection,
XX Claim 3; Page 81; 87pp; English.
XX This sequence is the HIV strain p896 chemokine. The HIV chemokine protein
XX has similarity with chemokine SDF-1. It is thought that the HIV chemokine
XX may play a role as a cofactor with glycoprotein 120 (gp120) in the
XX binding and entry of HIV to a target cell. The HIV chemokine gene
XX was deduced from the known sequence of the minus strand. The peptides
XX derived from the HIV chemokine gene or variants or modified versions of
XX the HIV chemokine may be used to block entry of target cell during
XX various phases of HIV infection and AIDS. Also, chemokine receptors may
XX provide a method by which the HIV chemokine may be isolated and purified
XX from HIV. The HIV chemokine and variants may also be useful in the
XX development of a vaccine for AIDS prevention. Isolated and purified HIV
XX chemokine or derived peptides may be used to generate antibodies useful
XX in diagnostic assays for detection of HIV chemokine in clinical samples.
XX SQ Sequence 106 AA;

Query Match 26.2%; Score 54; DB 20; Length 106;
Best Local Similarity 60.0%; Pred. No. 5.9;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 10 LCQSILHITQLILRC 24
DB 82 lccsllhlaqlv lac 96

RESULT 15
Y92001
ID Y92001 standard; Protein: 121 AA.
XX AC Y92001;
XX 19-JUL-2000 (first entry)
XX Human luteinizing hormone beta subunit.
XX human luteinizing hormone; beta subunit; CKGF; mutant;
KW cysteine knot growth factor; hairpin loop; thyroid stimulating hormone;
KW TSH; hypothyroidism; thyroid cancer.
XX OS Homo sapiens.
XX XX
XX Key Location/Qualifiers
FT Domain 8..33
FT /label= beta_hairpin_loop_1
FT Misc-difference 1..33
FT /note= "mutant optionally comprises one or more
FT substitutions in these residues, preferably
FT a basic residue"

FT Domain 58..87
 XX /label= beta_hairpin_loop_3
 PN WO200017360-A1.
 XX PD 30-MAR-2000.
 XX PF 19-MAR-1999; 99WO-US05908.
 XX PR 22-SEP-1998; 98WO-US19772.
 XX (UYMA-) UNIV MARYLAND BALTIMORE.
 PA Weintraub BD, Szkudlinski MW;
 PI WPI; 2000-283585/24.
 XX
 XX New mutant cystine knot growth factor proteins comprising one or more
 PT mutant subunits, useful for treating or preventing diseases e.g.
 PT hypothyroidism and thyroid cancer
 XX
 PS Claim 73; Page 297; 320pp; English.
 XX
 CC This is the wild type human luteinizing hormone beta subunit. Mutants
 CC comprise at least one electrostatic charge altering mutation in a beta
 CC hairpin loop, resulting in increased bioactivity.
 CC Mutant cystine knot growth factor (CKGF) proteins comprising one or more
 CC mutant subunits and having novel properties or improved pharmacological
 CC properties, compared to wild type CKGFs, are claimed. The CKGF
 CC superfamily comprises at least four families of growth factors: the
 CC glycoprotein hormones, the platelet-derived growth factor (PDGF) family,
 CC the neurotrophins and the transforming growth factor-beta family; the
 CC families are known to be structurally similar (especially comprising the
 CC cystine knot topology) and it was shown that mutations at certain
 CC positions in the CKGF hairpin loops of family members and other members
 CC of the CKGF superfamily could significantly alter the biological
 CC activities of the CKGF.
 CC A mutant thyroid stimulating hormone (TSH) heterodimer or analogue
 CC can be administered to treat or prevent hypothyroidism (claimed). They
 CC are also useful to treat or diagnose thyroid cancer, by administering the
 CC mutant heterodimer or analogue to stimulate iodine uptake, and
 CC subsequently administering radiolabeled iodine to treat the cancer or
 CC enable radiolabel detection (claimed).
 XX
 SQ Sequence 121 AA;

Query Match 26.2%; Score 54; DB 21; Length 121;
 Best Local Similarity 62.5%; Pred. No. 6.8;
 Matches 10; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 QY 22 LRCYCAPCRSGSSPG 37
 Db 86 lscrgcprstsdcg 101

Search completed: May 23, 2001, 15:28:25
 Job time: 402 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 23, 2001, 15:30:04 ; Search time 95.91 Seconds
(without alignments)
7.611 Million cell updates/sec

Title: US-08-887-977-10_COPY_1_38

Perfect score: 206

Sequence: 1 MFSTPVKILQCQILHITQLILRCVCAPCRSGSPG 38

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 185757 seqs, 19210857 residues

Total number of hits satisfying chosen parameters: 185757

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pap.*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pap.*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pap.*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pap.*
5: /cgn2_6/ptodata/2/iaa/PT05_COMB.pap.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	50	24.3	218	4	US-09-084-079-5
2	50	24.3	877	2	US-08-916-917-2
3	50	24.3	877	2	US-08-972-631-2
4	50	24.3	877	2	US-08-972-629-2
5	50	24.3	877	2	US-08-972-630-2
6	50	24.3	877	2	US-08-672-211-2
7	50	24.3	877	3	US-09-225-170-2
8	49	23.8	207	1	US-08-557-917A-2
9	49	23.8	207	4	US-09-084-153-2
10	49	23.8	207	4	US-09-084-079-2
11	49	23.8	447	4	US-09-378-255-2
12	49	23.8	880	2	US-08-916-917-12
13	49	23.8	880	3	US-09-225-170-12
14	49	23.8	880	4	US-09-378-255-6
15	49	23.8	880	4	US-09-141-212-2
16	49	23.8	880	4	US-09-141-212-4
17	48.5	23.5	114	1	US-08-425-673-7
18	48	23.3	462	2	US-08-477-451-24
19	46	22.3	88	2	US-08-327-362-2
20	46	22.3	88	2	US-08-709-924-24
21	46	22.3	88	2	US-08-709-925-24
22	46	22.3	88	4	US-09-158-565-2
23	46	22.3	98	2	US-08-709-924-23
24	46	22.3	98	2	US-08-709-925-23
25	46	22.3	145	1	US-08-425-673-1
26	46	22.3	145	1	US-08-425-673-2
27	46	22.3	145	1	US-08-475-213-10

Sequence 2, Appli
Sequence 4, Appli
Sequence 11, Appli
Sequence 12, Appli
Sequence 13, Appli
Sequence 14, Appli
Sequence 15, Appli
Sequence 16, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 8, Appli
Sequence 8, Appli
Sequence 9, Appli
Sequence 17, Appli
Sequence 2, Appli
Sequence 183, App

28 46 22.3 145 2 US-08-395-238-2
29 46 22.3 145 4 US-09-142-320-4
30 46 22.3 145 4 US-09-142-320-11
31 46 22.3 145 4 US-09-142-320-12
32 46 22.3 145 4 US-09-142-320-13
33 46 22.3 145 4 US-09-142-320-14
34 46 22.3 145 4 US-09-142-320-15
35 46 22.3 145 4 US-09-142-320-16
36 46 22.3 165 2 US-08-709-924-2
37 46 22.3 165 2 US-08-709-925-2
38 46 22.3 307 4 US-08-804-166-4
39 46 22.3 307 4 US-08-910-991-4
40 46 22.3 336 4 US-08-804-166-8
41 46 22.3 336 4 US-08-910-991-8
42 46 22.3 454 2 US-09-014-969-9
43 46 22.3 472 4 US-08-976-255-17
44 46 22.3 1040 2 US-08-254-989-2
45 45.5 22.1 771 4 US-09-188-930-183

ALIGNMENTS

RESULT 1

US-09-084-079-5

; Sequence 5, Application US/09084079

; Patent No. 6150136

; GENERAL INFORMATION:

; APPLICANT: Bronstein, Jeff M.

; APPLICANT: Seitz, Robert S.

; APPLICANT: Lallone, Roger L.

; TITLE OF INVENTION: Oligodendrocyte-specific Protein and Method for

; TITLE OF INVENTION: Diagnosing and Treating Disease

; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Sheldon & Max

; STREET: 225 S. Lake Avenue, 9th Floor

; CITY: Pasadena

; STATE: California

; ZIP: 91101

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage

; COMPUTER: IBM compatible

; OPERATING SYSTEM: Windows 95

; SOFTWARE: WordPerfect for Windows version 8.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/084.079

; FILING DATE: 22-MAY-1998

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Farah, David A.

; REGISTRATION NUMBER: 38,134

; REFERENCE/DOCKET NUMBER: 11201-1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (626)796-4000

; TELEFAX: (626)795-6321

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 218 amino acid residues

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-09-084-079-5

Query Match 24.3% Score 50; DB 4; Length 218;

Best Local Similarity 30.0%; Pred. No. 14;

Matches 9; Conservative 7; Mismatches 14; Indels 0; Gaps 0;

QY 8 IILCQSLHITQLILRCVCAPCRSGSPG 37

DB 84 LMTAASVLGLPAILLITVLPCIRMGPEPG 113

RESULT 3
US-08-972-631-2
; Sequence 2, Application US/08972631
; Patent No. 5856133
; GENERAL INFORMATION:
; APPLICANT: Stephens, Len
; APPLICANT: Hawkins, Phillip T.
; TITLE OF INVENTION: G-BETA-GAMMA REGULATED
; TITLE OF INVENTION: PHOSPHATIDYLINOSITOL-3, KINASE
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 2730 Sand Hill Road
; CITY: Menlo Park
; STATE: California

```

Query Match          24.3%; Score 50; DB 2; Length 877;
Best Local Similarity 33.3%; Pred. No. 64;
Matches 11; Conservative 5; Mismatches 17; Indels 0; Gaps 0;

QY      3 STPVKIILQSILHITOLIRCYCAPCRRSGSS 35
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RESULT      4
US-08-972-629-2
; Sequence 2, Application US/08972629
; Patent No. 5859201
; GENERAL INFORMATION:
; APPLICANT: Stephens, Len
; APPLICANT: Hawkins, Phillip T.
; TITLE OF INVENTION: G-BETA-GAMMA REGULATED
; TITLE OF INVENTION: PHOSPHATIDYLINOSITOL-3', KINASE
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: pennie & Edmonds
; STREET: 2730 Sand Hill Road
; CITY: Menlo Park
; STATE: California
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/972,629
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/672,211
; FILING DATE: 27-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Halluin, Albert P.
; REGISTRATION NUMBER: 25,277
; REFERENCE/DOCKET NUMBER: 8549-0005-999

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DB 809 SCFPAVCLDQDERKILQSVIRCEVSPCKPEKS 841
RESULT 6
US-08-672-211-2 ; Sequence 2, Application US/08672211
; Patent No. 5874273
; GENERAL INFORMATION:
; APPLICANT: Stephens, Len
; APPLICANT: Hawkins, Phillip T.
; TITLE OF INVENTION: G-BETA-GAMMA REGULATED
; TITLE OF INVENTION: PHOSPHATIDYLINOSITOL-3,
; KINASE

NUMBER OF SEQUENCES: 10
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: pennie & Edmonds
 STREET: 2730 Sand Hill Road
 CITY: Menlo Park
 STATE: California
 COUNTRY: USA
 ZIP: 94025

STREET: 2730 Sand Hill Road
CITY: Menlo Park
STATE: California
COUNTRY: USA
ZIP: 94025

CONTROLLER READABLE FORM.

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/672,211

FILING DATE: 27-JUN-1996

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Halluin, Albert P.

REGISTRATION NUMBER: 25,277

REFERENCE/DOCKET NUMBER: 8549-0005-999

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415)854-3660

TELEFAX: (415)854-3694

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 877 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: unknown

MOLECULE TYPE: peptide

PS-08-672-211-2

Query Match 24.3%; Score 50; DB 2; Length 877;
Best Local Similarity 33.3%; Pred. No. 64;
Matches 11; Conservative 5; Mismatches 17; Indels 0; Gaps 0;

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QY      3  STPVKIILQSIILHITQILIRCYCAPORRSGSS  35
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DB      809  SCFFAVCLDQERKILQSVIRCEVSPCYKPEKS' 841

RESULT  7
US-09-225-170-2
; Sequence 2, Application US/09225170
; Patent No. 6017763
; GENERAL INFORMATION:
; APPLICANT: Stephens, Len
; APPLICANT: Hawkins, Phillip Thomas
; APPLICANT: Braselmann, Sylvia
; TITLE OF INVENTION: G-BETA-GAMMA REGULATED
; TITLE OF INVENTION: PHOSPHATIDYLINOSITOL-3',
KINASE

```

ADDRESSEE: Pennie & Edmonds, LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA

STATE: NY
COUNTRY: USA

TELEPHONE: (818) 795-4000
TELEFAX: (818) 795-6321

TELEPHONE: (818) 796-4000
TELEFAX: (818) 795-5231

A;Molecule type: mRNA

Query Match 25.7%; Score 53; DB 2; Length 118;
 Best Local Similarity 56.2%; Pred. No. 7.3;
 Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 22 LRCYCPCRRSGSPG 37
 | | | | | | | | | |
 Db 86 LSCGCPCLRSSDCG 101

RESULT 9

PN0139

lutropin beta chain - minke whale

N:Alternate names: luteinizing hormone beta chain

C:Species: Balaenoptera acutorostrata (minke whale, lesser rorqual)

C>Date: 07-May-1993 #sequence_revision 07-May-1993 #text_change 08-Dec-1995

C:Accession: PN0139

R:Karasev, V.S.; Pankov, Y.A.

Biochimia 50, 1972-1986, 1985

A:Title: Amino acid sequence of reduced and carboxymethylated alpha- and beta-subunits of

A:Reference number: PN0138

A:Accession: PN0139

A:Molecule type: protein

A:Residues: 1-118 <KAR>

A:Note: article in Russian with English abstract

C:Superfamily: pituitary glycoprotein hormone beta chain

C:Keywords: glycoprotein; hormone

F:9-34,23-57,26-88,38-110,72-100,90-93/Disulfide bonds: #status predicted

F:13/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match

25.7%; Score 53; DB 2; Length 118;

Best Local Similarity 56.2%; Pred. No. 7.3;

Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 22 LRCYCPCRRSGSPG 37

| | | | | | | | | |

Db 86 LSCGCPCLRSSBCG 101

RESULT 10

UTPG8

lutropin beta chain precursor - pig

N:Alternate names: interstitial cell-stimulating hormone (ICSH) beta chain; luteinizing

C:Species: Sus scrofa domestica (domestic pig)

C>Date: 24-Apr-1984 #sequence_revision 30-Jun-1993 #text_change 16-Jun-2000

C:Accession: A48170; A30322; A01501; A60584

R:Ezashi, T.; Hirai, T.; Kato, T.; Wakabayashi, K.; Kato, Y.

J. Mol. Endocrinol. 5, 137-146, 1990

A:Title: The gene for the beta subunit of porcine LH: clusters of GC boxes and CACCC ele

A:Reference number: A48170; MUID:91063934

A:Accession: A48170

A:Molecule type: DNA

A:Residues: 1-141 <EZA>

A:Cross-references: GB:D00579; NID:g217693; PIDN:BAA00457.1; PID:g217694

R:Kato, Y.; Hirai, T.

Mol. Cell. Endocrinol. 62, 47-53, 1989

A:Title: Cloning and DNA sequence analysis of the cDNA for the precursor of porcine lute

A:Reference number: A30322; MUID:89306142

A:Accession: A30322

A>Status: not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-141 <KAT>

R:Maguini-Rogister, G.; Hennen, G.

Eur. J. Biochem. 39, 235-253, 1973

A:Title: Luteinizing hormone. The primary structures of the beta-subunit from bovine and

A:Reference number: A91212; MUID:74075724

A:Accession: A01501

A:Molecule type: protein

A:Residues: 21-29, 'Z', 31-39, 'D', 41-61, 'R', 63-82, 'I', 84-86, 'S', 88-121, 'PG', 124-133, 'P', 13

A:Note: 30-Arg was also found

A:Note: about half the chains lack one or both carboxyl-terminal leucines

R:Nomura, K.; Ohmura, K.; Nakamura, Y.; Horiba, N.; Shirakura, Y.; Sato, Y.; Ujihara, M.

Endocrinology 124, 712-719, 1989

C:Superfamily: Caenorhabditis elegans hypothetical protein ZK721.4

A:Title: Porcine luteinizing hormone isoform(s): relationship between their molecular
 A:Reference number: A60584; MUID:89107050

A:Accession: A60584

A:Molecule type: protein

A:Residues: 21-31;137-139 <NOM>

A:Note: the lutropin beta chain is heterogeneous at the carboxyl end; this form lacks

C:Genetics:

A:Introns: 5/3; 61/3

C:Superfamily: pituitary glycoprotein hormone beta chain

C:Keywords: blocked amino end; glycoprotein; hormone

F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-141/Product: lutropin beta chain #status experimental <MAT>

F:21/Modified site: blocked amino end (Ser) (in mature form) (probably acetylated) #s

F:29-54,43-77,46-108,58-130,92-120,110-113/Disulfide bonds: #status predicted

F:33/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match

25.7%; Score 53; DB 1; Length 141;

Best Local Similarity 56.2%; Pred. No. 8.4;

Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 22 LRCYCPCRRSGSPG 37

| | | | | | | | | |

Db 106 LSCGCPCLRSSDCG 121

RESULT 11

JG0177

LEP precursor - Korean leech

C:Species: Hirudo nipponia (Korean leech)

C>Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 19-May-2000

C:Accession: JG0177

R:Minakata, H.; Ikeda, T.; Nagahama, T.; Oumi, T.; Ukena, K.; Matsushima, O.; Kawano,

Biosci. Biotechnol. Biochem. 63, 443-445, 1999

A:Title: Comparison of precursor structures of the GNG peptides derived from the ear

A:Reference number: JG0176; MUID:99209006

A:Accession: JG0177

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-111 <MIN>

A:Cross-references: DDBJ:D63651

C:Superfamily: leech LEP precursor

Query Match

25.5%; Score 52.5; DB 2; Length 111;

Best Local Similarity 40.0%; Pred. No. 8.1;

Matches 12; Conservative 6; Mismatches 7; Indels 5; Gaps 1;

QY 8 ILQCQSLHITQLILRCYCPCRRSGSPG 37

: | | | | | | | | | |

Db 6 LVLCISLLHWTRGVERRY-----RLGSDEG 30

RESULT 12

T27983

hypothetical protein ZK721.4 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000

C:Accession: T27983

R:Miller, N.

submitted to the EMBL Data Library, November 1995

A:Description: The sequence of C. elegans cosmid ZK721.

A:Reference number: Z20450

A:Accession: T27983

A>Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-154 <MIL>

A:Cross-references: EMBL:U40951; PIDN:AAA81733.1; CESP:ZK721.4

C:Genetics:

A:Gene: CESP:ZK721.4

A:Introns: 30/3; 80/2

C:Superfamily: Caenorhabditis elegans hypothetical protein ZK721.4

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 23, 2001, 15:36:16 ; Search time 62.39 seconds
(without alignments)
20.864 Million cell updates/sec

Title: US-08-887-977-10_COPY_1_38
Perfect score: 206
Sequence: 1 MFSPVKILLQCSILHQLILRCYCPCRRSGSPGY 38

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	55	26.7	140	1	CO8B_RAT
2	55	26.7	411	1	RAPS_HUMAN
3	55	26.7	411	1	RAPS_MOUSE
4	54	26.2	141	1	LSHB_HUMAN
5	54	26.2	591	1	CO8B_HUMAN
6	53	25.7	118	1	LSHB_BALAC
7	53	25.7	118	1	LSHB_PHYCA
8	53	25.2	141	1	LSHB_PIG
9	52	25.2	315	1	VN35_ROTTL
10	51	24.8	411	1	RAPS_TORCA
11	51	24.8	444	1	XK_HUMAN
12	50	24.3	141	1	LSHB_BOVIN
13	50	24.3	141	1	LSHB_SHEEP
14	50	24.3	207	1	CLDB_HUMAN
15	50	24.3	877	1	P101_PIG
16	49	23.8	138	1	LSHB_CANFA
17	49	23.8	141	1	LSHB_CERSI
18	49	23.8	141	1	LSHB_MOUSE
19	49	23.8	141	1	LSHB_RAT
20	49	23.8	143	1	LSHB_FELCA
21	49	23.8	165	1	CGHB_PAPAN
22	49	23.8	207	1	CLDB_MOUSE
23	49	23.8	260	1	GLO2_HUMAN
24	49	23.8	260	1	GLO2_RAT
25	49	23.8	431	1	CGVK_HSVSA
26	49	23.8	590	1	CO8B_RABIT
27	48.5	23.5	131	1	KRA3_SHEEP
28	48	23.3	511	1	MVIN_ECOLI
29	47.5	23.1	48	1	RL33_MYCGA
30	47.5	23.1	299	1	SUTL_YEAST
31	47	22.8	128	1	LSHB_PHOSU
32	47	22.8	254	1	UL79_HSV7J
33	46.5	22.6	1896	1	RPB1_DROME

34	46	22.3	74	1	SGS7_DROME
35	46	22.3	165	1	CGHB_HUMAN
36	46	22.3	252	1	PHNP_ECOLI
37	46	22.3	328	1	YLM8_CAEEL
38	46	22.3	336	1	UL16_EBV
39	46	22.3	484	1	US15_HCMVA
40	46	22.3	524	1	MVIN_SALTY
41	46	22.3	971	1	Y029_HUMAN
42	46	22.3	1040	1	RAG1_MOUSE
43	46	22.3	1043	1	RAG1_HUMAN
44	46	22.3	1406	1	CPBX_DROME
45	45.5	22.1	183	1	KITH_FOWPV

ALIGNMENTS

RESULT 1
ID CO8B_RAT STANDARD; PRT; 140 AA.
AC P55314;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE COMPLEMENT COMPONENT C8 BETA CHAIN (FRAGMENT).
GN C8B.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BN/CRL; TISSUE=Liver;
RX MEDLINE=95394451; PubMed=7655162;
RA Kershaw E.B., Chua S.C., Williams J.A., Murphy E.M., Leibel R.L.;
RT "Molecular mapping of SSRs for Pgml and C8b in the vicinity of the
rat fatty locus".
RL Genomics 27:149-154(1995).

CC -!- FUNCTION: C8 IS A CONSTITUENT OF THE MEMBRANE ATTACK COMPLEX.
CC C8 BINDS TO THE C5B-7 COMPLEX, FORMING THE C5B-8 COMPLEX. C5-B8
CC BINDS C9 AND ACTS AS A CATALYST IN THE POLYMERIZATION OF C9.
CC -!- SUBUNIT: C8 IS COMPOSED OF THREE CHAINS: ALPHA, BETA AND GAMMA.
CC THE BETA CHAIN BINDS TO THE C8 ALPHA CHAIN AND TO THE C5B-C7
CC COMPLEX, PRESUMABLY TO C5B. IT IS ESSENTIAL TO THE INCORPORATION
CC OF C8 INTO THE C5B-C8 COMPLEX.
CC -!- SIMILARITY: TO COMPLEMENT FACTORS C6, C7, C9, AND TO PERFORIN.
CC -!- SIMILARITY: CONTAINS 2 TSP TYPE-1 DOMAINS.
CC -!- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
CC -!- SIMILARITY: CONTAINS 1 LDL-RECEPTOR CLASS A DOMAIN.
CC -----
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CC -----
CC EMBL; U20194; AAA82890.1; -
CC InterPro; IPR000561; -
CC InterPro; IPR000884; -
CC InterPro; IPR001862; -
CC InterPro; IPR002172; -
CC Pfam; PF00090; tsp_1; 1.
CC PROSITE; PS00022; EGF_1; 1.
CC PROSITE; PS01186; EGF_2; FALSE NEG.
CC PROSITE; PS01209; LDLRA_1; PARTIAL.
CC PROSITE; PS00068; LDLRA_2; PARTIAL.
CC PROSITE; PS00279; MAC_PERFORIN; PARTIAL.
CC PROSITE; PS00092; TSP1; 1.
CC Complement pathway; Complement alternate pathway; Glycoprotein;
KW Plasma; Membrane attack complex; Cytolysis; EGF-like domain;
KW Repeat.

```
FT NON_TER 1 1 EGF-LIKE.
FT DOMAIN 49 85 TYPE-1 TSP 2.
FT SEQUENCE 92 140
SQ SEQUENCE 140 AA; 15331 MW; F7FDE36325EC0488 CRC64;

Query Match 26.7%; Score 55; DB 1; Length 140;
Best Local Similarity 31.2%; Pred. No. 1.2;
Matches 10; Conservative 9; Mismatches 13; Indels 0; Gaps 0;

QY 2 FSTPVKILQCSILHITQILRCYCPCRRSG 33
Db 31 YSTVKQNMKALEEFOKEVSSCRAPCRNNG 62

RESULT 2
RAPS_HUMAN STANDARD; PRT; 411 AA.
AC Q13702;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE 43 KDA RECEPTOR-ASSOCIATED PROTEIN OF THE SYNAPSE (RAPSYN)
DE (ACETYLCHOLINE RECEPTOR-ASSOCIATED 43 KDA PROTEIN) (43 KDA
DE POSTSYNAPTIC PROTEIN).
GN RAPSN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Muscle;
RX MEDLINE=97001170; PubMed=8812503;
RA Buckel A., Beeson D., James M., Vincent A.;
RT "Cloning of cDNA encoding human rapsyn and mapping of the RAPSN gene
RL locus to chromosome 11p11.2-pl1.1.";
RL Genomics 35:613-616(1996).
CC -!- FUNCTION: THOUGHT TO PLAY SOME ROLE IN ANCHORING OR STABILIZING
CC THE NICOTINIC ACETYLCHOLINE RECEPTOR AT SYNAPTIC SITES. IT MAY
CC LINK THE RECEPTOR TO THE UNDERLYING POSTSYNAPTIC CYTOSKELETON,
CC POSSIBLY BY DIRECT ASSOCIATION WITH ACTIN OR SPECTRIN.
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC SURFACE OF POSTSYNAPTIC
CC MEMBRANES.
CC -!- DOMAIN: A CYSTEINE-RICH REGION HOMOLOGOUS TO PART OF THE
CC REGULATORY DOMAIN OF PROTEIN KINASE C MAY BE IMPORTANT IN
CC INTERACTIONS OF THIS PROTEIN WITH THE LIPID BILAYER.
CC -!- SIMILARITY: BELONGS TO THE RAPSN FAMILY.
CC -----
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CC -----
CC EMBL; Z33905; CAA83954.1;
CC MIM; 601592;
CC InterPro: IPR001237;
CC PRINTS; PR00217; POSTSYNAPTIC.
CC PROSITE; PS00405; 43_KD_POSTSYNAPTIC; 1.
CC Synapse; Postsynaptic membrane; Cytoskeleton; Phosphorylation;
CC Myristate.
CC INIT_MET 0 0 BY SIMILARITY.
CC LIPID 1 1 MYRISTATE (BY SIMILARITY).
CC MOD_RES 195 195 PHOSPHORYLATION (POTENTIAL).
CC FT MOD_RES 404 404 PHOSPHORYLATION (POTENTIAL).
CC FT DOMAIN 362 398 INVOLVED IN MEMBRANE ASSOCIATION
CC (POTENTIAL).
CC SEQUENCE 411 AA; 46199 MW; 6A9FBA4B95E58BC CRC64;
```

```
Query Match 26.7%; Score 55; DB 1; Length 411;
Best Local Similarity 37.1%; Pred. No. 3.2;
Matches 13; Conservative 1; Mismatches 9; Indels 12; Gaps 2;

QY 11 CQSILHITQILRCY-----CAPCRSSGSSSPCY 38
Db 381 CSHIFH-----LRCLQNNGTRSCPCNRRSSMKPGF 410

RESULT 3
RAPS_MOUSE STANDARD; PRT; 411 AA.
AC P12672;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE 43 KDA RECEPTOR-ASSOCIATED PROTEIN OF THE SYNAPSE (RAPSYN)
DE (ACETYLCHOLINE RECEPTOR-ASSOCIATED 43 KDA PROTEIN) (43 KDA
DE POSTSYNAPTIC PROTEIN).
GN RAPSN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Muscle;
RX MEDLINE=89289985; PubMed=2737281;
RA Froehner S.C.;
RT "Expression of RNA transcripts for the postsynaptic 43 kDa protein in
RL innervated and denervated rat skeletal muscle.";
RL FEBS Lett. 249:229-233(1989).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Muscle;
RX MEDLINE=89008468; PubMed=3170600;
RA Fraill D.E., McLaughlin L.L., Mudd J., Merlie J.P.;
RT "Identification of the mouse muscle 43,000-dalton acetylcholine
RL receptor-associated protein (RAPSYN) by cDNA cloning.";
RL J. Biol. Chem. 263:15602-15607(1988).
CC -!- FUNCTION: THOUGHT TO PLAY SOME ROLE IN ANCHORING OR STABILIZING
CC THE NICOTINIC ACETYLCHOLINE RECEPTOR AT SYNAPTIC SITES. IT MAY
CC LINK THE RECEPTOR TO THE UNDERLYING POSTSYNAPTIC CYTOSKELETON,
CC POSSIBLY BY DIRECT ASSOCIATION WITH ACTIN OR SPECTRIN.
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC SURFACE OF POSTSYNAPTIC
CC MEMBRANES.
CC -!- DOMAIN: A CYSTEINE-RICH REGION HOMOLOGOUS TO PART OF THE
CC REGULATORY DOMAIN OF PROTEIN KINASE C MAY BE IMPORTANT IN
CC INTERACTIONS OF THIS PROTEIN WITH THE LIPID BILAYER.
CC -!- SIMILARITY: BELONGS TO THE RAPSN FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X15788; CAA33789.1;
CC DR EMBL; J03962; AAA40030.1;
CC DR PIR; S04488; S04488.
CC DR PIR; A31995; A31995.
CC DR MGD; MGI:99422; Rapsn.
CC InterPro: IPR001237;
CC PRINTS; PR00217; POSTSYNAPTIC.
CC PROSITE; PS00405; 43_KD_POSTSYNAPTIC; 1.
CC Synapse; Postsynaptic membrane; Cytoskeleton; Phosphorylation;
CC Myristate.
CC INIT_MET 0 0 MYRISTATE.
CC LIPID 1 1 PHOSPHORYLATION (POTENTIAL).
CC FT MOD_RES 195 195 PHOSPHORYLATION (POTENTIAL).
CC FT MOD_RES 404 404 PHOSPHORYLATION (POTENTIAL).
```

RT	resonance
RL	Mol. 1
RN	[7]

DR Pfam; PF00007; Cys_knot; 1.
 DR PRINTS; PR00438; GFCYSKNOT.
 DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
 DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; FALSE_NEG.
 KW Hormone; Glycoprotein.
 FT DISULFID 9 57 BY SIMILARITY.
 FT DISULFID 23 72 BY SIMILARITY.
 FT DISULFID 26 110 BY SIMILARITY.
 FT DISULFID 34 88 BY SIMILARITY.
 FT DISULFID 38 90 BY SIMILARITY.
 FT DISULFID 93 100 BY SIMILARITY.
 FT CARBOHYD 13 13 N-LINKED (GLCNAC...).
 SQ SEQUENCE 118 AA; 12414 MW; 039F229EFC480F5D CRC64;

Query Match 25.7%; Score 53; DB 1; Length 118;
 Best Local Similarity 56.2%; Pred. No. 2;
 Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 22 LRCYCAPCRRSGSSPG 37
 I I I I I I I I
 DB 86 LSCGCGPCLSSBSCG 101

RESULT 7

LSHB_PHYCA STANDARD; PRT; 118 AA.
 AC P25330;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE LUTROPIN BETA CHAIN (LUTEINIZING HORMONE BETA SUBUNIT) (LSH-BETA)
 DE (LSH-B) (LH-B).
 GN LHB.
 OS Physeter catodon (Sperm whale) (Physeter macrocephalus).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti;
 OC Physeteridae; Physeter.
 OX NCBI_TaxID=9755;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=87032654; PubMed=3771098;
 RA Pankov Y.A., Karasov V.S.;
 RT "Primary structure of sperm whale luteinizing hormone.";
 RL Int. J. Pept. Protein Res. 28:124-129(1986).
 RN [2]
 RP SEQUENCE.
 RX MEDLINE=84281133; PubMed=6466737;
 RA Pankov Y.A., Karasev V.S.;
 RT "Luteinizing hormone of the sperm whale. Amino acid sequences of reduced and carboxymethylated beta-subunits.";
 RL Biochimica 49:1004-1018(1984).
 CC -!- FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.
 CC -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN, LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
 CC -!- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN FAMILY.
 CC PIR; P0141; P0141.
 DR HSP; P01233; 1HRP.
 DR InterPro; IPR000359; -
 DR InterPro; IPR001545; -
 DR InterPro; IPR002400; -
 Pfam; PF00007; Cys_knot; 1.
 DR PRINTS; PR00438; GFCYSKNOT.
 DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
 DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
 KW Hormone; Glycoprotein.
 FT DISULFID 9 57 BY SIMILARITY.
 FT DISULFID 23 72 BY SIMILARITY.
 FT DISULFID 26 110 BY SIMILARITY.
 FT DISULFID 34 88 BY SIMILARITY.

FT DISULFID 38 90 BY SIMILARITY.
 FT DISULFID 93 100 BY SIMILARITY.
 FT CARBOHYD 13 13 N-LINKED (GLCNAC...).
 SQ SEQUENCE 118 AA; 12412 MW; 81177A56382F15E7 CRC64;

Query Match 25.7%; Score 53; DB 1; Length 118;
 Best Local Similarity 56.2%; Pred. No. 2;
 Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 22 LRCYCAPCRRSGSSPG 37
 I I I I I I I I
 DB 86 LSCGCGPCLSSDCG 101

RESULT 8

LSHB_PIG STANDARD; PRT; 141 AA.
 AC P01232;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE LUTROPIN BETA CHAIN PRECURSOR (LUTEINIZING HORMONE BETA SUBUNIT) (LSH-BETA) (LH-B).
 GN LHB.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91063934; PubMed=1701088;
 RA Ezashi T., Hirai T., Kato T., Wakabayashi K., Kato Y.;
 RT "The gene for the beta subunit of porcine LH: clusters of GC boxes and CACC elements.";
 RL J. Mol. Endocrinol. 5:137-146(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89306142; PubMed=2744222;
 RA Kato Y., Hirai T.;
 RT "Cloning and DNA sequence analysis of the cDNA for the precursor of porcine luteinizing hormone (LH) beta subunit.";
 RL Mol. Cell. Endocrinol. 62:47-53(1989).
 RN [3]
 RP SEQUENCE OF 21-139.
 RX MEDLINE=74075724; PubMed=4770795;
 RA Maghain-Rogister G., Hennen G.;
 RT "Luteinizing hormone. The primary structures of the beta-subunit from bovine and porcine species.";
 RL Eur. J. Biochem. 39:235-253(1973).
 CC -!- FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.
 CC -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN, LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
 CC -!- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN FAMILY.
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 CC EMBL; D00579; BAA00457.1; -
 DR PIR; A30322; UTEGB.
 DR PIR; A48170; A48170.
 DR HSP; P01233; 1HRP.
 DR InterPro; IPR000359; -
 DR InterPro; IPR001545; -
 DR InterPro; IPR002400; -

DR Pfam: PF00007; Cys_knot; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR PROSITE; PS00261; GLYCO.HORMONE.BETA_1; 1.
DR PROSITE; PS00689; GLYCO.HORMONE.BETA_2; 1.
KW Hormone; Signal; Glycoprotein.
FT SIGNAL 1 20
FT CHAIN 21 141 LUTROPIN BETA CHAIN.
FT DISULFID 29 77 BY SIMILARITY.
FT DISULFID 43 92 BY SIMILARITY.
FT DISULFID 46 130 BY SIMILARITY.
FT DISULFID 54 108 BY SIMILARITY.
FT DISULFID 58 110 BY SIMILARITY.
FT DISULFID 113 120 BY SIMILARITY.
FT CARBOHYD 33 33 N-LINKED (GLCNAC. . .).
FT MOD_RES 21 21 BLOCKED.
FT VARIANT 30 30 R -> Z.
FT CONFLICT 40 40 N -> D (IN REF. 3).
FT CONFLICT 62 62 V -> R (IN REF. 3).
FT CONFLICT 83 83 S -> I (IN REF. 3).
FT CONFLICT 87 87 I -> S (IN REF. 3).
FT CONFLICT 122 123 GP -> PG (IN REF. 3).
SQ SEQUENCE 141 AA; 14889 MW; 803E8E7C59F3C2CF CRC64;

Query Match 25.7%; Score 53; DB 1; Length 141;
Best Local Similarity 56.2%; Pred. No. 2.3;
Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 22 LRCYCPCRRSGSPG 37
| : | : | : | : | : |
DB 106 LSCGCGPCLSSDCG 121

RESULT 9
VN35_ROT1 STANDARD; PRT; 315 AA.
AC Q03244;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE NONSTRUCTURAL RNA-BINDING PROTEIN 35 (NS35) (NCVP3).
GN S7.
OS Turkey rotavirus (serotype 7 / strain Ty-1).
OC Viruses; dsRNA viruses; Reoviridae; Rotavirus.
OX NCBI_TaxID=36445;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93134787; PubMed=8380660;
RA Patton J.T., Salter-Cid L., Kalbach A., Mansell E.A., Kattoura M.;
RT "Nucleotide and amino acid sequence analysis of the rotavirus
nonstructural RNA-binding protein NS35.";
RL Virology 192:438-446(1993).
CC -!- FUNCTION: ESSENTIAL FOR GENOME REPLICATION AND FOR THE FORMATION
OF THE VYROPLASM. IT MAY ALSO BE IMPORTANT IN VIRAL RNA PACKAGING.
CC
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or send an email to license@isb-sib.ch).
CC
CC EMBL; L04533; AAA47300.1; .
KW Nonstructural protein; RNA-binding.
FT DOMAIN 204 240 RNA-BINDING (POTENTIAL).
SQ SEQUENCE 315 AA; 35930 MW; B4FB84AB69EA65C6 CRC64;

Query Match 25.2%; Score 52; DB 1; Length 315;
Best Local Similarity 57.1%; Pred. No. 6.3;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 22 LRCYCPCRRSGSS 35
| : | : | : | : | : |
DB 4 LACFCVPCDREGAS 17

RESULT 10
RAPS_TORCA STANDARD; PRT; 411 AA.
AC P09108;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DE 30-KDA RECEPTOR-ASSOCIATED PROTEIN OF THE SYNAPSE (RAPSYN)
DE 43 KDA RECEPTOR-ASSOCIATED 43 KDA PROTEIN (43 KDA
DE (ACETYLCHOLINE RECEPTOR-ASSOCIATED 43 KDA PROTEIN)
DE POSTSYNAPTIC PROTEIN).
GN RAPSIN.
OS Torpedo californica (Pacific electric ray).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Squalia; Hymnosqualia; Pristiorajae; Batoidae;
OC Torpediniformes; Torpedinoidei; Torpedinidae; Torpedo.
OX NCBI_TaxID=7787;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87317641; PubMed=3476945;
RA Fraill D.E., Mudd J., Shah V., Carr C., Cohen J.B., Merlie J.P.;
RT "cDNAs for the postsynaptic 43-kDa protein of Torpedo electric organ
encode two proteins with different carboxyl termini.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:6302-6306(1987).
RN [2]
RP SEQUENCE OF 8-412.
RX MEDLINE=88107644; PubMed=3427060;
RA Carr C., McCourt D., Cohen J.B.;
RT "The 43-kilodalton protein of Torpedo nicotinic postsynaptic
membranes: purification and determination of primary structure.";
RL Biochemistry 26:7090-7102(1987).
RN [3]
RP MYRISTOYLATION.
RX MEDLINE=88331095; PubMed=3417776;
RA Musil L.S., Carr C., Cohen J.B., Merlie J.P.;
RT "Acetylcholine receptor-associated 43K protein contains covalently
bound myristate.";
RL J. Cell Biol. 107:1113-1121(1988).
CC -!- FUNCTION: THOUGHT TO PLAY SOME ROLE IN ANCHORING OR STABILIZING
THE NICOTINIC ACETYLCHOLINE RECEPTOR AT SYNAPTIC SITES. IT MAY
LINK THE RECEPTOR TO THE UNDERLYING POSTSYNAPTIC CYTOSKELETON,
POSSIBLY BY DIRECT ASSOCIATION WITH ACTIN OR SPECTRIN.
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC SURFACE OF POSTSYNAPTIC
MEMBRANES.
CC -!- ALTERNATIVE PRODUCTS: THERE ARE AT LEAST TWO DISTINCT PROTEINS
EXPRESSED, WHICH DIFFER IN THEIR C-TERMINUS.
CC -!- DOMAIN: A CYSTEINE-RICH REGION HOMOLOGOUS TO PART OF THE
REGULATORY DOMAIN OF PROTEIN KINASE C MAY BE IMPORTANT IN
INTERACTIONS OF THIS PROTEIN WITH THE LIPID BILAYER.
CC -!- SIMILARITY: BELONGS TO THE RAPSIN FAMILY.
CC
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CC
CC EMBL; J02952; AAA49282.1; .
DR EMBL; J02953; AAA49283.1; .
DR PIR; A28009; A28009.
DR InterPro; IPR001237; .
DR InterPro; IPR001841; .
DR Pfam; PF00097; zf-C3HC4; 1.
DR PRINTS; PS00217; POSTSYNAPTIC.
DR PROSITE; PS00405; 43 KD POSTSYNAPTIC; 1.
KW Synapse; Postsynaptic membrane; Cytoskeleton; Phosphorylation;
Myristate; Alternative splicing.

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FT INTL_MET 0 0 MYRISTATE.
FT LIPID 1 1
FT MOD_RES 195 195 PHOSPHORYLATION (POTENTIAL).
FT MOD_RES 404 404 PHOSPHORYLATION (POTENTIAL).
FT DOMAIN 362 398 INVOLVED IN MEMBRANE ASSOCIATION
(POTENTIAL).
FT VARSPLIC 399 411 MISSING (IN SHORT ISOFORM).
FT CONFLICT 361 361 Y -> T (IN REF. 2).
FT CONFLICT 393 393 N -> D (IN REF. 2).
FT CONFLICT 410 410 Y -> T (IN REF. 2).
SQ SEQUENCE 411 AA; 46321 MW; 4D26262679C9B4D CRC64;

Query Match 24.8%; Score 51; DB 1; Length 411;
Best Local Similarity 25.6%; Pred. No. 11;
Matches 11; Conservative 8; Mismatches 12; Indels 12; Gaps 2;

Qy 3 STPVKIIICQSLHITQLILRCY-----CAPCRSGSGSPGY 38
Db 373 NSQALPCSHLFH-----LKQLTNGRCPCNKRSSVKPGY 410

RESULT 11
XK_HUMAN
AC P51811; STANDARD; PRT; 444 AA.
DT 01-OCT-1996 (Rel. 34, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DE 01-OCT-2000 (Rel. 40, Last annotation update)
DE MEMBRANE TRANSPORT PROTEIN XK (KX ANTIGEN).
GN XK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=94273191; PubMed=8004674;
RT "Isolation of the gene for McLeod syndrome that encodes a novel
membrane transport protein.";
RL Cell 77:869-880(1994).
RN [2]
RP REVISIONS TO 204-205.
RA Ho M.F.;
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: MAY BE INVOLVED IN SODIUM-DEPENDENT TRANSPORT OF NEUTRAL
AMINO ACIDS OR OLIGOPEPTIDES.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
CC -!- TISSUE SPECIFICITY: HIGH LEVELS IN SKELETAL MUSCLE, HEART, BRAIN,
AND PANCREAS; LOW LEVELS IN PLACENTA, LUNG, LIVER, AND KIDNEY.
CC -!- POLYMORPHISM: XK IS RESPONSIBLE FOR THE KX BLOOD GROUP SYSTEM.
CC -!- DISEASE: DEFECTS IN XK ARE THE CAUSE OF MCLEOD SYNDROME, AN X-
LINKED MULTISYSTEM DISORDER CHARACTERIZED BY ABNORMALITIES IN THE
NEUROMUSCULAR AND HEMATOPOIETIC SYSTEMS.
CC -----
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CC -----
CC EMBL; 232684; CAA83632.1;
CC MIM; 314850;
DR Transmembrane; Transport; Amino-acid transport; Blood group antigen.
KW DOMAIN 1 2 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 3 23 POTENTIAL.
FT DOMAIN 24 37 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 38 58 POTENTIAL.
FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 69 89 POTENTIAL.

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FT DOMAIN 90 140 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 141 161 POTENTIAL.
FT DOMAIN 162 171 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 172 192 POTENTIAL.
FT DOMAIN 193 208 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 209 229 POTENTIAL.
FT DOMAIN 230 235 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 236 256 POTENTIAL.
FT DOMAIN 257 277 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 278 298 POTENTIAL.
FT DOMAIN 299 317 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 318 338 POTENTIAL.
FT DOMAIN 339 349 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 350 370 POTENTIAL.
FT DOMAIN 371 444 CYTOPLASMIC (POTENTIAL).
SQ SEQUENCE 444 AA; 50876 MW; E94BDD0E3BEF7AB2 CRC64;

Query Match 24.8%; Score 51; DB 1; Length 444;
Best Local Similarity 36.7%; Pred. No. 12;
Matches 11; Conservative 4; Mismatches 15; Indels 0; Gaps 0;

Qy 2 FSTPVKIIICQSLHITQLILRCYCACPQR 31
Db 372 FFHCKKLFSSVSEGFQWLRCFCWACRQ 401

RESULT 12
LSHB_BOVIN
ID LSHB_BOVIN STANDARD; PRT; 141 AA.
AC P04651;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE LUTROPIN BETA CHAIN PRECURSOR (LUTEINIZING HORMONE BETA SUBUNIT) (LSH-
BETA) (LSH-B) (LH-B).
GN LHB.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=85207729; PubMed=2987241;
RA Virgin J.B., Silver B.J., Thomson A.R., Nilson J.H.;
RT "The gene for the beta subunit of bovine luteinizing hormone encodes
a gonadotropin mRNA with an unusually short 5'-untranslated region.";
J. Biol. Chem. 260:7072-7077(1985).
RN [2]
RP SEQUENCE FROM N.A.
RA MEDLINE=85182575; PubMed=3838746;
RA Maurer R.A.;
RT "Analysis of several bovine lutropin beta subunit cDNAs reveals
heterogeneity in nucleotide sequence.";
J. Biol. Chem. 260:4684-4687(1985).
RN [3]
RP SEQUENCE OF 21-139.
RX MEDLINE=74075724; PubMed=4770795;
RA Maghuln-Rogister G., Hennen G.;
RT "Luteinizing hormone. The primary structures of the beta-subunit from
bovine and porcine species.";
Eur. J. Biochem. 39:235-253(1973).
CC -!- FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING
THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.
CC -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
CC -!- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN
FAMILY.
CC -----
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DR EMBL; M10077; AAA30623.1; -;
 DR EMBL; M11506; AAB59267.1; -;
 DR PIR; A01499; UTBOB.
 DR HSSP; P01233; LHRP.
 DR GlycoSuiteDB; P04651; -;
 DR InterPro; IPR000359; -;
 DR InterPro; IPR001545; -;
 DR InterPro; IPR002400; -;
 DR Pfam; PF00007; Cys_knot; 1.
 DR PRINTS; PR00438; GFCYSKNOT.
 DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
 DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
 KW Hormone; Signal; Glycoprotein.
 FT SIGNAL 1 20
 FT CHAIN 21 141 LUTROPIN BETA CHAIN.
 FT DISULFID 29 77 BY SIMILARITY.
 FT DISULFID 43 92 BY SIMILARITY.
 FT DISULFID 46 130 BY SIMILARITY.
 FT DISULFID 54 108 BY SIMILARITY.
 FT DISULFID 58 110 BY SIMILARITY.
 FT DISULFID 113 120 BY SIMILARITY.
 FT CARBOHYD 33 33 N-LINKED (GLCNAC...).
 FT CONFLICT 1 2 MISSING (IN REF. 2).
 FT CONFLICT 74 74 Q -> E (IN REF. 3).
 FT CONFLICT 112 112 P -> S (IN REF. 2).
 FT CONFLICT 122 123 GP -> PG (IN REF. 3).
 FT CONFLICT 126 126 Q -> E (IN REF. 3).
 SQ SEQUENCE 141 AA; 15202 MW; 44Pb1CBD4901BC95 CRC64;

Query Match 24.3%; Score 50; DB 1; Length 141;
 Best Local Similarity 50.0%; Pred. No. 5.8;
 Matches 8; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 22 LRCYCAPCRSGSSPG 37

DB 106 LSCHCPCRLSSTDCG 121

RESULT 13

LSHB_SHEEP
 ID LSHB_SHEEP STANDARD; PRT; 141 AA.
 AC P01231;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE LUTROPIN BETA CHAIN PRECURSOR (LUTEINIZING HORMONE BETA SUBUNIT) (LSH-
 DE BETA) (LSH-B) (LH-B) (INTERSTITIAL CELL STIMULATING HORMONE).
 GN LHB.
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Ovis.
 OX NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93351742; PubMed=8349025;
 RA Brown P., McNeilly J.R., Wallace R.M., McNeilly A.S., Clark A.J.;
 FT "Characterization of the ovine LH beta-subunit gene: the promoter
 FT directs gonadotrope-specific expression in transgenic mice.";
 RL Mol. Cell. Endocrinol. 93:157-165(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Pituitary;
 RX MEDLINE=90245669; PubMed=2336396;
 RA D'Angelo-Bernard G., Mounni M., Jutisz M., Counis R.;
 FT "Cloning and sequence analysis of the cDNA for the precursor of the

RT beta subunit of ovine luteinizing hormone.";
 RL Nucleic Acids Res. 18:2175-2175(1990).
 RN [3]
 RX SEQUENCE OF 21-139.
 RA MEDLINE=72211145; PubMed=4556309;
 RT Liu W.-K., Nahm H.S., Sweeney C.M., Holcomb G.N., Ward D.N.;
 RT "The primary structure of ovine luteinizing hormone. II. The amino
 RT acid sequence of the reduced, S-carboxymethylated A-subunit (LH-
 RT beta).";
 RL J. Biol. Chem. 247:4365-4381(1972).
 RN [4]
 RP SEQUENCE OF 21-139.
 RX MEDLINE=73190035; PubMed=4575435;
 RA Sairam M.R., Samy T.S.A., Pakkoff H., Li C.H.;
 RT "The primary structure of ovine interstitial cell-stimulating
 RT hormone. II. The beta-subunit.";
 RL Arch. Biochem. Biophys. 153:572-586(1972).
 RN [5]
 RP PRELIMINARY ASSIGNMENT OF DISULFIDE BONDS.
 RX MEDLINE=76068152; PubMed=1201911;
 RA Chung D., Sairam M.R., Li C.H.;
 RT "The primary structure of ovine interstitial cell stimulating
 RT hormone. IV: Disulfide bridges of the beta subunit.";
 RL Int. J. Pept. Protein Res. 7:487-493(1975).
 RN [6]
 RP STRUCTURE OF CARBOHYDRATE.
 RX MEDLINE=91006170; PubMed=2209620;
 RA Weisshaar G., Hiyama J., Renwick A.G.C.;
 RT "Site-specific N-glycosylation of ovine lutropin. Structural analysis
 RT by one- and two-dimensional 1H-NMR spectroscopy.";
 RL Eur. J. Biochem. 192:741-751(1990).
 CC -1- FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING
 CC THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.
 CC -1- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
 CC CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
 CC LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
 CC -1- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN
 CC FAMILY.
 CC -----
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 CC -----
 DR EMBL; S64695; AAB27819.1; -;
 DR EMBL; X52488; CAA36729.1; -;
 DR PIR; A01500; UTSNB.
 DR PIR; S09232; S09232.
 DR HSSP; P01233; LHRP.
 DR GlycoSuiteDB; P01231; -;
 DR InterPro; IPR000359; -;
 DR InterPro; IPR001545; -;
 DR InterPro; IPR002400; -;
 DR Pfam; PF00007; Cys_knot; 1.
 DR PRINTS; PR00438; GFCYSKNOT.
 DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
 DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
 KW Hormone; Signal; Glycoprotein.
 FT SIGNAL 1 20
 FT CHAIN 21 141 LUTROPIN BETA CHAIN.
 FT DISULFID 29 77 BY SIMILARITY.
 FT DISULFID 43 92
 FT DISULFID 46 130
 FT DISULFID 54 108 BY SIMILARITY.
 FT DISULFID 58 110 BY SIMILARITY.
 FT DISULFID 113 120
 FT MOD_RES 21 21
 FT CARBOHYD 33 33
 FT VARIANT 138 141
 FT CONFLICT 30 30
 FT N-LINKED (GLCNAC...).
 FT MISSING (IN SOME MOLECULES).
 FT Q -> E (IN REF. 4).

Query Match 24.3%; Score 50; DB 1; Length 207;
Best Local Similarity 30.0%; Pred. No. 8.1;
Matches 9; Conservative 7; Mismatches 14; Indels 0; Gaps 0;

Job time: 648 sec

Search completed: May 23, 2001, 15:36:17
Job time: 648 sec

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OM protein - protein search, using sw model

Run on: May 23, 2001, 15:35:10 ; Search time 189.03 Seconds
(without alignments)
23.562 Million cell updates/sec

Title: US-08-887-977-10_COPY_1_38

Perfect score: 206

Sequence: 1 MFSTPVKIIILCSILHITLILCYCAPCRSGSPGY 38

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL15:*

1: sp.archaea:*

2: sp.bacteria:*

3: sp.fungi:*

4: sp.human:*

5: sp.invertebrate:*

6: sp.mammal:*

7: sp.mhc:*

8: sp.organelle:*

9: sp.phage:*

10: sp.plant:*

11: sp.rodent:*

12: sp.unclassified:*

13: sp.vertebrate:*

14: sp.virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	63	30.6	365	5 Q9W2E0	Q9W2E0 drosophila
2	56.5	27.4	120	1 Q9VAD0	Q9VAD0 aeropyrum p
3	56	27.2	227	4 Q9NV51	Q9NV51 homo sapien
4	54	26.2	279	2 P71734	P71734 mycobacteri
5	54	26.2	9376	2 O85168	O85168 pseudomonas
6	53.5	26.0	111	5 Q25104	Q25104 hirudo nipp
7	53	25.7	678	4 Q9NUT5	Q9NUT5 homo sapien
8	52.5	25.5	111	5 Q25102	Q25102 hirudo nipp
9	52.5	25.5	198	4 Q9P0S8	Q9P0S8 homo sapien
10	51.5	25.0	924	5 Q20016	Q20016 caenorhabdi
11	51	24.8	383	14 O89609	O89609 equine herp
12	50.5	24.5	816	5 Q9U274	Q9U274 caenorhabdi
13	50.5	24.5	1880	5 O18465	O18465 hirudo medi
14	50	24.3	578	11 Q9WU80	Q9WU80 mus musculus
15	50	24.3	1518	10 Q9SH34	Q9SH34 arabidopsis
16	49.5	24.0	249	6 Q9XSD3	Q9XSD3 macaca mula
17	49	23.8	38	6 Q46621	Q46621 tapirus ind
18	49	23.8	61	2 Q50154	Q50154 mycobacteri
19	49	23.8	80	11 Q63013	Q63013 rattus norv

20	49	23.8	82	6	O46622	ceratotheri
21	49	23.8	86	2	Q9WWL8	Q9WWL8 synchococc
22	49	23.8	129	5	O20552	O20552 caenorhabdi
23	49	23.8	135	6	O19102	O19102 ceratotheri
24	49	23.8	139	11	O62778	Q82778 rattus norv
25	49	23.8	141	6	O77835	O77835 ceratotheri
26	49	23.8	141	11	O60844	O60844 mus musculu
27	49	23.8	143	6	O77805	O77805 felis silve
28	49	23.8	157	6	O28306	O28306 canis famil
29	49	23.8	286	4	O9P2V3	O9P2V3 homo sapien
30	49	23.8	315	14	O55586	O55586 avian rotav
31	49	23.8	430	14	O9YTM9	O9YTM9 ateline her
32	49	23.8	687	3	O42955	O42955 schizosacch
33	49	23.8	880	4	O9V2Y2	O9V2Y2 homo sapien
34	48.5	23.5	123	1	O9VBC7	O9VBC7 aeropyrum p
35	48.5	23.5	413	13	O98860	O98860 cynops pyrr
36	48.5	23.5	446	11	O9QX17	O9QX17 mus musculu
37	48.5	23.5	683	3	O9P7Z1	O9P7Z1 schizosacch
38	48.5	23.5	1305	13	O91952	O91952 coturnix co
39	48	23.3	63	14	O64830	O64830 human adeno
40	48	23.3	198	5	O9ULD7	O9ULD7 leishmania
41	48	23.3	219	13	O99370	O99370 gallus gall
42	48	23.3	568	5	O23637	O23637 caenorhabdi
43	48	23.3	658	5	O18215	O18215 caenorhabdi
44	48	23.3	682	11	O9JH13	O9JH13 rattus norv
45	48	23.3	913	5	O9V7G6	O9V7G6 drosophila

ALIGNMENTS

RESULT	1
Q9W2E0	
ID	Q9W2E0 PRELIMINARY; PRT; 365 AA.
AC	Q9W2E0;
DT	01-MAY-2000 (TREMBlrel. 13, Created)
DT	01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DE	01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE	CG15679 PROTEIN.
GN	CG15679.
OS	Drosophila melanogaster (Fruit fly).
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC	Ephydroidea; Drosophilidae; Drosophila.
OX	NCBI_TaxID=7227;
RP	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=BERKELEY;
RX	MEDLINE=20196006; PubMed=10731132;
RA	Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA	Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA	George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA	Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA	Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA	Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA	Abriel J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA	Baliew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA	Beeson K.Y., Benos P.V., Bertram B.P., Bhandari D., Bolshakov S.,
RA	Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA	Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA	Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., de
RA	de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA	Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA	Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA	Fosler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA	Glocke A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA	Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA	Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA	Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA	Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA	Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA	Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA	Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*."
 RL Science 287:2185-2195(2000).
 DR EMBL; AF003454; AAF46752.1; -;
 DR FLYBASE; FBgn0034653; CG15679.
 SQ SEQUENCE 365 AA; 40978 MW; 1BE51C4E809B0198 CRC64;

Query Match 30.6%; Score 63; DB 5; Length 365;
 Best Local Similarity 35.1%; Pred. No. 0.26;
 Matches 13; Conservative 7; Mismatches 9; Indels 8; Gaps 2;

QY 7 KILCOSILHI-----TQILRCYCAPCRSGSSP 36

Db 163 KVFCCSRVNRVDPPTGDETEMKQCFCICPCCR-GSRP 198

RESULT 2

QYAD0 PRELIMINARY; PRT; 120 AA.
 AC QYAD0;
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DE 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
 DE HYPOTHETICAL 13.0 KDA PROTEIN APE2009.
 GN APE2009.
 OS Aeropyrum pernix.
 OC Archaea; Crenarchaeota; Desulfurococcales; Desulfurococcaceae;
 OC Aeropyrum.
 OX NCBI_TaxID=56636;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K1;
 RX MEDLINE=99310339; PubMed=10382966;
 RA Kavarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y.,
 RA Jin-no K., Takahashi M., Sekine M., Baba S., Ankai A., Kosugi H.,
 RA Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,
 RA Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,
 RA Yamazaki J., Kushida N., Oguchi A., Aoki K., Kubota K., Nakamura Y.,
 RA Nomura N., Sako Y., Kikuchi H.;
 RT "Complete genome sequence of an aerobic hyper-thermophilic
 crenarchaeon, *Aeropyrum pernix* K1."
 RL DNA Res. 6:83-101(1999).
 DR EMBL; AP000063; BAA81019.1; -;
 KW Hypothetical protein.
 SQ SEQUENCE 120 AA; 12969 MW; F796EE35809F4660 CRC64;

Query Match 27.4%; Score 56.5; DB 1; Length 120;
 Best Local Similarity 39.5%; Pred. No. 0.9;
 Matches 15; Conservative 5; Mismatches 11; Indels 7; Gaps 1;

QY 6 VKIILCQSLHITQILRC-----YCAPCRSGSSP 36

Db 19 VLLILSSLLILTSULLRLCYWSAAYIFGPRKPGYSP 56

RESULT 3

Q9NV51 PRELIMINARY; PRT; 227 AA.
 ID Q9NV51
 AC Q9NV51;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
 DE CDNA FLJ10920 FTS, CLONE OVARC1000384.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=OVARIAN CANCER;
 RA Isogai T., Oca T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
 RA Nishikawa T., Nagai K., Sugano S., Ishibashi T., Fujimori K.,
 RA Tanai H., Kimata M., Watanabe M., Hiraoka S., Ishii S., Kawai Y.,
 RA Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K.,
 RA Masuho Y., Kanemori K.;
 RT "NEDO human cDNA sequencing project."
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK001782; BAA91907.1; -;
 SQ SEQUENCE 227 AA; 24072 MW; 03146D66E6FC4E30 CRC64;

Query Match 27.2%; Score 56; DB 4; Length 227;
 Best Local Similarity 31.2%; Pred. No. 1.8;
 Matches 15; Conservative 3; Mismatches 10; Indels 20; Gaps 2;

QY 4 TPVKIILCQSLHITQILI-----LRC-YCAPCRR 31

Db 129 TPAGVFLAESALHMAGLAEYPMQGLASAISSGKKRRCGMCAPCRR 176

RESULT 4

P71734 PRELIMINARY; PRT; 279 AA.
 ID P71734
 AC P71734;
 DT 01-FEB-1997 (TrEMBLrel. 02, Created)
 DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
 DE 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
 DE HYPOTHETICAL 31.0 KDA PROTEIN.
 GN RV2409C OR MTCY253.11.
 OS Mycobacterium tuberculosis.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1773;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=H37RV;
 RX MEDLINE=96295987; PubMed=9634230;
 RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
 RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,
 RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
 RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
 RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
 RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
 RA Rutter S., Seeger K., Skellon S., Squares S., Squires R., Sulston J.E.,
 RA Taylor K., Whitehead S., Barrell B.G.;
 RT "Deciphering the biology of *Mycobacterium tuberculosis* from the
 complete genome sequence."
 RL Nature 393:537-544(1998).
 DR EMBL; Z81368; CAB03718.1; -;
 DR TUBERCULIST; RV2409C; -;
 DR INTERPRO; IPR002931; -;
 DR PFAM; PF01841; Transglut_core; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 279 AA; 31029 MW; 0719C275EC8C9908 CRC64;

Query Match 26.2%; Score 54; DB 2; Length 279;
 Best Local Similarity 38.1%; Pred. No. 4.2;
 Matches 8; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 10 LCQSLHITQILRCYCAPCR 30

Db 174 VQDFVHLSLMLVLRSMGIPCR 194

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RESULT 5
O85168 PRELIMINARY; PRT; 9376 AA.
AC O85168;
DT 01-NOV-1998 (TReMBLrel. 08, Created)
DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
DE SYRINGOMYCIN SYNTHETASE.
GN SYRE.
OS Pseudomonas syringae (pv. syringae).
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=321;
RN [1]
RP SEQUENCE FROM N.A.
RA Guenzi E., Grandi G.;
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF047828; AAC80285.1; -
DR HSSP; P14687; IAMU.
DR INTERPRO; IPR000255; -
DR INTERPRO; IPR000873; -
DR INTERPRO; IPR001031; -
DR INTERPRO; IPR001242; -
DR PFAM; PF00501; AMP-binding; 8.
DR PFAM; PF00668; DUF4; 9.
DR PFAM; PF00975; Thioesterase; 1.
DR PRINTS; PR00154; AMPBINDING.
DR PROSITE; PS00012; PHOSPHOTANTHEINE; UNKNOWN_5.
DR PROSITE; PS00455; AMP_BINDING; 8.
DR PROSITE; PS00075; ACP DOMAIN; 9.
SQ SEQUENCE 9376 AA; 1029843 MW; F770C08975EF9CE5 CRC64;

Query Match 26.2%; Score 54; DB 2; Length 9376;
Best Local Similarity 50.0%; Pred. No. 80;
Matches 9; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

Qy 5 PVKILQCSILHITLIL 22
Db 1099 PQVVLQRAELHVTLELL 1116

RESULT 6
Q25104 PRELIMINARY; PRT; 111 AA.
AC Q25104;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-JAN-1998 (TReMBLrel. 05, Last annotation update)
DE PRECURSOR PROTEIN OF LEP.
OS Hirudo nipponia.
OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
OC Arynchobdellida; Hirudiniiformes; Hirudinidae; Hirudo.
OX NCBI_TaxID=42736;
RN [1]
RP SEQUENCE FROM N.A.
RA Kawano T., Ukena K., Ikeda T., Matsushima O., Minakata H.;
RL (In) Nishi N. (eds.);
RL Peptide chemistry, pp.1-1, Protein Research Foundation, Osaka (1995).
DR EMBL; D63651; BAA09804.1; -
SQ SEQUENCE 111 AA; 13032 MW; 7F1E49E158F367A4 CRC64;

Query Match 26.0%; Score 53.5; DB 5; Length 111;
Best Local Similarity 40.0%; Pred. No. 2.3;
Matches 12; Conservative 6; Mismatches 7; Indels 5; Gaps 1;

Qy 8 IILQCSILHITLILRCYCPCRRSGSPG 37
Db 6 LVLCISLLHVTGVERRY-----RLGSDEG 30

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RESULT 7
Q9NUT5 PRELIMINARY; PRT; 678 AA.
AC Q9NUT5;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
DE CDNA FLJ11152 FIS, CLONE PLACE1006901 (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Ishibashi T., Fujimori K.,
RA Tanai H., Kimata M., Watanabe M., Hiraoka S., Ishii S., Kawai Y.,
RA Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K.,
RA Masuho Y., Kanehori K.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK002014; BAA92035.1; -
FT NON_TER 678
SQ SEQUENCE 678 AA; 77715 MW; 44F86BEC221108C1 CRC64;

Query Match 25.7%; Score 53; DB 4; Length 678;
Best Local Similarity 37.5%; Pred. No. 12;
Matches 12; Conservative 4; Mismatches 16; Indels 0; Gaps 0;

Qy 3 STPVKILQCSILHITLILRCYCPCRRSGS 34
Db 517 STPVTPFLCPRIVLVLEVLVLRISISEQCRRVSS 548

RESULT 8
Q25102 PRELIMINARY; PRT; 111 AA.
AC Q25102;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-JAN-1998 (TReMBLrel. 05, Last annotation update)
DE PRECURSOR PROTEIN OF LEP.
OS Hirudo nipponia.
OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
OC Arynchobdellida; Hirudiniiformes; Hirudinidae; Hirudo.
OX NCBI_TaxID=42736;
RN [1]
RP SEQUENCE FROM N.A.
RA Kawano T., Ukena K., Ikeda T., Matsushima O., Minakata H.;
RL (In) Nishi N. (eds.);
RL Peptide chemistry, pp.1-1, Protein Research Foundation, Osaka (1995).
DR EMBL; D63649; BAA09802.1; -
SQ SEQUENCE 111 AA; 13006 MW; 7B5A19F119F467D3 CRC64;

Query Match 25.5%; Score 52.5; DB 5; Length 111;
Best Local Similarity 40.0%; Pred. No. 3.2;
Matches 12; Conservative 6; Mismatches 7; Indels 5; Gaps 1;

Qy 8 IILQCSILHITLILRCYCPCRRSGSPG 37
Db 6 LVLCISLLHVTGVERRY-----RLGSDEG 30

RESULT 9
Q9P0S8 PRELIMINARY; PRT; 198 AA.
AC Q9P0S8;
DT 01-OCT-2000 (TReMBLrel. 15, Created)

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DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DE 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
DI HSPC195.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=UMBILICAL CORD BLOOD;
RA Ye M., Zhang Q.H., Zhou J., Shen Y., Wu X.Y., Guan Z.Q., Wang L.,
RA Fan H.Y., Mao Y.F., Dai M., Huang Q.H., Chen S.J., Chen Z.;
RT "Human full length cDNA cloned from cd34+ stem cells.";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF151029; AAF36115.1; -
SQ SEQUENCE 198 AA; 21272 MW; EB6E198F2CE6AE58 CRC64;

Query Match 25.5%; Score 52.5; DB 4; Length 198;
Best Local Similarity 35.9%; Pred. No. 5.2;
Matches 14; Conservative 5; Mismatches 13; Indels 7; Gaps 1;

OY 4 TPVKIILCOQSLHTLIQTLI-----LRCYCAPCRSGSS 35
|| : : : || : : : | |||||
DB 100 TPAGVFLAESALHAGLAEPYMQGELPLPSAPARRSGNA 138

RESULT 10
Q20016 PRELIMINARY; PRT; 924 AA.
ID Q20016 PRELIMINARY;
AC Q20016; Q22838;
DT 01-NOV-1998 (TReMBLrel. 08, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
DE HYPOTHETICAL 104.3 KDA PROTEIN T27F2.2.
GN T27F2.2.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA White S.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Lennard N.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z74032; CAA98469.2; -
DR EMBL; Z74045; CAA98469.2; JOINED.
DR EMBL; Z74045; CAA98554.2; -
DR EMBL; Z74032; CAA98554.2; JOINED.
DR INTERPRO; IPR000331; -
DR PFAM; PF02145; Rap_GAP; 1.
KW Hypothetical protein.
SQ SEQUENCE 924 AA; 104330 MW; 3F2EF474E885C1FB CRC64;

Query Match 25.0%; Score 51.5; DB 5; Length 924;
Best Local Similarity 34.1%; Pred. No. 26;
Matches 14; Conservative 4; Mismatches 14; Indels 9; Gaps 1;

OY 1 MFSPPVKIILCOQSL-----RITQILRCYCACPGRS 32
:|||| : : ||||| |
DB 590 LFSPTHSIIGWTSDTGLKLYYDHGDQLLRCYSETCTDS 630

RESULT 11
Q89609 PRELIMINARY; PRT; 383 AA.
ID Q89609
AC Q89609;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)

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ID O18465 PRELIMINARY; PRT; 1880 AA.
AC O18465;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE TRACTIN.
OS Hirudo medicinalis (Medicinal leech).
OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
OC Arynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.
OX NCBI_TaxID=6421;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92198663; PubMed=1550678;
RA Johansen K.M., Kopp D.M., Jellies J., Johansen J.;
RT "Tract formation and axon fasciculation of molecularly distinct
RT peripheral neuron subpopulations during leech embryogenesis.";
RL Neuron 8:559-572(1992).
RN [2]
RN SEQUENCE FROM N.A.
RX MEDLINE=97362067; PubMed=9214388;
RA Huang Y., Jellies J., Johansen K.M., Johansen J.;
RT "Differential glycosylation of tractin and LeechCAM, two novel Ig
RT superfamily members, regulates neurite extension and fascicle
RT formation.";
RL J. Cell Biol. 138:143-157(1997).
DR HSSP; P20241; 1CFB.
DR INTERPRO; IPR000087; -.
DR INTERPRO; IPR001777; -.
DR INTERPRO; IPR003006; -.
DR PFAM; PF00041; fn3; 4.
DR PFAM; PF00047; ig; 6.
DR PRINTS; PR00014; FNTYPELII.
SQ SEQUENCE 1880 AA; 199867 MW; 174EC84DAC540DF0 CRC64;

Query Match 24.5%; Score 50.5; DB 5; Length 1880;
Best Local Similarity 37.9%; Pred. No. 66;
Matches 11; Conservative 5; Mismatches 12; Indels 1; Gaps 1;

Oy 8 IILCOSILHITOLILRCYCPCRRSGSP 36
Db 1755 LLICLLMLLMLLMLLILC-CIRCNRRGGIYP 1782

RESULT 14
Q9WU80 PRELIMINARY; PRT; 578 AA.
AC Q9WU80;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE CAMP INDUCIBLE 1 PROTEIN.
GN CIL.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Miyata M., Takahashi Y., Zheng P., Smith J.D.;
RT "Identification of three genes markedly induced by CAMP treatment of
RT RAW264 cells.";
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF121080; AAD24570.1; -.
DR INTERPRO; IPR000109; -.
DR PFAM; PF00854; PTR2; 2.
DR PROSITE; PS01023; PTR2_2; UNKNOWN_1.
SQ SEQUENCE 578 AA; 64022 MW; 9B56BEE7C3AB65A5 CRC64;

Query Match 24.3%; Score 50; DB 11; Length 578;
Best Local Similarity 30.6%; Pred. No. 29;

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Matches 11; Conservative 9; Mismatches 14; Indels 2; Gaps 1;

Oy 1 MFSTPVKIIILCOSILHITOLILRCY--CAPCRSGS 34
Db 245 LFATPVFTKPTGSGVSSMLKLAIFONCCPKRSS 280

RESULT 15
Q9SH34 PRELIMINARY; PRT; 1518 AA.
AC Q9SH34;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE F2K11.14.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
OC Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Shann P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Khan S.,
RA Kim C., Altafi H., Bei Q., Chin C., Chiou J., Choi E., Conn L.,
RA Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B., Lee J.,
RA Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M.,
RA Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A.,
RA Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A.,
RA Ecker J.R.;
RT "Genomic sequence for Arabidopsis thaliana BAC F2K11 from chromosome
RT I.";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC008047; AAF19696.1; -.
DR INTERPRO; IPR000561; -.
DR INTERPRO; IPR001965; -.
DR INTERPRO; IPR002363; -.
DR PFAM; PF00628; PHD; 2.
DR PROSITE; PS01109; RIBOSOMAL_L10; 1.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
SQ SEQUENCE 1518 AA; 173125 MW; 9750189E2A3DBDAD CRC64;

Query Match 24.3%; Score 50; DB 10; Length 1518;
Best Local Similarity 40.0%; Pred. No. 66;
Matches 8; Conservative 5; Mismatches 5; Indels 2; Gaps 1;

Oy 9 ILCQSILHITOLILRCYCPC 28
Db 623 IICQOFLHLSAIV--CNCRP 640

Search completed: May 23, 2001, 15:35:12
Job time: 618 sec

```


GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 23, 2001, 15:28:25 ; Search time 184.73 Seconds
(without alignments)
8.045 Million cell updates/sec

Title: US-08-887-977-10_COPY_39_64

Perfect score: 127

Sequence: 1 LVRIAYSLICVLGLNLIWITFAF 26

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 390729 seqs, 57163235 residues

Total number of hits satisfying chosen parameters: 390729

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_0401.*
1: /SID56/gcgdata/geneseq/geneseq/AA1980.DAT.*
2: /SID56/gcgdata/geneseq/geneseq/AA1981.DAT.*
3: /SID56/gcgdata/geneseq/geneseq/AA1982.DAT.*
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6: /SID56/gcgdata/geneseq/geneseq/AA1985.DAT.*
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8: /SID56/gcgdata/geneseq/geneseq/AA1987.DAT.*
9: /SID56/gcgdata/geneseq/geneseq/AA1988.DAT.*
10: /SID56/gcgdata/geneseq/geneseq/AA1989.DAT.*
11: /SID56/gcgdata/geneseq/geneseq/AA1990.DAT.*
12: /SID56/gcgdata/geneseq/geneseq/AA1991.DAT.*
13: /SID56/gcgdata/geneseq/geneseq/AA1992.DAT.*
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21: /SID56/gcgdata/geneseq/geneseq/AA2000.DAT.*
22: /SID56/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	127	100.0	365	19 W48086	Human dendritic ce
2	127	100.0	365	21 Y97077	Primate (human) ch
3	75	59.1	358	15 R53745	Partial sequence o
4	75	59.1	358	21 B21689	Human 7TM receptor
5	75	59.1	361	20 W97348	An Epstein-Barr vi
6	75	59.1	378	15 R54079	Epstein Barr virus
7	75	59.1	378	15 R53744	Putative seven tra
8	75	59.1	378	19 W48724	Human V31 seven tr
9	75	59.1	378	19 W56164	G-protein coupled
10	75	59.1	378	19 W53622	Epstein Barr virus
11	75	59.1	378	21 B21688	Human 7TM receptor

12	75	59.1	378	21	Y90629	Human G protein-co
13	75	59.1	378	21	Y90663	Human mutant G pro
14	75	59.1	378	22	B50859	Human CCR7. Homo
15	75	59.1	410	15	R53743	Putative seven tra
16	75	59.1	410	19	W48723	Polypeptide sequen
17	75	59.1	410	21	B21687	Genomic clone of 7
18	71	55.9	359	15	R53747	Seven transmembran
19	71	55.9	359	19	W48728	Murine V31 seven t
20	71	55.9	359	21	B21691	Murine 7TM recepto
21	71	55.9	378	21	B21699	7TM receptor prote
22	69	54.3	372	20	W86323	Kidney injury asso
23	67	52.8	374	20	Y05643	Mouse Burkitt's ly
24	65	51.2	372	13	R27793	New platelet facto
25	65	51.2	372	16	R92239	Chemokine superfam
26	65	51.2	372	16	R68813	Human lymphocyte p
27	65	51.2	372	20	Y06644	Human Burkitt's ly
28	65	51.2	372	21	Y90627	Human G protein-co
29	65	51.2	372	21	Y90661	Human mutant G pro
30	63	49.6	355	15	R39995	Peptide effecting
31	63	49.6	355	15	R52749	C-C chemokine rece
32	63	49.6	355	18	W26588	Human MIP-1 alpha/
33	63	49.6	355	18	W25751	Human MIP-1alpha/R
34	63	49.6	355	21	R20571	Human CC-chemokine
35	62	48.8	428	14	R39264	Murine somatostati
36	61	48.0	30	18	W34015	Human mu opioid re
37	61	48.0	356	15	R65188	Murine mu-subtype
38	61	48.0	371	15	R65503	Murine delta opioi
39	61	48.0	372	15	R48629	Sequence of murine
40	61	48.0	372	16	R67682	Rat delta opiate r
41	61	48.0	372	16	R67670	Mouse delta opioi
42	61	48.0	372	19	W44938	Mouse delta opiate
43	61	48.0	372	21	Y80495	Mouse delta-opioi
44	61	48.0	390	21	Y68885	A murine mu-opioi
45	61	48.0	391	21	Y68886	A murine mu-opioi

ALIGNMENTS

RESULT 1
W48086
ID W48086 standard; Protein; 365 AA.
XX
AC W48086;
XX
DT 11-JUN-1998 (first entry)
XX
Human dendritic cell chemokine receptor.

XX
Human; thymus expressed chemokine; TECK; MIP-3alpha; MIP-3beta;
KW receptor; dendritic cell; macrophage; inflammation; asthma.
XX
OS Homo sapiens.

XX
FH Key Location/Qualifiers
FT Misc-difference 193
FT /note= "encoded by CAN"
XX
XX W09801557-A2.
XX
XX 15-JAN-1998.
XX
XX 02-JUL-1997; 97WO-US10819.
XX
XX 04-JUN-1997; 97US-0048593.
PR 05-JUL-1996; 96US-0675814.
PR 11-OCT-1996; 96US-0028329.
XX
XX (SCHE) SCHERING CORP.
PA
XX Gish KC, Schall TJ, Vicari A, Wang W, Zlotnik A;
PI
XX WPI; 1998-101054/09.

DR N-PSDB; V15418.
XX Novel chemokines, e.g. thymus expressed chemokine - used for
PT treating inflammatory conditions including asthma.
XX
PS Claim 3; Page 94-95; 202pp; English.
XX
CC The present sequence represents human dendritic cell chemokine receptor.
CC Antibodies which bind to the protein can be used in detecting or
CC diagnosing various immunological conditions related to expression
CC of the protein. The nucleic acid can be used for screening and
CC isolating DNA clones for the chemokines, especially from other
CC species. The chemokine can be used in the treatment of conditions
CC associated with abnormal physiology or development, including
CC inflammatory conditions such as asthma.
XX
SQ Sequence 365 AA;

Query Match 100.0%; Score 127; DB 19; Length 365;
Best Local Similarity 100.0%; Pred. No. 7.6e-11;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LYRIAYSLICVLGLGNILVITFAF 26
DB 39 lyriayslicvlgllgnilvittaf 64

RESULT 2
Y97077
ID Y97077 standard; Protein; 365 AA.
XX
XX Y97077;
AC
XX
DT 04-DEC-2000 (first entry)
DE
DE Primate (human) chemokine receptor CCR6.
KW MIP-3-alpha; chemokine; CCR6 receptor; ligand; cytostatic; agonist;
KW antagonist; anti-psoriatic; dermatological; immunosuppressive;
KW anti-inflammatory.
XX
XX Homo sapiens.
XX
XX OS
XX
XX Key Location/Qualifiers
XX Misc-difference 193 /note= "Encoded by CAN#"
XX
XX WO200046248-A1.
XX
XX 10-AUG-2000.
XX
XX
XX 02-FEB-2000; 2000WO-US00511.
XX
XX 03-FEB-1999; 99US-0244281.
XX
XX (SCHE) SCHERING CORP.
XX
XX Oldham ER, Homey B, Dieu-Nosjean M, Caux C, Zlotnik A;
XX
XX WPI; 2000-543477/49.
XX
XX N-PSDB; A51971.
XX
XX Novel methods for modulating the migration of cells within or to the
XX skin using MIP-3-alpha or CCR6 agonists or antagonists, useful for
XX treating skin disorders, e.g. cancer
XX
XX Disclosure; Page 53-54; 61pp; English..
XX
XX The MIP-3-alpha chemokine is expressed in inflamed skin cells. This
XX chemokine is the ligand for the CCR6 receptor. MIP-3-alpha or CCR6
XX agonists or antagonists can be used to modulate the migration of a cell
XX within or to the skin of a mammal. MIP-3-alpha can be used to purify a

CC population of cells expressing a MIP-3-alpha receptor. The methods are
CC useful for treating a mammalian subject with a skin disease or condition,
CC e.g. cancer, metastasis, psoriasis, atopic or contact dermatitis,
CC systemic lupus erythematosus and lichen ruber planus, or for treating
CC skin transplants or grafts.
XX
SQ Sequence 365 AA;

Query Match 100.0%; Score 127; DB 21; Length 365;
Best Local Similarity 100.0%; Pred. No. 7.6e-11;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LYRIAYSLICVLGLGNILVITFAF 26
DB 39 lyriayslicvlgllgnilvittaf 64

RESULT 3
R53745
ID R53745 standard; Protein; 358 AA.
XX
XX R53745;
AC
XX
DT 02-FEB-1995 (first entry)
XX
DE Partial sequence of seven transmembrane receptor (V31).
XX
XX KW Primer; seven transmembrane receptor; receptor; amplification; PCR;
KW polymerase chain reaction.
XX
XX OS Homo sapiens.
XX
XX WO9412635-A.
XX
XX 09-JUN-1994.
XX
XX 17-NOV-1993; 93WO-US11153.
XX
XX 17-NOV-1992; 92US-0977452.
XX
XX (ICOS-) ICOS CORP.
XX
XX Godiska R, Gray PW, Schweickart VL;
XX
XX WPI; 1994-200264/24.
XX
XX N-PSDB; Q66162.
XX
XX DNA encoding seven transmembrane receptors - used to develop
XX prods. for use as therapeutic or diagnostic agents for conditions
XX involving the receptors.
XX
XX Example 3; Page 56-57; 100pp; English.
XX
XX Two primers (Q66148, Q66149) were used to amplify human genomic DNA
XX purified from leukocytes. Approximately 1000 clones were isolated
XX after the initial amplification reaction and probed with sequences
XX specific for seven transmembrane receptors IL8R1, AT2R and R20.
XX Clones which did not hybridise were then chosen for sequence
XX analysis. Three new clones were identified that appeared to encode
XX seven transmembrane receptor segments. Two more primers (Q66151,
XX Q66152) were used to isolate a full length version of one of these
XX clones designated V31 (See Q66153). This is the sequence encoded
XX by exon 3 of the V31 genomic clone
XX
XX Sequence 358 AA;

Query Match 59.1%; Score 75; DB 15; Length 358;
Best Local Similarity 60.9%; Pred. No. 0.0029;
Matches 14; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 4 IAYSLICVLGLGNILVITFAF 26

XX FH Key Location/Qualifiers
 FT Domain 58..86
 FT Domain /note= "Transmembrane domain 1"
 FT Domain 96..119
 FT Domain /note= "Transmembrane domain 2"
 FT Domain 131..152
 FT Domain /note= "Transmembrane domain 3"
 FT Domain 171..196
 FT Domain /note= "Transmembrane domain 4"
 FT Domain 219..247
 FT Domain /note= "Transmembrane domain 5"
 FT Domain 264..285
 FT Domain /note= "Transmembrane domain 6"
 FT Domain 306..331
 FT Domain /note= "Transmembrane domain 7"
 XX
 PN US5759804-A.
 XX
 XX 02-JUN-1998.
 PD
 XX
 XX 17-NOV-1993; 93US-0153848.
 XX
 XX 17-NOV-1992; 92US-0977452.
 PR
 XX (ICOS-) ICOS CORP.
 PA
 XX
 XX Godiska R, Gray PW, Schweickart VL;
 PI
 XX
 XX WPI; 1998-332132/29.
 DR
 XX N-PSDB; V18347.
 DR
 XX
 XX DNA encoding V28 seven transmembrane receptor polypeptide - useful
 PT for producing recombinant polypeptide and anti-V28 antibodies, and
 PT in screening assays for V28 agonists and antagonists
 PT
 XX
 XX Example 3; Columns 39-42; 56pp; English.
 PS
 XX
 XX The present sequence represents the V31 seven transmembrane (7TM)
 CC receptor encoded by the V31 cDNA (V18347). The invention claims for
 CC a full length V28 genomic DNA (V18343) and the V28 protein it
 CC encodes (W48722). V28 and V31 proteins are 7TM receptors which
 CC are probably involved in signal transduction. The invention also
 CC claims that cells transformed with V28 DNA can be used to produce the
 CC recombinant polypeptide, to produce anti-V28 antibodies or in screening
 CC assays for V28 agonists or antagonists. The antibodies, agonists and
 CC antagonists could then be used to modulate V28 receptor-ligand binding,
 CC for e.g. in immunological and/or inflammatory events in vivo.
 XX
 XX Sequence 378 AA;
 SQ
 Query Match 59.1%; Score 75; DB 19; Length 378;
 Best Local Similarity 60.9%; Pred. No. 0.003;
 Matches 14; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
 Qy 4 TAYSLICVLGLGNLIVITFAF 26
 Db 63 imysicfvglnglglvltviy 85
 RESULT 9
 W56164
 ID W56164 standard; Protein; 378 AA.
 XX
 AC W56164;
 XX
 XX 20-JUL-1998 (first entry)
 DT
 XX G-protein coupled receptor (R7G) designated EB11.
 DE
 XX Lymphocyte R7G; EB11; G-protein coupled receptor;
 KW opiate/opioid recognition site; opiate; opioid; opiod binding protein;
 KW

KW screening; lymphocyte receptor; compound; agonist; antagonist;
 KW lymphocyte receptor protein; immune-cell specific lymphocyte receptor;
 KW neuronal type opiod receptor.
 XX Homo sapiens.
 XX US5753516-A.
 PN
 XX 19-MAY-1998.
 PD
 XX 03-FEB-1995; 95US-0383751.
 PF
 XX 03-FEB-1995; 95US-0383751.
 PR
 XX (FINB/) FINBERG R W.
 XX (HEAG/) HEAGY W E.
 PA
 PA Finberg RW, Heagy WE;
 XX
 PI WPI; 1998-311410/27.
 DR
 XX N-PSDB; V22684.
 DR
 XX Screening assay for lymphocyte opiod receptor ligands - using
 PT recombinant receptor protein
 PT
 XX Claim 1; Columns 87-88; 70pp; English.
 PS
 XX The present sequence represents a novel lymphocyte R7G, termed EB11. R7G
 CC proteins are part of the G-protein coupled receptor superfamily. EB11 is
 CC a functional opiate/opioid recognition site that probably plays a major
 CC role in mediating the effects that opiate/opioids have on lymphocytes.
 CC The EB11 protein is an opiod binding protein that is displayed on the
 CC surface of lymphocytes. A process for screening a candidate substance for
 CC ability to interact with a lymphocyte receptor comprises selecting a
 CC candidate substance having a chemical structure or biological activity
 CC suggestive of an ability to mimic the biological activity of an
 CC opiate, opiod drug or opiod peptide having known binding affinity for
 CC EB11. The ability of the candidate substance is tested to interact with
 CC the lymphocyte receptor protein. This method can be used to screen for
 CC agonists or antagonists to the lymphocyte receptor protein. The method
 CC can be modified and used to screen for agonists or antagonists to the
 CC immune-cell specific lymphocyte receptor polypeptide or the neuronal type
 CC opiod receptor polypeptide.
 XX
 XX Sequence 378 AA;
 SQ
 Query Match 59.1%; Score 75; DB 19; Length 378;
 Best Local Similarity 60.9%; Pred. No. 0.003;
 Matches 14; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
 Qy 4 TAYSLICVLGLGNLIVITFAF 26
 Db 63 imysicfvglnglglvltviy 85
 RESULT 10
 W53622
 ID W53622 standard; Protein; 378 AA.
 XX
 AC W53622;
 XX
 XX 09-JUL-1998 (first entry)
 DT
 XX Epstein Barr virus induced protein 1 (EBI-1).
 DE
 XX Assessing; monitoring; foetal development; placental development;
 KW Epstein Barr virus; EBV; induced gene 1; EBI-1.
 KW
 XX Homo sapiens.
 XX
 XX US5744301-A.
 PN

PD 28-APR-1998.
 XX
 PF 02-FEB-1995; 95US-0383750.
 XX
 PR 02-FEB-1995; 95US-0383750.
 PR 25-NOV-1992; 92US-0980518.
 PR 30-NOV-1994; 94US-0352678.
 XX
 PA (BGHM) BRIGHAM & WOMENS HOSPITAL.
 XX
 PI Birkenbach M, Kieff E;
 XX
 DR WPI; 1998-271060/24.
 DR N-PSDB; V25490.
 XX
 XX Assessing or monitoring foetal or placental development - comprises
 PT detecting the level or size of Epstein Barr virus induced nucleic
 PT acid or protein in maternal serum samples
 XX
 PS Example 2; Columns 37-40; 45pp; English.
 XX
 CC The present sequence was used in the development of a novel method
 CC for assessing or monitoring foetal or placental development. The
 CC method comprises taking a maternal serum sample, and detecting the
 CC level or size of Epstein Barr virus (EBV) induced gene or protein 3
 CC (EBI-3) to obtain a result, which can be compared to a control to
 CC assess or monitor foetal or placental development.
 XX
 SQ Sequence 378 AA;

Query Match 59.1%; Score 75; DB 19; Length 378;
 Best Local Similarity 60.9%; Pred. NO. 0.003;
 Matches 14; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 4 IAYSLICVLGLGNILVWITFAF 26
 | | | | | : | | | | | : | | | | | :
 Db 63 imyslicvfgllnglvltiy 85

RESULT 11
 B21688
 ID B21688 standard; Protein; 378 AA.
 XX
 AC B21688;
 XX
 DT 26-JAN-2001 (first entry)
 XX
 DE Human 7TM receptor V31-B cDNA clone protein.
 XX
 KW Seven transmembrane receptor; 7TM; heptahelical; serpentine;
 KW G-protein-coupled; V28; V31; V112; R20; R2; R12; RM3; gene therapy;
 KW cancer.
 XX
 OS Homo sapiens.
 XX
 PN US6107475-A.
 XX
 PD 22-AUG-2000.
 XX
 PF 26-APR-1999; 99US-0299843.
 XX
 PR 17-MAY-1994; 94US-0245242.
 PR 01-JUN-1998; 98US-0083337.
 PR 17-NOV-1992; 92US-0977452.
 PR 17-NOV-1993; 93US-0153848.
 XX
 PA (ICOS-) ICOS CORP.
 XX
 PI Schweickart VL, Gray PW, Godiska R;
 XX
 DR WPI; 2000-571335/53.
 DR N-PSDB; A91707.

XX Polynucleotide encoding seven transmembrane receptors, antibody
 PT specific to the receptor, agonist and antagonist of the receptor useful
 PT for treating inflammation in a mammal
 XX
 PS Example 3; Columns 41-44; 61pp; English.
 XX
 CC The present sequence is a novel seven transmembrane (7TM) receptors
 CC (also known as heptahelical, serpentine or G-protein-coupled receptors).
 CC The coding sequence for the present sequence may be used for gene
 CC therapy for diseases such as cancer.
 XX
 SQ Sequence 378 AA;

Query Match 59.1%; Score 75; DB 21; Length 378;
 Best Local Similarity 60.9%; Pred. NO. 0.003;
 Matches 14; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 4 IAYSLICVLGLGNILVWITFAF 26
 | | | | | : | | | | | : | | | | | :
 Db 63 imyslicvfgllnglvltiy 85

RESULT 12
 Y90629
 ID Y90629 standard; Protein; 378 AA.
 XX
 AC Y90629;
 XX
 DT 21-AUG-2000 (first entry)
 XX
 DE Human G protein-coupled receptor EB11.
 XX
 KW G protein-coupled receptor; GPCR; constitutively active;
 KW intracellular loop 3; transmembrane domain 6; drug screening;
 KW agonist; antagonist.
 XX
 OS Homo sapiens.
 XX
 PN WO200022129-A1.
 XX
 PD 20-APR-2000.
 XX
 PF 12-OCT-1999; 99WO-US23938.
 XX
 PR 13-OCT-1998; 98US-0170496.
 XX
 PA (AREN-) ARENA PHARM INC.
 XX
 PI Behan DP, Chalmers DT, Liaw CW;
 XX
 DR WPI; 2000-329165/28.
 DR N-PSDB; A30632.
 XX
 PT Non-endogenous constitutively activated human G protein-coupled
 PT receptors, useful for identifying agonists for use as pharmaceutical
 PT agents
 XX
 PS Example 1; Page 158-159; 341pp; English.
 XX
 CC The invention relates to constitutively active, non-endogenous versions
 CC of endogenous human orphan G protein-coupled receptors (GPCRs, Y90643-
 CC Y90677 and Y90683-Y90687), and to DNA encoding them (A30709-A30743 and
 CC A30775-A30779). The mutant proteins of the invention contain a
 CC mutation in a portion of the protein comprising intracellular loop 3
 CC (IC3) and transmembrane domain 6 (TM6). A non-endogenous amino acid, X,
 CC is substituted for an endogenous residue in IC3 at a position 16 amino
 CC acids N-terminal of an endogenous proline in TM6 to form a sequence
 CC X-(AA)15-Pro. The endogenous amino acid is selected from Lys, His, Arg or
 CC Ala, and is preferably Lys. When the endogenous residue at this position
 CC is Lys, this residue is replaced by His, Arg or preferably Ala. The 15
 CC amino acid stretch between the substituted amino acid and the Pro may be

CC endogenous, non-endogenous, or a mixture of endogenous and non-endogenous
 CC residues. The constitutively active GPCRs are useful for identifying
 CC antagonists, agonists and partial agonists for use as pharmaceutical
 CC agents. The mutant proteins are also useful in research settings for
 CC elucidating the roles of the receptors in normal and diseased conditions.
 CC Antagonists for a particular GPCR are useful for treating diseases and
 CC disorders associated with that receptor. Because the novel mutant GPCRs
 CC are constitutively active, they can be used directly for screening of
 CC compounds without the need for endogenous ligands. The present
 CC sequence represents a human wild-type GPCR referred to in an
 CC exemplification of the invention.

XX
 SQ Sequence 378 AA;

Query Match 59.1%; Score 75; DB 21; Length 378;
 Best Local Similarity 60.9%; Pred. No. 0.003;
 Matches 14; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 4 IAYSLICVLGLNGLVITFAF 26
 | | | | | : | | | | | | | | | : :
 Db 63 imysiicfvglnglvltviy 85

RESULT 13
 ID Y90663 standard; Protein; 378 AA.
 XX
 AC Y90663;
 XX
 DT 21-AUG-2000 (first entry)
 XX
 DE Human mutant G protein-coupled receptor EB11 (I262K).
 XX
 KW G protein-coupled receptor; GPCR; constitutively active;
 KW intracellular loop 3; transmembrane domain 6; drug screening;
 KW agonist; antagonist; mutant; mutain.
 XX
 OS Homo sapiens.
 OS Synthetic.

XX WO200022129-A1.
 XX
 XX 20-APR-2000.
 XX
 XX 12-OCT-1999; 99WO-US23938.
 XX
 XX 13-OCT-1998; 98US-0170496.
 XX
 XX (AREN-) ARENA PHARM INC.
 XX
 XX Behan DP, Chalmers DT, Liaw CW;
 XX
 XX WPI; 2000-329165/28.
 XX
 XX N-PSDB; A30729.
 XX
 XX Non-endogenous constitutively activated human G protein-coupled
 PT receptors, useful for identifying agonists for use as pharmaceutical
 PT agents -
 XX
 XX Example 2; Page 259-260; 341pp; English.

XX The invention relates to constitutively active, non-endogenous versions
 CC of endogenous human orphan G protein-coupled receptors (GPCRs, Y90643-
 CC Y90677 and Y90683-Y90687), and to DNA encoding them (A30709-A30743 and
 CC A30775-A30779). The mutant proteins of the invention contain a
 CC mutation in a portion of the protein comprising intracellular loop 3
 CC (IC3) and transmembrane domain 6 (TM6). A non-endogenous amino acid, X,
 CC is substituted for an endogenous residue in IC3 at a position 16 amino
 CC acids N-terminal of an endogenous proline in TM6 to form a sequence
 CC X-(AA)15-Pro. The endogenous amino acid is selected from Lys, His, Arg or
 CC Ala, and is preferably Lys. When the endogenous residue at this position
 CC is Lys, this residue is replaced by His, Arg or preferably Ala. The 15

CC amino acid stretch between the substituted amino acid and the Pro may be
 CC endogenous, non-endogenous, or a mixture of endogenous and non-endogenous
 CC residues. The constitutively active GPCRs are useful for identifying
 CC antagonists, agonists and partial agonists for use as pharmaceutical
 CC agents. The mutant proteins are also useful in research settings for
 CC elucidating the roles of the receptors in normal and diseased conditions.
 CC Antagonists for a particular GPCR are useful for treating diseases and
 CC disorders associated with that receptor. Because the novel mutant GPCRs
 CC are constitutively active, they can be used directly for screening of
 CC compounds without the need for endogenous ligands. Sequences Y90643-
 CC Y90677 and Y90683-Y90687 the mutant human GPCRs of the invention.

XX
 SQ Sequence 378 AA;

Query Match 59.1%; Score 75; DB 21; Length 378;
 Best Local Similarity 60.9%; Pred. No. 0.003;
 Matches 14; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 4 IAYSLICVLGLNGLVITFAF 26
 | | | | | : | | | | | | | | | : :
 Db 63 imysiicfvglnglvltviy 85

RESULT 14
 ID B50859 standard; protein; 378 AA.
 XX
 AC B50859;
 XX
 DT 16-MAR-2001 (first entry)
 XX
 DE Human CCR7.
 XX
 KW Human; chemokine receptor 7; CCR7; chemokine beta-9; Ckbeta-9;
 KW allergy; autoimmune disease; ischaemia; atherosclerosis; cancer;
 KW chronic inflammatory disorder; organ transplant; tissue graft;
 KW chronic myelogenous leukaemia; Infection.
 XX
 OS Homo sapiens.

XX US6153441-A.
 XX
 XX 28-NOV-2000.
 XX
 XX 17-FEB-1999; 99US-0251545.
 XX
 XX 17-FEB-1998; 98US-0074883.
 XX
 XX (SMIK) SMITHKLINE BEECHAM CORP.
 XX
 XX Appelbaum ER, White JR, Sarau HM;
 PI
 XX WPI; 2001-049151/06.
 XX
 XX Identifying agonists or antagonists of interaction between human
 PT protein, chemokine beta-9 and human CC chemokine receptor 7, by
 PT contacting cell expressing receptor with test compound -
 XX
 XX Claim 1; Fig 1; 20pp; English.

XX The present sequence is human chemokine receptor 7 (CCR7), a cellular
 CC receptor for chemokine beta-9 (Ckbeta-9). The sequence may be
 CC used in a method for discovering agonists and antagonists of the
 CC interaction between Ckbeta-9 and CCR7. A cell expressing CCR7
 CC polypeptide on its surface, associated with a component capable of
 CC providing a detectable signal in response to binding of Ckbeta-9, is
 CC contacted with a compound in the presence of labelled or unlabelled
 CC Ckbeta-9. The compound is identified as an agonist/antagonist by
 CC determining whether it activates or inhibits the detectable signal.
 CC The method is useful for identifying agonists and antagonists of the
 CC interaction between Ckbeta-9 and CCR7 which are useful for treating
 CC diseases including allergic disorders, autoimmune diseases,

CC ischaemia/reperfusion injury, development of atherosclerotic plaques,
CC cancer, chronic inflammatory disorders, chronic rejection of
CC transplanted organs or tissue grafts, chronic myelogenous leukaemia, and
CC infection by HIV and other pathogens.

Db 95 imysiicfvllgnglvvltiy 117

Search completed: May 23, 2001, 15:28:26
Job time: 403 sec

Sequence	378 AA;
SQ	

Query Match 59.1%; Score 75; DB 22; Length 378;

Query Match 59.1%; Score 75; DB 22; Length 378;
Best Local Similarity 60.9%; Pred. No. 0.003;
Matches 14; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 4 IAYS LICVLGLGNILVITFAF 26

```

Db      | | | | | : | | | | | | | | | :
63 imysii c f v g l l n g l v l t y i y 85

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RESULT 15

R53743
ID R53743 standard; Protein; 410 AA.

AC R53743;

DT 02-FEB-1995 (first entry)

DE Putative seven transmembrane receptor (V31).

Primer; seven transmembrane receptor; receptor; amplification; PCR; polymerase chain reaction.

OS Homo sapiens.

PN WO9412635-A.

09-JUN-1994.

AA
PF 17-NOV-1993; 93WO-US11153.

PR 17-NOV-1992; 92US-0977452.

PA (ICOS-) ICOS CORP.

PI Godiska R, Gray PW, Schweickart VL:

AA
DR WPI: 1994-200264/24.

XX
XX
N-ESDB; Q00133.

PT DNA encoding seven trans:membrane receptors - used to develop
PT prods. for use as therapeutic or diagnostic agents for conditions
PT involving the receptors.

PS Example 2; Page 46-48; 100pp; English.

Two primers (Q66148, Q66149) were used to amplify human genomic DNA purified from leukocytes. Approximately 1000 clones were isolated after the initial amplification reaction and probed with sequences specific for seven transmembrane receptors IL8R1, AN2R and R20. Clones which did not hybridise were then chosen for sequence analysis. Three new clones were identified that appeared to encode seven transmembrane receptor segments. Two more primers (Q66151, Q66152) were used to isolate a full length version of one of these clones, one of which was designated V31 and encoded this polypeptide.

AA	Sequence	410 AA:
SQ		

Query Match

Best Local Similarity 60.9%;
 Matches 14; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 4 IAYSLICVLGLLGNILVVITFAF 26

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..
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—

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 23, 2001, 15:30:04 ; Search time 95.91 Seconds
(without alignments)
5.208 Million cell updates/sec

Title: US-08-887-977-10_COPY_39_64

Perfect score: 127

Sequence: 1 LRYIAVSLICVLGLLGNILVITFAF 26

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 185757 seqs, 19210857 residues

Total number of hits satisfying chosen parameters: 185757

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents_AA.*
- 1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
 - 2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
 - 3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
 - 4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
 - 5: /cgn2_6/ptodata/2/iaa/PTUS_COMB.pep.*
 - 6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	75	59.1	358	1 US-08-153-848-19	Sequence 19, Appl
2	75	59.1	358	5 US-09-299-843A-19	Sequence 19, Appl
3	75	59.1	358	5 PCT-US93-11153-19	Sequence 19, Appl
4	75	59.1	361	2 US-08-902-294-2	Sequence 2, Appl
5	75	59.1	361	3 US-09-178-637-2	Sequence 2, Appl
6	75	59.1	378	1 US-08-383-750-2	Sequence 2, Appl
7	75	59.1	378	1 US-08-383-751A-2	Sequence 2, Appl
8	75	59.1	378	1 US-08-153-848-15	Sequence 15, Appl
9	75	59.1	378	3 US-08-352-678-2	Sequence 15, Appl
10	75	59.1	378	3 US-09-299-843A-15	Sequence 15, Appl
11	75	59.1	378	4 US-09-251-545-1	Sequence 1, Appl
12	75	59.1	378	5 PCT-US93-09636-2	Sequence 2, Appl
13	75	59.1	378	5 PCT-US93-11153-15	Sequence 15, Appl
14	75	59.1	410	1 US-08-153-848-7	Sequence 7, Appl
15	75	59.1	410	3 US-09-299-843A-7	Sequence 7, Appl
16	75	59.1	410	5 PCT-US93-11153-7	Sequence 7, Appl
17	71	55.9	359	1 US-08-153-848-24	Sequence 24, Appl
18	71	55.9	359	3 US-09-299-843A-24	Sequence 24, Appl
19	71	55.9	359	5 PCT-US93-11153-24	Sequence 24, Appl
20	71	55.9	378	3 US-09-299-843A-66	Sequence 66, Appl
21	67	52.8	374	4 US-08-982-493-6	Sequence 6, Appl
22	65	51.2	372	1 US-08-202-056-5	Sequence 5, Appl
23	65	51.2	372	1 US-08-076-093A-6	Sequence 6, Appl
24	65	51.2	372	1 US-08-701-265-6	Sequence 6, Appl
25	65	51.2	372	2 US-08-284-586-6	Sequence 6, Appl
26	65	51.2	372	2 US-08-805-478-6	Sequence 6, Appl
27	65	51.2	372	2 US-08-802-627A-6	Sequence 6, Appl

28	65	51.2	372	2	US-08-801-238-6	Sequence 6, Appl
29	65	51.2	372	2	US-08-801-228-6	Sequence 6, Appl
30	65	51.2	372	3	US-09-104-296-6	Sequence 6, Appl
31	65	51.2	372	4	US-08-982-493-8	Sequence 8, Appl
32	63	49.6	355	1	US-08-012-988A-2	Sequence 2, Appl
33	63	49.6	355	1	US-08-450-393A-5	Sequence 5, Appl
34	63	49.6	355	4	US-08-446-669-5	Sequence 5, Appl
35	63	49.6	355	5	PCT-US95-00476-5	Sequence 5, Appl
36	62	48.8	428	1	US-07-816-283-12	Sequence 12, Appl
37	62	48.8	428	1	US-08-417-103-12	Sequence 12, Appl
38	61	48.0	367	2	US-08-454-549-4	Sequence 4, Appl
39	61	48.0	367	3	US-08-454-552-4	Sequence 4, Appl
40	61	48.0	367	3	US-08-676-351-3	Sequence 3, Appl
41	61	48.0	372	1	US-08-149-093A-6	Sequence 6, Appl
42	61	48.0	372	2	US-08-911-245-6	Sequence 6, Appl
43	61	48.0	372	2	US-08-411-859-10	Sequence 10, Appl
44	61	48.0	372	3	US-09-170-331-6	Sequence 6, Appl
45	61	48.0	372	3	US-08-147-592A-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1
US-08-153-848-19
; Sequence 19, Application US/08153848
; Patent No. 5759804
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schweikart, Vicki L.
; TITLE OF INVENTION: No. 5759804e1 Seven Transmembrane Receptors
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/153,848
; APPLICATION NUMBER: 514
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/977,452
; FILING DATE: 17-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5759804and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31794
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 358 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-153-848-19

Query Match 59.1%; Score 75; DB 1; Length 358;
Best Local Similarity 60.9%; Pred. No. 0.0031;
Matches 14; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

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Qy 4 IAYSILCVLGLGNLIVITFAF 26
    | |||| :|||| |||: :
Db 43 IMYSIICFVGLLGNLVLVTIY 65

RESULT 2
US-09-299-843A-19
; Sequence 19, Application US/09299843A
; Patent No. 6107475
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; APPLICANT: Gray, Patrick W.
; TITLE OF INVENTION: Novel Seven Transmembrane Receptors
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/299,843A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/088,337
; FILING DATE: 01-JUN-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Jill E. Uhl
; REGISTRATION NUMBER: 43,213
; REFERENCE/DOCKET NUMBER: 27866/32059B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX:
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 358 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-299-843A-19

Query Match 59.1%; Score 75; DB 3; Length 358;
Best Local Similarity 60.9%; Pred. No. 0.0031;
Matches 14; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 4 IAYSILCVLGLGNLIVITFAF 26
    | |||| :|||| |||: :
Db 43 IMYSIICFVGLLGNLVLVTIY 65

RESULT 3
PCT-US93-11153-19
; Sequence 19, Application PC/TUS9311153
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
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; APPLICANT: Gray, Patrick W.
; TITLE OF INVENTION: Novel Seven Transmembrane Receptors
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/11153
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/977,452
; FILING DATE: 17-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Noland, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31794
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 358 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US93-11153-19

Query Match 59.1%; Score 75; DB 5; Length 358;
Best Local Similarity 60.9%; Pred. No. 0.0031;
Matches 14; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 4 IAYSILCVLGLGNLIVITFAF 26
    | |||| :|||| |||: :
Db 43 IMYSIICFVGLLGNLVLVTIY 65

RESULT 4
US-08-902-294-2
; Sequence 2, Application US/08902294
; Patent No. 5874252
; GENERAL INFORMATION:
; APPLICANT: ZHU, YUAN
; TITLE OF INVENTION: A NOVEL SPLICING VARIANT OF
; THE EPSTEIN-BARR VIRUS-INDUCED G-PROTEIN COUPLED
; RECEPTOR
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RATNER & PRESTIA
; STREET: P. O. BOX 980
; CITY: VALLEY FORGE
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
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APPLICATION NUMBER: US/08/902,294
FILING DATE: 29-JUL-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: PRESTIA, PAUL F
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GP-70177
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
TELEFAX: 610-407-0701
TELEX: 846169
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 361 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-902-294-2

Query Match 59.1%; Score 75; DB 2; Length 361;
Best Local Similarity 60.9%; Pred. No. 0.0031;
Matches 14; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 4 IAYSLLICVLGLNGLNVLVITFAF 26
| ||| : |||| | : :
Db 63 IMYSIIICFVGLLGNGLVLTYY 85

RESULT 5
US-09-178-637-2
Sequence 2, Application US/09178637
Patent No. 6001972
GENERAL INFORMATION:
APPLICANT: ZHU, YUAN
TITLE OF INVENTION: A No. 6001972el Splicing Variant of
TITLE OF INVENTION: the Epstein-Barr Virus-Induced G-Protein Coupled Receptor
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSER: RATNER & PRESTIA
STREET: P.O. BOX 980
CITY: VALLEY FORGE
STATE: PA
COUNTRY: USA
ZIP: 19482
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/178,637
FILING DATE: 26-OCT-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/902,294
FILING DATE: 29-JUL-1998
ATTORNEY/AGENT INFORMATION:
NAME: PRESTIA, PAUL F
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GP-70177-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
TELEFAX: 610-407-0701
TELEX: 846169
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 361 amino acids
TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-178-637-2

Query Match 59.1%; Score 75; DB 3; Length 361;
Best Local Similarity 60.9%; Pred. No. 0.0031;
Matches 14; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 4 IAYSLLICVLGLNGLNVLVITFAF 26
| ||| : |||| | : :
Db 63 IMYSIIICFVGLLGNGLVLTYY 85

RESULT 6
US-08-383-750-2
Sequence 2, Application US/08383750
Patent No. 5744301
GENERAL INFORMATION:
APPLICANT: Birkenbach, Mark
APPLICANT: Kieff, Elliot
TITLE OF INVENTION: Epstein Barr Virus Induced Genes
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSER: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, N.W.,
SUITE: Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/383,750
FILING DATE: Herewith
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Fox, Samuel, L.
REGISTRATION NUMBER: 30,353
REFERENCE/DOCKET NUMBER: 0627.3300001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 378 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-383-750-2

Query Match 59.1%; Score 75; DB 1; Length 378;
Best Local Similarity 60.9%; Pred. No. 0.0032;
Matches 14; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 4 IAYSLLICVLGLNGLNVLVITFAF 26
| ||| : |||| | : :
Db 63 IMYSIIICFVGLLGNGLVLTYY 85

RESULT 7
US-08-383-751A-2
Sequence 2, Application US/08383751A
Patent No. 5753516
GENERAL INFORMATION:
APPLICANT: Heavy, Wyrta E.
APPLICANT: Finberg, Robert W.
TITLE OF INVENTION: Identification and Uses of Opioid

; TITLE OF INVENTION: Receptors
 ; NUMBER OF SEQUENCES: 8
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Arnold, White & Durkee
 ; STREET: P.O. Box 4433
 ; CITY: Houston
 ; STATE: Texas
 ; COUNTRY: US
 ; ZIP: 77210
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/383,751A
 ; FILING DATE: 03-FEB-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Wilson, Mark B.
 ; REGISTRATION NUMBER: 37,259
 ; REFERENCE/DOCKET NUMBER: DFCI:001/WIM
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (512) 418-3000
 ; TELEFAX: (512) 474-7577
 ; TELEX: 79-0924
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 378 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-383-751A-2

Query Match 59.1%; Score 75; DB 1; Length 378;
 Best Local Similarity 60.9%; Pred. No. 0.0032;
 Matches 14; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 4 IAYSILCVLGLNGLNVLVITFAF 26
 Db 63 IMYSICFVGLLGLNGLVLTYY 85

RESULT 8
 US-08-153-848-15
 ; Sequence 15, Application US/08153848
 ; Patent No. 5759804
 ; GENERAL INFORMATION:
 ; APPLICANT: Godiska, Ronald
 ; APPLICANT: Gray, Patrick W.
 ; APPLICANT: Schwellart, Vicki L.
 ; TITLE OF INVENTION: No. 5759804el Seven Transmembrane Receptors
 ; NUMBER OF SEQUENCES: 64
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
 ; ADDRESSEE: Bicknell
 ; STREET: 6300 Sears Tower, 233 South Wacker Drive
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: USA
 ; ZIP: 60606
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/153,848
 ; FILING DATE:
 ; CLASSIFICATION: 514
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/977,452
 ; FILING DATE: 17-NOV-1992

; ATTORNEY/AGENT INFORMATION:
 ; NAME: No. 5759804and, Greta E.
 ; REGISTRATION NUMBER: 35,302
 ; REFERENCE/DOCKET NUMBER: 31794
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (312) 474-6300
 ; TELEFAX: (312) 474-0448
 ; TELEX: 25-3856
 ; INFORMATION FOR SEQ ID NO: 15:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 378 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-153-848-15

Query Match 59.1%; Score 75; DB 1; Length 378;
 Best Local Similarity 60.9%; Pred. No. 0.0032;
 Matches 14; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 4 IAYSILCVLGLNGLNVLVITFAF 26
 Db 63 IMYSICFVGLLGLNGLVLTYY 85

RESULT 9
 US-08-352-678-2
 ; Sequence 2, Application US/08352678
 ; Patent No. 6043351
 ; GENERAL INFORMATION:
 ; APPLICANT: Birkenbach, Mark
 ; APPLICANT: Kieff, Elliott
 ; TITLE OF INVENTION: EPSTEIN BARR VIRUS INDUCED GENES
 ; NUMBER OF SEQUENCES: 6
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
 ; STREET: 600 Atlantic Avenue
 ; CITY: Boston
 ; STATE: MA
 ; COUNTRY: USA
 ; ZIP: 02210
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/352,678
 ; FILING DATE: 30-NOV-1994
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/980,518
 ; FILING DATE: 25-NOV-1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Gates, Edward R.
 ; REGISTRATION NUMBER: 31,616
 ; REFERENCE/DOCKET NUMBER: B0801/7044
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 617-720-3500
 ; TELEFAX: 617-720-2441
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 378 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-352-678-2

Query Match 59.1%; Score 75; DB 3; Length 378;
 Best Local Similarity 60.9%; Pred. No. 0.0032;
 Matches 14; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 4 IAYSILCVLGLGNILVITFAF 26
| | | | | : | | | | | : | | | | | :
Db 63 IMYSIIICFVGLGNGLVLTYYI 85

RESULT 10

US-09-299-843A-15
; Sequence 15, Application US/09299843A
; Patent No. 6107475
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schweikart, Vicki L.
; TITLE OF INVENTION: No. 6107475el Seven Transmembrane Receptors
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS: 66
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/299,843A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/088,337
; FILING DATE: 01-JUN-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/153,848
; FILING DATE: 17-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/977,452
; FILING DATE: 17-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Jill E. Uhl
; REGISTRATION NUMBER: 43,213
; REFERENCE/DOCKET NUMBER: 27866/32059B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX:
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 378 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-299-843A-15

Query Match 59.1%; Score 75; DB 3; Length 378;
Best Local Similarity 60.9%; Pred. No. 0.0032;
Matches 14; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 4 IAYSILCVLGLGNILVITFAF 26
| | | | | : | | | | | : | | | | | :
Db 63 IMYSIIICFVGLGNGLVLTYYI 85

RESULT 11

US-09-251-545-1
; Sequence 1, Application US/09251545
; Patent No. 6153441
; GENERAL INFORMATION:

; APPLICANT: Edward R. Appelbaum
; APPLICANT: Henry M. Sarau
; APPLICANT: John R. White
; TITLE OF INVENTION: METHODS OF SCREENING FOR AGONISTS AND
; TITLE OF INVENTION: ANTAGONISTS OF THE INTERACTION BETWEEN HUMAN CCR7 RECEPTOR
; FILE REFERENCE: P50753
; CURRENT APPLICATION NUMBER: US/09/251,545
; CURRENT FILING DATE: 1999-02-17
; EARLIER APPLICATION NUMBER: 60/074,883
; EARLIER FILING DATE: 1998-02-17
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 378
; TYPE: PRT
; ORGANISM: Human
US-09-251-545-1

Query Match 59.1%; Score 75; DB 4; Length 378;
Best Local Similarity 60.9%; Pred. No. 0.0032;
Matches 14; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 4 IAYSILCVLGLGNILVITFAF 26
| | | | | : | | | | | : | | | | | :
Db 63 IMYSIIICFVGLGNGLVLTYYI 85

- RESULT 12

PCT-US93-09636-2
; Sequence 2, Application PC/TUS9309636
; GENERAL INFORMATION:
; APPLICANT: Birkenbach, Mark
; APPLICANT: Kieff, Elliot
; TITLE OF INVENTION: Epstein Barr Virus Induced Genes
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue N.W., Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/09636
; FILING DATE: herewith
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2500
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 378 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
PCT-US93-09636-2

Query Match 59.1%; Score 75; DB 5; Length 378;
Best Local Similarity 60.9%; Pred. No. 0.0032;
Matches 14; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 4 IAYSILCVLGLGNILVITFAF 26
| | | | | : | | | | | : | | | | | :
Db 63 IMYSIIICFVGLGNGLVLTYYI 85

RESULT 13
PCT-US93-11153-15
; Sequence 15, Application PC/TUS9311153
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schweikart, Vicki L.
; TITLE OF INVENTION: Novel Seven Transmembrane Receptors
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/11153
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/977,452
; FILING DATE: 17-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Noland, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31794
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 378 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US93-11153-15

Query Match 59.1%; Score 75; DB 5; Length 378;
Best Local Similarity 60.9%; Pred. No. 0.0032;
Matches 14; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 4 IAYSLICVLGLGNILVITFAF 26
| | | | | : | | | | | : | | | | | : | | | | | :
Db 63 IMYSICFVGLLGNLVLTYIY 85

RESULT 14
US-08-153-848-7
; Sequence 7, Application US/08153848
; Patent No. 5759804
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schweikart, Vicki L.
; TITLE OF INVENTION: Novel Seven Transmembrane Receptors
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/153,848
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/977,452
; FILING DATE: 17-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5759804and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31794
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 410 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-153-848-7

Query Match 59.1%; Score 75; DB 1; Length 410;
Best Local Similarity 60.9%; Pred. No. 0.0035;
Matches 14; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 4 IAYSLICVLGLGNILVITFAF 26
| | | | | : | | | | | : | | | | | : | | | | | :
Db 95 IMYSICFVGLLGNLVLTYIY 117

RESULT 15
US-09-299-843A-7
; Sequence 7, Application US/09299843A
; Patent No. 6107475
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schweikart, Vicki L.
; TITLE OF INVENTION: No. 6107475el Seven Transmembrane Receptors
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/299,843A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/088,337
; FILING DATE: 01-JUN-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/153,848
; FILING DATE: 17-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/977,452

FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Jill E. Uhl
REGISTRATION NUMBER: 43,213
REFERENCE/DOCKET NUMBER: 27866/32059B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX:
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 410 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-299-843A-7

Query Match 59.1%; Score 75; DB 3; Length 410;
Best Local Similarity 60.9%; Pred. NO. 0.0035;
Matches 14; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
QY 4 IAYSLICVLGLNLTIVITAF 26
Db 95 IMYSIICFVGLGNGLVLTYY 117

Search completed: May 23, 2001, 15:30:05
Job time: 412 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 23, 2001, 15:31:58 ; Search time 110.15 Seconds
(without alignments)
16.221 Million cell updates/sec

Title: US-08-887-977-10_COPY_39_64
Perfect score: 127
Sequence: 1 LYRIAYSLICVLGLGNILVITFAF 26

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 198801 seqs, 68722935 residues

Total number of hits satisfying chosen parameters: 198801

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_67: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	107	84.3	369	JC5068	G protein-coupled
2	75	59.1	378	A45680	G protein-coupled
3	75	59.1	378	B5735	lymphocyte-specifi
4	71	55.9	371	JC5498	G protein-coupled
5	71	55.9	378	A55735	G protein-coupled
6	69	54.3	371	JC5796	probable chemoattr
7	69	54.3	373	JE0087	delta opioid recep
8	67	52.8	374	S42628	G protein-coupled
9	67	52.8	374	S32785	G protein-coupled
10	65	51.2	327	S56162	MDCR15 protein - h
11	65	51.2	372	S26667	G protein-coupled
12	63	49.6	355	A45177	chemokine (C-C) re
13	62	48.8	428	A44021	somatostatin recep
14	62	48.8	428	S30508	probable G protein
15	61	48.0	372	B48227	delta opioid recep
16	61	48.0	372	S34592	delta opioid recep
17	61	48.0	372	S38532	delta opioid recep
18	61	48.0	392	S56933	opioid receptor mu
19	61	48.0	398	S56504	mu opioid receptor
20	61	48.0	398	S56517	mu opioid receptor
21	61	48.0	398	A57510	mu opioid receptor
22	61	48.0	400	S56553	mu opiate receptor
23	61	48.0	418	A46226	somatostatin recep
24	60	47.2	359	S49341	MIP-1 alpha recep
25	59	46.5	384	JC4629	somatostatin recep
26	59	46.5	384	A47249	brain-specific som
27	59	46.5	388	JN0605	somatostatin recep
28	58	45.7	359	JC1104	angiotensin II rec
29	58	45.7	359	S44425	angiotensin II rec

ALIGNMENTS

RESULT 1

JC5068

G protein-coupled receptor CKR-L3 - human

C:Species: Homo sapiens (man)

C:Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 21-Jul-2000

C:Accession: JC5068

R:Zaballos, A.; Varona, R.; Gutierrez, J.; Lind, P.; Marquez, G.

Biochem. Biophys. Res. Commun. 227, 846-853, 1996

A:Title: Molecular cloning and RNA expression of two new human chemokine receptor-lik

A:Reference number: JC5067; MUID:97040707

A:Accession: JC5068

A:Molecule type: DNA

A:Residues: 1-369 <ZAB>

A:Cross-references: EMBL:Z79784; NID:gl668737; PIDN:CA802144.1; PID:gl668738

C:Comment: This protein belongs to the family of alpha chemokine receptors.

C:Genetics:

A:Gene: GDB:CKBR6; STRL22: GPR29; CCR6; CKR-L3; GPR-CY4

A:Cross-references: GDB:5370639; OMIM:601835

A:Map position: 6q27-6q27

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor; transmembrane protein

F;42-68/Domain: transmembrane #status predicted <TM1>

F;75-99/Domain: transmembrane #status predicted <TM2>

F;115-136/Domain: transmembrane #status predicted <TM3>

F;160-180/Domain: transmembrane #status predicted <TM4>

F;212-233/Domain: transmembrane #status predicted <TM5>

F;250-271/Domain: transmembrane #status predicted <TM6>

F;292-315/Domain: transmembrane #status predicted <TM7>

Query Match 84.3%; Score 107; DB 2; Length 369;

Best Local Similarity 95.7%; Pred. No. 2e-07;

Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 IAYSLICVLGLGNILVITFAF 26

DB 46 IAYSLICVLGLGNILVITFAF 68

RESULT 2

A45680

G protein-coupled peptide receptor EBI 1 - human

C:Species: Homo sapiens (man)

C:Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 24-Nov-1999

C:Accession: A45680

R:Birkenbach, M.; Josefsen, K.; Yalamanchili, R.; Lenoir, G.; Kieff, E.

J. Virol. 67, 2209-2220, 1993

A:Title: Epstein-Barr virus-induced genes: first lymphocyte-specific G protein-couple

A:Reference number: A45680; MUID:93188173

A:Accession: A45680

A>Status: preliminary

A:Molecule type: nucleic acid

A:Residues: 1-378 <BIR>
A:Cross-references: GB:L08176; NID:g183484; PID:g183485
A:Experimental source: B-lymphocytes
A:Note: sequence extracted from NCBI backbone (NCBIN:127094, NCBI:P.127095)
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 59.1%; Score 75; DB 2; Length 378;
Best Local Similarity 60.9%; Pred. No. 0.005;
Matches 14; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 4 IAYSLICVLGLGNILVITFAF 26
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 63 IMYSIICFVGLLGNLGLVLTIIY 85

RESULT 3
B55735
Lymphocyte-specific G protein-coupled receptor EB11 - human
N:Alternate names: Burkitt's lymphoma receptor 2; Epstein-Barr virus induced protein 1
C:Species: Homo sapiens (man)
C:Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 19-May-2000
C:Accession: B55735; S52443
R:Schweickart, V.L.; Raport, C.J.; Godiska, R.; Byers, M.G.; Eddy Jr., R.L.; Shows, T.B.
Genomics 23, 643-650, 1994
A:Title: Cloning of human and mouse EB11, a lymphoid-specific G-protein-coupled receptor
A:Reference number: A55735; MUID:95154835
A:Accession: B55735
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-378 <SCH>
A:Cross-references: GB:L31581; NID:g468319; PID:AAA74231.1; PID:g468320
R:Burgstahler, R.; Kempkes, B.; Staube, K.; Lipp, M.
submitted to the EMBL Data Library, February 1995
A:Description: The expression of the chemokine receptor BLR2/EB11 is specifically transcribed in the brain.
A:Reference number: S52443
A:Accession: S52443
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 21-378 <BUR>
A:Cross-references: EMBL:X84702
C:Genetics:
A:Gene: GDB:CMKBR7; EB11; BLR2; CCR7
A:Cross-references: GDB:342065; OMIM:600242
A:Map position: 17q12-17q21.2
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor

Query Match 59.1%; Score 75; DB 2; Length 378;
Best Local Similarity 60.9%; Pred. No. 0.005;
Matches 14; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 4 IAYSLICVLGLGNILVITFAF 26
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 63 IMYSIICFVGLLGNLGLVLTIIY 85

RESULT 4
JC5498
G protein-coupled receptor DEZ - mouse
C:Species: Mus musculus (house mouse)
C:Date: 07-Jul-1997 #sequence_revision 29-Aug-1997 #text_change 19-May-2000
C:Accession: JC5498
R:Metzner, A.; Herney, G.; Schinke, B.; Hermans-Borgmeyer, I.
Biochem. Biophys. Res. Commun. 233, 336-342, 1997
A:Title: A novel G protein-coupled receptor with homology to neuropeptide and chemotactic factor 1.
A:Reference number: JC5498; MUID:97289630
A:Contents: Brain
A:Accession: JC5498
A:Molecule type: mRNA
A:Residues: 1-371 <MET>

A:Cross-references: GB:U79525; NID:g1732346; PID:AA53789.1; PID:g1732347
C:Comment: This protein is involved in the bone metabolism.
C:Superfamily: vertebrate rhodopsin
F:110-187/Disulfide bonds: #status predicted

Query Match 55.9%; Score 71; DB 2; Length 371;
Best Local Similarity 56.5%; Pred. No. 0.017;
Matches 13; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 4 IAYSLICVLGLGNILVITFAF 26
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 43 VIYSLVCFVGLLGNLGLVITAF 65

RESULT 5
A55735
G protein-coupled receptor EB11 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 24-Nov-1999
C:Accession: A55735
R:Schweickart, V.L.; Raport, C.J.; Godiska, R.; Byers, M.G.; Eddy Jr., R.L.; Shows, T.B.
Genomics 23, 643-650, 1994
A:Title: Cloning of human and mouse EB11, a lymphoid-specific G-protein-coupled receptor
A:Reference number: A55735; MUID:95154835
A:Accession: A55735
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-378 <SCH>
A:Cross-references: GB:L31580; NID:g468340; PID:AAA74232.1; PID:g468341
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor

Query Match 55.9%; Score 71; DB 2; Length 378;
Best Local Similarity 52.2%; Pred. No. 0.018;
Matches 12; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 4 IAYSLICVLGLGNILVITFAF 26
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 63 LMYSVICFVGLLGNLGLVLTIIY 85

RESULT 6
JC5796
Probable chemoattractant receptor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 24-Jan-1998 #sequence_revision 13-Mar-1998 #text_change 20-Jun-2000
C:Accession: JC5796
R:Owman, C.; Lolait, S.J.; Santen, S.; Olde, B.
Biochem. Biophys. Res. Commun. 241, 390-394, 1997
A:Title: Molecular cloning and tissue distribution of cDNA encoding a novel chemoattractant receptor.
A:Reference number: JC5796; MUID:98086361
A:Accession: JC5796
A:Molecule type: mRNA
A:Residues: 1-371 <OWM>
A:Cross-references: DDBJ:AJ002745; NID:g2624397; PIDN:CAA05715.1; PID:g2624398
A:Experimental source: liver
C:Comment: This protein regulates the trafficking of immune cells during a microbial infection.
C:Superfamily: glycoprotein; receptor; transmembrane protein
F:39-62/Domain: transmembrane #status predicted <TM1>
F:74-94/Domain: transmembrane #status predicted <TM2>
F:112-135/Domain: transmembrane #status predicted <TM3>
F:156-177/Domain: transmembrane #status predicted <TM4>
F:206-237/Domain: transmembrane #status predicted <TM5>
F:259-280/Domain: transmembrane #status predicted <TM6>
F:302-317/Domain: transmembrane #status predicted <TM7>
F:7,190/Binding site: carbohydrate (Asn) #status predicted

Query Match 54.3%; Score 69; DB 2; Length 371;
Best Local Similarity 52.2%; Pred. No. 0.033;

A:Map position: 15q26.1-15q26.1

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 51.2%; Score 65; DB 2; Length 372;
Best Local Similarity 57.9%; Pred. No. 0.12;
Matches 11; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

QY 4 IAYSLICVLGLGNILVVI 22

Db 56 VAYSLIFLGVIGNVLV 74

RESULT 12

A45177

Chemokine (C-C) receptor 1 - human

N:Alternate names: C-C CKR-1; macrophage inflammatory protein-1-alpha receptor

C:Species: Homo sapiens (man)

C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 13-Aug-1999

C:Accession: A45177; 155671

R:Neote, K.; DiGregorio, D.; Mak, J.Y.; Horuk, R.; Schall, T.J.

Cell 72, 415-425, 1993

A:Title: Molecular cloning, functional expression, and signaling characteristics of a C-
A:Reference number: A45177; MUID:93161416

A:Accession: A45177

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-355 <NEO>

A:Cross-references: GB:L10918; NID:9292416; PIDN:AAA36543.1; PID:g292417

A:Experimental source: HL60 cells

A:Note: sequence extracted from NCBI backbone (NCBIP:124876)

R:Gao, J.

J. Exp. Med. 177, 1421-1427, 1993

A:Title: Structure and functional expression of the human macrophage inflammatory 1 alpha
A:Reference number: 155671; MUID:93240122

A:Accession: 155671

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: mRNA

A:Residues: 1-355 <RES>

A:Cross-references: GB:L10918; NID:9292416; PIDN:AAA36543.1; PID:g292417

C:Genetics:

A:Gene: GDB:CMKBR1; CMKR-1

A:Cross-references: GDB:138446; OMIM:601159

A:Map position: 3p21-3p21

C:Superfamily: vertebrate rhodopsin

C:Keywords: disulfide bond; G protein-coupled receptor; glycoprotein; phosphoprotein; tr

F:36-60/Domain: transmembrane #status predicted <TM1>

F:71-91/Domain: transmembrane #status predicted <TM2>

F:108-129/Domain: transmembrane #status predicted <TM3>

F:147-171/Domain: transmembrane #status predicted <TM4>

F:205-223/Domain: transmembrane #status predicted <TM5>

F:240-264/Domain: transmembrane #status predicted <TM6>

F:288-305/Domain: transmembrane #status predicted <TM7>

F:5/Binding site: carboxylate (Asn) (covalent) #status predicted

F:24-273,106-183/Disulfide bonds: #status predicted

F:345/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted

Query Match

Best Local Similarity 49.6%; Score 63; DB 2; Length 355;

Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 6 YSLICVLGLGNILVVI 22

Db 41 YSLVFVIGLVGNILV 57

RESULT 13

A44021

somatostatin receptor SSTR3 - mouse

C:Species: Mus musculus (house mouse)

C:Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 11-Jan-2000

C:Accession: A44021

R:Yasuda, K.; Rens-Domiano, S.; Breder, C.D.; Law, S.F.; Saper, C.B.; Reisine, T.; Be

J. Biol. Chem. 267, 20422-20428, 1992

A:Title: Cloning of a novel somatostatin receptor, SSTR3, coupled to adenylylcyclase.

A:Reference number: A44021; MUID:93015924

A:Accession: A44021

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: nucleic acid

A:Residues: 1-428 <YAS>

A:Cross-references: GB:M91000; NID:g201065; PIDN:AAA40144.1; PID:g201066

A:Note: sequence extracted from NCBI backbone (NCBIP:115746)

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 48.8%; Score 62; DB 2; Length 428;

Best Local Similarity 52.4%; Pred. No. 0.34;

Matches 11; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 LYRIAYSLICVLGLGNILV 21

Db 47 LISLVLVVCVVGILGNSLVI 67

RESULT 14

S30508

probable G protein-coupled receptor - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 11-Jan-2000

C:Accession: S30508

R:Meyerhof, W.; Wulfsen, I.; Schoenrock, C.; Fehr, S.; Richter, D.

Proc. Natl. Acad. Sci. U.S.A. 89, 10267-10271, 1992

A:Title: Molecular cloning of a somatostatin-28 receptor and comparison of its expres

A:Reference number: S30508; MUID:93066220

A:Accession: S30508

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-428 <MEY>

A:Cross-references: EMBL:X63574; NID:g56315; PIDN:CAA45130.1; PID:g56316

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 48.8%; Score 62; DB 2; Length 428;

Best Local Similarity 52.4%; Pred. No. 0.34;

Matches 11; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 LYRIAYSLICVLGLGNILV 21

Db 47 LISLVLVVCVVGILGNSLVI 67

RESULT 15

B48227

delta opioid receptor 1 - mouse

C:Species: Mus musculus (house mouse)

C:Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 24-Nov-1999

C:Accession: B48227; S37807; A48685; S36745

R:Yasuda, K.; Raynor, K.; Kong, H.; Breder, C.D.; Takeda, J.; Reisine, T.; Bell, G.I.

Proc. Natl. Acad. Sci. U.S.A. 90, 6736-6740, 1993

A:Title: Cloning and functional comparison of kappa and delta opioid receptors from m

A:Reference number: A48227; MUID:93342064

A:Accession: B48227

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-372 <YAS>

A:Cross-references: GB:L11064; NID:g348246; PIDN:AAA37520.1; PID:g348247

R:Kieffer, B.L.; Befort, K.; Gaveriaux-Ruff, C.; Hirth, C.G.

submitted to the EMBL Data Library, February 1993

A:Reference number: S37807

A:Accession: S37807

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-372 <KIE>
A:Cross-references: EMBL:L06322; NID:g192942; PIDN:AAA37522.1; PID:g192943
R:Bzdega, T.; Chin, H.; Kim, H.; Jung, H.H.; Kozak, C.A.; Klee, W.A.
Proc. Natl. Acad. Sci. U.S.A. 90, 9305-9309, 1993
A:Title: Regional expression and chromosomal localization of the delta opiate receptor gene
A:Reference number: A48685; MUID:94022364
A:Accession: A48685
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 8-372 <B2D>
A:Cross-references: GB:S66181; NID:g435781; PIDN:AAB28546.1; PID:g435782
A:Experimental source: NCI08-15 hybrid cells
A:Note: sequence extracted from NCBI backbone (NCBIN:138618, NCBIP:138619)
R:Kieffer, B.L.; Befort, K.; Gaveriaux-Ruff, C.; Hirth, C.G.
Proc. Natl. Acad. Sci. U.S.A. 89, 12048-12052, 1992
A:Title: The delta-opioid receptor: isolation of a cDNA by expression cloning and pharmacological characterization
A:Reference number: S36745; MUID:93101664
A:Accession: S36745
A:Molecule type: mRNA
A:Residues: 1-189, 'N', 191, 'GMVQ', 207-208, 'ACSSSPVQLVL', 210-372 <KIW>
A:Cross-references: EMBL:L06322
C:Superfamily: vertebrate rhodopsin
C:Keywords: brain; G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane protein

\ Query Match 48.0%; Score 61; DB 2; Length 372;
Best Local Similarity 62.5%; Pred. No. 0.41;
Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 6 YSLICVLGLLGNILVY 21
|| : ||||| : ||
Db 56 YSAVCAVGLLGNVLVY 71

Search completed: May 23, 2001, 15:31:58
Job time: 505 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 23, 2001, 15:36:17 ; Search time 62.39 Seconds
(without alignments)
14.275 Million cell updates/sec

Title: US-08-887-977-10_COPY_39_64

Perfect score: 127

Sequence: 1 LYRIAYSLICVLGLGNILVITPAF 26

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	107	84.3	374	1	CKR6_HUMAN
2	102	80.3	367	1	CKR6_MOUSE
3	75	59.1	378	1	CKR7_HUMAN
4	71	55.9	371	1	CML1_MOUSE
5	71	55.9	378	1	CKR7_MOUSE
6	69	54.3	371	1	CH23_HUMAN
7	69	54.3	371	1	CML1_RAT
8	69	54.3	373	1	CML1_HUMAN
9	69	54.3	399	1	OPS2_PATYE
10	67	52.8	374	1	CCR5_MOUSE
11	67	52.8	374	1	CCR5_RAT
12	65	51.2	372	1	CCR5_HUMAN
13	63	49.6	355	1	CKR1_HUMAN
14	62	48.8	428	1	SSR3_MOUSE
15	62	48.8	428	1	SSR3_RAT
16	61	48.0	372	1	OPRD_HUMAN
17	61	48.0	372	1	OPRD_MOUSE
18	61	48.0	372	1	OPRD_RAT
19	61	48.0	398	1	OPRM_MOUSE
20	61	48.0	398	1	OPRM_RAT
21	61	48.0	400	1	OPRM_HUMAN
22	61	48.0	401	1	OPRM_BOVIN
23	61	48.0	401	1	OPRM_PIG
24	61	48.0	418	1	SSP3_HUMAN
25	60	47.2	359	1	AG2R_SHEEP
26	60	47.2	359	1	CKR3_MOUSE
27	60	47.2	408	1	NK1R_RANCA
28	59	46.5	359	1	CKR3_RAT
29	59	46.5	384	1	SSP4_MOUSE
30	59	46.5	384	1	SSP4_RAT
31	59	46.5	388	1	SSR4_HUMAN
32	58	45.7	355	1	CKR1_MACMU
33	58	45.7	359	1	AG2R_BOVIN

34	58	45.7	359	1	AG2R_CANFA	P43240 canis famli
35	58	45.7	359	1	AG2R_CAVPO	Q9WV26 cavia porce
36	58	45.7	359	1	AG2R_HUMAN	P30556 homo sapien
37	58	45.7	359	1	AG2R_MERUN	O35210 meriones un
38	58	45.7	359	1	AG2R_MOUSE	P29754 mus musculu
39	58	45.7	359	1	AG2R_PIG	P30555 sus scrofa
40	58	45.7	359	1	AG2R_RAT	P25095 rattus norv
41	58	45.7	359	1	AG2S_HUMAN	Q13725 homo sapien
42	58	45.7	359	1	AG2S_MOUSE	P29755 mus musculu
43	58	45.7	359	1	AG2S_RAT	P29089 rattus norv
44	57	44.9	308	1	P2Y5_CHICK	P32250 gallus gall
45	57	44.9	350	1	IL8A_HUMAN	P25024 homo sapien

ALIGNMENTS

RESULT 1

CKR6_HUMAN

ID CKR6_HUMAN STANDARD; PRT; 374 AA.

AC P51684; Q92846; P78553;

DT 01-OCT-1996 (Rel. 34, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 01-OCT-2000 (Rel. 40, Last annotation update)

DE C-C CHEMOKINE RECEPTOR TYPE 6 (C-C CKR-6) (CCR-6) (IARC

DE RECEPTOR) (GPR-CY4) (GPCY4) (CHEMOKINE RECEPTOR-LIKE 3) (CKR-L3)

DE (DRY6).

GN CKR6 OR CMKBR6 OR STRL22 OR GPR29 OR CKRL3.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A., AND FUNCTION.

RX MEDLINE=97313465; PubMed=9169459;

RA Baba M., Imal T., Nishimura M., Kakizaki M., Takagi S., Hieshima K.,

RA Nomiya H., Yoshie O.;

RT "Identification of CKR6, the specific receptor for a novel

RT lymphocyte-directed CC chemokine LARC.,"

RL J. Biol. Chem. 272:14893-14898(1997).

RN [2]

RP SEQUENCE FROM N.A.

RA Lautens L.L., Modi W., Bonner T.I.;

RT Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.

RN [3]

RP SEQUENCE FROM N.A.

RX MEDLINE=97040707; PubMed=8886020;

RA Zaballos A., Varona R., Gutierrez J., Lind P., Marquez G.;

RT "Molecular cloning and RNA expression of two new human chemokine

RT receptor-like genes.,"

RN Biochem. Biophys. Res. Commun. 227:846-853(1996).

RN [4]

RP SEQUENCE FROM N.A.

RA McCoy R., Perlmutter D.H.;

RT Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.

RN [5]

RP SEQUENCE FROM N.A.

RX MEDLINE=97224503; PubMed=9070937;

RA Liao F., Lee H.-H., Farber J.M.;

RT "Cloning of STRL22, a new human gene encoding a G-protein-coupled

RT receptor related to chemokine receptors and located on chromosome

RT 6q27.,"

RN Genomics 40:175-180(1997).

CC -1- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-3-

CC ALPHA/LARC AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE

CC INTRACELLULAR CALCIUM IONS LEVEL.

CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

CC -1- TISSUE SPECIFICITY: SPLEEN, LYMPH NODES, APPENDIX, AND FETAL

CC LIVER. EXPRESSED IN LYMPHOCYTES, T CELLS AND B CELLS BUT NOT IN

CC NATURAL KILLER CELLS, MONOCYTES, OR GRANULOCYTES.

CC -1- INDUCTION: INTERLEUKIN-2.

CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

CC -1- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-6 IS THE INITIATOR.

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 DR EMBL; U45984; AAB62714.1; -;
 DR EMBL; 279784; CAB02144.1; ALT_INIT.
 DR EMBL; U60000; AAB06949.1; -;
 DR EMBL; U68030; AAC51124.1; -;
 DR EMBL; U68032; AAC51125.1; -;
 DR HSSP; P34996; IDDD.
 DR GCRdb; GCR_1037; -;
 DR GCRdb; GCR_1075; -;
 DR GCRdb; GCR_1906; -;
 DR GCRdb; GCR_1919; -;
 DR GCRdb; GCR_1941; -;
 DR GCRdb; GCR_2110; -;
 DR MIM; 601835; -;
 DR InterPro; IPR000276; -;
 DR Pfam; PF00001; 7tm1.1; 1.
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PROSITE; PS00237; G-PROTEIN_RECP_FL_1; 1.
 DR PROSITE; PS0262; G-PROTEIN_RECP_FL_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 47
 FT TRANSMEM 48 74
 FT DOMAIN 75 83
 FT TRANSMEM 84 104
 FT DOMAIN 105 119
 FT TRANSMEM 120 141
 FT DOMAIN 142 159
 FT TRANSMEM 160 180
 FT DOMAIN 181 211
 FT TRANSMEM 212 238
 FT DOMAIN 239 254
 FT TRANSMEM 255 279
 FT DOMAIN 280 303
 FT TRANSMEM 304 321
 FT DOMAIN 322 374
 FT DISULFID 118 197
 FT CARBOHYD 23 23
 FT CONFLICT 60 60
 FT CONFLICT 74 74
 FT CONFLICT 86 86
 FT CONFLICT 164 164
 FT CONFLICT 182 182
 FT CONFLICT 192 192
 FT CONFLICT 206 206
 FT CONFLICT 225 225
 FT CONFLICT 370 374
 SQ SEQUENCE 374 AA; 42494 MW; D7F963534E990BC4 CRC64;

Query Match 84.3%; Score 107; DB 1; Length 374;
 Best Local Similarity 95.7%; Pred. No. 1.2e-07;
 Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 IAYSILCVGLGNILVITFAF 26
 ||||| ||||| ||||| ||||| |||||
 Db 51 IAYSILCVGLGNILVITFAF 73

RESULT 2
 ID_CK6_MOUSE STANDARD; PRT; 367 AA.
 AC O54689;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE C-C CHEMOKINE RECEPTOR TYPE 6 (C-C CKR-6) (CCR-6) (KY411).
 GN CKR6 OR CKMR6.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Yanagihara S., Komura E., Yamaguchi Y.;
 RT "Mouse G protein-coupled receptor KY411";
 RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99077268; PubMed=9862452;
 RA Varona R., Zaballos A., Gutierrez J., Martin P., Roncal F.,
 RA Albar J.P., Ardavin C., Marquez G.;
 RT "Molecular cloning, functional characterization and mRNA expression
 RT analysis of the murine chemokine receptor CCR6 and its specific ligand
 RT MIP-3alpha";
 RL FEBS Lett. 440:188-194 (1998).
 CC !- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-3-
 CC ALPHA/LARC AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE
 CC INTRACELLULAR CALCIUM IONS LEVEL.
 CC !- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC !- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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 DR EMBL; AB009369; BAA23776.1; -;
 DR EMBL; AJ222714; CAA10956.1; -;
 DR MGD; MGI:1333797; Cmkbr6.
 DR InterPro; IPR000276; -;
 DR Pfam; PF00001; 7tm1.1; 1.
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PROSITE; PS00237; G-PROTEIN_RECP_FL_1; 1.
 DR PROSITE; PS0262; G-PROTEIN_RECP_FL_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 39
 FT TRANSMEM 40 66
 FT DOMAIN 67 75
 FT TRANSMEM 76 96
 FT DOMAIN 97 111
 FT TRANSMEM 112 133
 FT DOMAIN 134 151
 FT TRANSMEM 152 172
 FT DOMAIN 173 203
 FT TRANSMEM 204 230
 FT DOMAIN 231 246
 FT TRANSMEM 247 271
 FT DOMAIN 272 295
 FT TRANSMEM 296 313
 FT DOMAIN 314 367
 FT DISULFID 110 189
 FT CARBOHYD 2 2
 FT CARBOHYD 35 35
 SQ SEQUENCE 367 AA; 42102 MW; 6A309AF833B117E CRC64;

Query Match 80.3%; Score 102; DB 1; Length 367;
 Best Local Similarity 87.0%; Pred. No. 5.7e-07;
 Matches 20; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 4 IAYSILCVGLGNILVITFAF 26
 ||||| ||||| ||||| ||||| |||||
 Db 43 IAYSILCVGLGNILVITFAF 65

```

RESULT 3
CKR7_HUMAN
ID CKR7_HUMAN STANDARD; PRT; 378 AA.
AC P32248;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE C-C CHEMOKINE RECEPTOR TYPE 7 PRECURSOR (C-C CKR-7) (CCR-7)
DE (MIP-3 BETA RECEPTOR) (EBV-INDUCED G PROTEIN-COUPLED RECEPTOR 1)
DE (EBI1) (BLR2).
GN CKR7 OR CMKBR7 OR EBI1 OR EVI1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93188173; PubMed=8383238;
RA Birkenbach M.P., Josefsen K., Yalanchilli R.R., Lenoir G.M.,
RA Elliott K.;
RT "Epstein-Barr virus-induced genes: first lymphocyte-specific G
RT protein-coupled peptide receptors.";
RL J. Virol. 67:2209-2220(1993).
RN [2]
RP SEQUENCE FROM N.A.
RX TISSUE=Placenta;
RX MEDLINE=95154835; PubMed=7851893;
RA Schweickart V.L., Raport C.J., Godiska R., Byers M.G., Eddy R.L. Jr.,
RA Shows T.B., Gray P.W.;
RT "Cloning of human and mouse EB1, a lymphoid-specific
RT G-protein-coupled receptor encoded on human chromosome 17q12-q21.2.";
RL Genomics 23:643-650(1994).
CC -!- FUNCTION: RECEPTOR FOR THE MIP-3-BETA CHEMOKINE. PROBABLE MEDIATOR
CC OF EBV EFFECTS ON B LYMPHOCYTES OR OF NORMAL LYMPHOCYTE FUNCTIONS.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN VARIOUS LYMPHOID TISSUES AND
CC ACTIVATED B AND T LYMPHOCYTES, STRONGLY UPREGULATED IN B CELLS
CC INFECTED WITH EPSTEIN-BARR VIRUS AND T CELLS INFECTED WITH
CC HERPESVIRUS 6 OR 7.
CC -!- INDUCTION: BY EBV.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
-----
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-----
DR EMBL; L08176; AAA58615.1; -
DR EMBL; L31584; AAA74230.1; -
DR EMBL; L31582; AAA74230.1; JOINED.
DR EMBL; L31583; AAA74230.1; JOINED.
DR EMBL; L31581; AAA74231.1; -
DR PIR; A45680; A45680.
DR HSSP; P34996; 1DDD.
DR GCRDb; GCR_0492; -
DR GCRDb; GCR_0958; -
DR MTM; 600242; -
DR InterPro; IPR000276; -
DR InterPro; IPR001718; -
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODSPN.
DR PRINTS; PR00641; CHEMOKINER7.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
DR G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 378 C-C CHEMOKINE RECEPTOR TYPE 7.
FT DOMAIN 25 59 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 60 86 1 (POTENTIAL).

```

```

FT DOMAIN 87 95 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 96 116 2 (POTENTIAL).
FT DOMAIN 117 130 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 131 152 3 (POTENTIAL).
FT DOMAIN 153 170 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 171 191 4 (POTENTIAL).
FT DOMAIN 192 219 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 220 247 5 (POTENTIAL).
FT DOMAIN 248 263 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 264 289 6 (POTENTIAL).
FT DOMAIN 290 313 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 314 331 7 (POTENTIAL).
FT DOMAIN 332 378 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 36 36 N-LINKED (GLCNAC. .) (POTENTIAL).
FT DISULFID 129 210 BY SIMILARITY.
FT CONFLICT 182 183 IW -> SA (IN REF. 1).
FT CONFLICT 337 337 L -> I (IN REF. 1).
SQ SEQUENCE 378 AA; 42874 MW; D4CB4213841AIBD4 CRC64;

Query Match 59.1%; Score 75; DB 1; Length 378;
Best Local Similarity 60.9%; Pred. No. 0.0028;
Matches 14; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 4 IAYSLLICVLGLGNLVLVITFAF 26
DB 63 IMYSIIICFVLGLGNLVLVITYI 85

RESULT 4
CM1L_MOUSE STANDARD; PRT; 371 AA.
ID CM1L_MOUSE
AC P97468;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE CHEMOKINE RECEPTOR-LIKE 1 (G-PROTEIN COUPLED RECEPTOR DEZ).
GN CMKLR1 OR DEZ OR GPCR27.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Brain;
RX MEDLINE=97289630; PubMed=9144535;
RA Methner A., Hermey G., Schinke B., Hermans-Borgmeyer I.;
RA "A novel G protein-coupled receptor with homology to neuropeptide and
RA chemoattractant receptors expressed during bone development.";
RL Biochem. Biophys. Res. Commun. 233:336-342(1997)
CC -!- FUNCTION: ORPHAN RECEPTOR. COULD BE A CHEMOTACTIC PEPTIDE
CC RECEPTOR. MAY HAVE A FUNCTION IN BONE METABOLISM.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- DEVELOPMENTAL STAGE: EXPRESSED DURING BONE DEVELOPMENT AND IN
CC ADULT PARATHYROID GLANDS. EXPRESSED AT DAY E11 IN THE CAUDAL PART
CC OF THE TONGUE AND THE UMBILICAL CORD AND THE EXPRESSION IN THE
CC TONGUE WAS MAINTAINED THROUGHOUT ADULTHOOD. EXPRESSION INCREASES
CC IN BONE AND CARTILAGINOUS FORMING ZONES OF EMBRYO UPTO STAGE E14.5
CC AND AT E16.5 EXPRESSION IS SEEN IN THE LUNG.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
-----
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CC or send an email to license@isb-sib.ch)
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DR EMBL; U79525; AAB53789.1; -
DR GCRDb; GCR_1301; -
DR MGI; MGI:109603; Cmk1r1.
DR InterPro; IPR000276; -

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DR InterPro: IPR002258;
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCRHHODOPS.
DR InterPro: IPR002276;
DR InterPro: IPR001718;
DR PROSITE: PS00237; G-PROTEIN_RECF_F1_1; 1.
DR PROSITE: PS00262; G-PROTEIN_RECF_F1_2; 1.
DR G-protein coupled receptor; Transmembrane; Glycoprotein.
KW DOMAIN 1 39 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 1 39
FT TRANSMEM 40 62 1 (POTENTIAL).
FT DOMAIN 63 73 2 (POTENTIAL).
FT TRANSMEM 74 95 3 (POTENTIAL).
FT DOMAIN 96 112 4 (POTENTIAL).
FT TRANSMEM 113 133 5 (POTENTIAL).
FT DOMAIN 134 152 6 (POTENTIAL).
FT TRANSMEM 153 174 7 (POTENTIAL).
FT DOMAIN 175 222 8 (POTENTIAL).
FT TRANSMEM 223 243 9 (POTENTIAL).
FT DOMAIN 244 259 10 (POTENTIAL).
FT TRANSMEM 260 280 11 (POTENTIAL).
FT DOMAIN 281 298 12 (POTENTIAL).
FT TRANSMEM 299 318 13 (POTENTIAL).
FT DOMAIN 319 371 14 (POTENTIAL).
FT CARBOHYD 7 7 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 190 190 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 110 187 POTENTIAL.
SQ SEQUENCE 371 AA; 41815 MW; CDBE19305244C0B3 CRC64;

Query Match 55.9%; Score 71; DB 1; Length 371;
Best Local Similarity 56.5%; Pred. No. 0.0096; 6; Indels 0; Gaps 0;
Matches 13; Conservative 4; Mismatches 6;

QY 4 IAYSLICVLGLLGNLVITFAF 26
DB 43 VYSLVCFGLLGNLVITFAF 65

RESULT 5
CKR7_MOUSE
ID CKR7_MOUSE STANDARD; PRT; 378 AA.
AC P47774;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE C-C CHEMOKINE RECEPTOR TYPE 7 PRECURSOR (C-C CKR-7) (CCR-7)
DE (MIP-3 BETA RECEPTOR) (EBV-INDUCED G PROTEIN-COUPLED RECEPTOR 1)
DE (EBI1).
DE CKR7 OR CMKBR7 OR EBI1 OR EBIH.
GN Mus musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=B6/CBA; TISSUE=Thymus;
RC MEDLINE=95154835; PubMed=7851893;
RA Schweickart V.L., Raport C.J., Godiska R., Byers M.G., Eddy R.L. Jr.,
RA Shows T.B., Gray P.W.;
RA "Cloning of human and mouse EBI1, a lymphoid-specific
RT G-protein-coupled receptor encoded on human chromosome 17q12-q21.2.";
RL Genomics 23:643-650(1994).
CC -!- FUNCTION: RECEPTOR FOR THE MIP-3-BETA CHEMOKINE. PROBABLE MEDIATOR
CC OF EBV EFFECTS ON B LYMPHOCYTES OR OF NORMAL LYMPHOCYTE FUNCTIONS.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC
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CC EMBL: L31580; AAA74232.1;
DR MGD; MGI:103011; Cmkbr7.
DR InterPro: IPR000276;
DR InterPro: IPR001718;
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCRHHODOPS.
DR PRINTS: PR00641; CHEMOKINER7.
DR PROSITE: PS00237; G-PROTEIN_RECF_F1_1; 1.
DR PROSITE: PS00262; G-PROTEIN_RECF_F1_2; 1.
DR G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
KW DOMAIN 1 24 POTENTIAL.
FT DOMAIN 1 24
FT CHAIN 25 378 C-C CHEMOKINE RECEPTOR TYPE 7.
FT TRANSMEM 25 59 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 60 86 1 (POTENTIAL).
FT TRANSMEM 87 95 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 96 116 2 (POTENTIAL).
FT DOMAIN 117 130 3 (POTENTIAL).
FT TRANSMEM 131 152 4 (POTENTIAL).
FT DOMAIN 153 170 5 (POTENTIAL).
FT TRANSMEM 171 191 6 (POTENTIAL).
FT DOMAIN 192 219 7 (POTENTIAL).
FT TRANSMEM 220 247 8 (POTENTIAL).
FT DOMAIN 248 263 9 (POTENTIAL).
FT TRANSMEM 264 289 10 (POTENTIAL).
FT DOMAIN 290 313 11 (POTENTIAL).
FT TRANSMEM 314 331 12 (POTENTIAL).
FT DOMAIN 332 378 13 (POTENTIAL).
FT CARBOHYD 36 36 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 129 210 BY SIMILARITY.
SQ SEQUENCE 378 AA; 42941 MW; ACBIA422CF54AA54 CRC64;

Query Match 55.9%; Score 71; DB 1; Length 378;
Best Local Similarity 52.2%; Pred. No. 0.0097; 7; Indels 0; Gaps 0;
Matches 12; Conservative 7; Mismatches 4;

QY 4 IAYSLICVLGLLGNLVITFAF 26
DB 63 LMYSVICFVGLLGNLVITFAF 85

RESULT 6
CH23_HUMAN
ID CH23_HUMAN STANDARD; PRT; 371 AA.
AC O75748;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE PROBABLE G PROTEIN-COUPLED RECEPTOR CHEMR23.
DE CHEMR23.
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98264639; PubMed=9603476;
RA Samson M., Edinger A.L., Stordeur P., Rucker J., Verhasselt V.,
RA Sharron M., Govaerts C., Mollereau C., Vassart G., Doms R.W.,
RA Parmentier M.;
RA "ChemR23, a putative chemotactant receptor, is expressed in
RT monocyte-derived dendritic cells and macrophages and is a coreceptor
RT for HIV and some primary HIV-1 strains.";
RL Eur. J. Immunol. 28:1689-1700(1998).
CC -!- FUNCTION: ORPHAN RECEPTOR. COULD BE A CHEMOATTRACTANT RECEPTOR.
CC USED AS A CORECEPTOR FOR SEVERAL HIV STRAINS (SIVMAC316,
CC SIVMAC239, SIVMAC17E-FR AND SIVMAC62A), AS WELL AS A PRIMARY HIV-1
CC STRAIN (92UG024-2). STRAIN (92UG024-2).
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC
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 CC EMBL; Y14838; CAA75112.1; -
 DR InterPro; IPR000276; -
 DR InterPro; IPR002258; -
 DR Pfam; PF00001; 7tm.1; 1.
 DR PRINTS; PR00237; GPCRHHODOPSN.
 DR PRINTS; PR01126; DEZORPHANR.
 DR PROSITE; PS00237; G-PROTEIN_RECP_F1_1; 1.
 DR PROSITE; PS00237; G-PROTEIN_RECP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 38
 FT TRANSMEM 39 61
 FT DOMAIN 62 72
 FT TRANSMEM 73 95
 FT DOMAIN 96 111
 FT TRANSMEM 112 133
 FT DOMAIN 134 154
 FT TRANSMEM 155 175
 FT DOMAIN 176 216
 FT TRANSMEM 217 242
 FT DOMAIN 243 258
 FT TRANSMEM 259 281
 FT DOMAIN 282 296
 FT TRANSMEM 297 317
 FT DOMAIN 318 363
 FT CARBOHYD 7 7
 FT CARBOHYD 190 190
 FT DISULFID 110 187
 SQ SEQUENCE 371 AA; 42034 MW; 944E7AB541FB2898 CRC64;

Query Match 54.3%; Score 69; DB 1; Length 371;
 Best Local Similarity 52.2%; Pred. No. 0.018;
 Matches 12; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

Oy 4 IAYSILCVLGLNGLVITFAF 26
 : ||||| ||||| |||||
 Db 43 VVYSIVCFGLGNGLVIVITAF 65

RESULT 7
 CML1_RAT ID CML1_RAT STANDARD; PRT; 371 AA.
 AC O35786;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE CHEMOKINE RECEPTOR-LIKE 1 (G-PROTEIN COUPLED RECEPTOR DEZ) (G-PROTEIN
 DE COUPLED CHEMOATTRACTANT-LIKE RECEPTOR).
 GN CMLR1 OR DEZ.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ALBINO; TISSUE=Anterior pituitary;
 RX MEDLINE=98086361; PubMed=9425281;
 RA Owan C.S.O., Lolait S.J., Santen S., Olde B.;
 RT "Molecular cloning and tissue distribution of cDNA encoding a novel
 RT chemoattractant-like receptor".
 RL Biochem. Biophys. Res. Commun. 241:390-394 (1997).
 CC -!- FUNCTION: ORPHAN RECEPTOR. COULD BE A CHEMOTACTIC PEPTIDE
 CC RECEPTOR. MAY HAVE A FUNCTION IN BONE METABOLISM.
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -!- TISSUE SPECIFICITY: HIGH EXPRESSION IN HEART AND LUNG. LOW IN
 CC SMALL INTESTINES, COLON, KIDNEY, LIVER, UTERUS, AND BRAIN.

CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

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 DR EMBL; AJ002745; CAA05715.1; -
 DR GCRDB; GCR_2583; -
 DR InterPro; IPR000276; -
 DR InterPro; IPR002258; -
 DR Pfam; PF00001; 7tm.1; 2.
 DR PRINTS; PR00237; GPCRHHODOPSN.
 DR PRINTS; PR01126; DEZORPHANR.
 DR PROSITE; PS00237; G-PROTEIN_RECP_F1_1; 1.
 DR PROSITE; PS00237; G-PROTEIN_RECP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 39
 FT TRANSMEM 40 62
 FT DOMAIN 63 73
 FT TRANSMEM 74 95
 FT DOMAIN 96 112
 FT TRANSMEM 113 133
 FT DOMAIN 134 152
 FT TRANSMEM 153 174
 FT DOMAIN 175 222
 FT TRANSMEM 223 243
 FT DOMAIN 244 259
 FT TRANSMEM 260 280
 FT DOMAIN 281 298
 FT TRANSMEM 299 318
 FT DOMAIN 319 371
 FT CARBOHYD 7 7
 FT CARBOHYD 190 190
 FT DISULFID 110 187
 SQ SEQUENCE 371 AA; 41722 MW; 3AE308603FEC7801 CRC64;

Query Match 54.3%; Score 69; DB 1; Length 371;
 Best Local Similarity 52.2%; Pred. No. 0.018;
 Matches 12; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

Oy 4 IAYSILCVLGLNGLVITFAF 26
 : ||||| ||||| |||||
 Db 43 VVYSIVCFGLGNGLVIVITAF 65

RESULT 8
 CML1_HUMAN ID CML1_HUMAN STANDARD; PRT; 373 AA.
 AC Q99788; Q99789;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE CHEMOKINE RECEPTOR-LIKE 1 (G-PROTEIN COUPLED RECEPTOR DEZ).
 GN CMLR1 OR DEZ.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97289630; PubMed=9144535;
 RA Mather A., Herney G., Schinke B., Hermans-Borgmeyer I.;
 RT "A novel G protein-coupled receptor with homology to neuropeptide and
 RT chemoattractant receptors expressed during bone development".
 RL Biochem. Biophys. Res. Commun. 233:336-342 (1997).
 CC -!- FUNCTION: ORPHAN RECEPTOR. COULD BE A CHEMOTACTIC PEPTIDE
 CC RECEPTOR. MAY HAVE A FUNCTION IN BONE METABOLISM.
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

CC -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A (SHOWN HERE) AND B; ARE
CC PRODUCED BY ALTERNATIVE SPLICING.
CC -!- TISSUE SPECIFICITY: PROMINENTLY EXPRESSED IN DEVELOPING OSSEOUS
CC AND CARTILAGINOUS TISSUE. ALSO FOUND IN ADULT PARATHYROID GLANDS.
CC -!- DEVELOPMENTAL STAGE: EXPRESSED DURING BONE DEVELOPMENT.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC -----
DR EMBL; U79526; AAC51258.1; -
DR EMBL; U79527; AAC51259.1; -
DR GCRDB; GCR_1326; -
DR GCRDB; GCR_1327; -
DR MIM; 602351; -
DR InterPro; IPR000276; -
DR InterPro; IPR002258; -
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR01126; DEZORPHANR.
DR PRINTS; PR00237; GPCRHOOPS.
DR PROSITE; PS00237; G-PROTEIN_RECEPT_F1_1; 1.
DR PROSITE; PS0262; G-PROTEIN_RECEPT_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Alternative splicing.
FT DOMAIN 1 41 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 42 64 1 (POTENTIAL).
FT DOMAIN 65 75 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 76 97 2 (POTENTIAL).
FT DOMAIN 98 114 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 115 135 3 (POTENTIAL).
FT DOMAIN 136 154 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 155 176 4 (POTENTIAL).
FT DOMAIN 177 224 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 225 245 5 (POTENTIAL).
FT DOMAIN 246 261 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 262 282 6 (POTENTIAL).
FT DOMAIN 283 300 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 301 320 7 (POTENTIAL).
FT DOMAIN 321 373 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 9 9 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 192 192 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 112 189 POTENTIAL.
FT CONFLICT 1 2 MISSING (IN ISOFORM B).
FT SEQUENCE 248 248 H -> Q (IN AAC51259).
SQ SEQUENCE 373 AA; 42331 MW; 5244B964BEC7082D CRC64;

Query Match 54.3%; Score 69; DB 1; Length 373;
Best Local Similarity 52.2%; Pred. No. 0.018;
Matches 12; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

Oy 4 IAYSILCVLGLGNILVITFA 26
| : : : : | : : : : | : : : : | : : : : |
Db 45 VYISVCFGLGNGLVIIATF 67

RESULT 9
ID OPS2_PATYE STANDARD; PRT; 399 AA.
AC O15974;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE RHODOPSIN, G0-COUPLED (G0-RHODOPSIN).
GN SCOP2.
OS Patopecten yessoensis (Ezo giant scallop) (Yesso scallop).
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Pectinoidea;
OC Pectinoidea; Pectinidae; Patingopecten.

OX NCBI_TaxID=6573;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=EYE;
RX MEDLINE-97435252; PubMed-9287291;
RA Kojima D., Terakita A., Ishikawa T., Tsukahara Y., Maeda A.,
RA Shichida Y.;
RT "A novel Go-mediated phototransduction cascade in scallop visual
RT cells.";
RL J. Biol. Chem. 272:22979-22989(1997).
CC -!- FUNCTION: VISUAL PIGMENTS ARE THE LIGHT-ABSORBING MOLECULES THAT
CC MEDIATE VISION. THEY CONSIST OF AN APOPROTEIN, OPSIN, COVALENTLY
CC LINKED TO CIS-RETINAL.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- TISSUE SPECIFICITY: RETINA. EXPRESSED IN THE HYPERPOLARIZING CELL
CC LAYER OF THE PHOTORECEPTOR CELLS WITH ITS PHOTORECEPTIVE REGION
CC ADJACENT TO THE LENS.
CC -!- PTM: SOME OR ALL OF THE CARBOXYL-TERMINAL SER OR THR RESIDUES MAY
CC BE PHOSPHORYLATED (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC OPSIN SUBFAMILY.
CC -----
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CC -----
DR EMBL; AB006455; BAA22218.1; -
DR InterPro; IPR000276; -
DR InterPro; IPR001760; -
DR Pfam; PF00001; 7tm.1; 1.
DR PROSITE; PS00237; G-PROTEIN_RECEPT_F1_1; FALSE_NEG.
DR PROSITE; PS0262; G-PROTEIN_RECEPT_F1_2; 1.
DR PROSITE; PS00238; OPSIN; 1.
KW Photoreceptor; Retinal protein; Transmembrane; Glycoprotein; Vision;
KW Phosphorylation; G-protein coupled receptor.
FT DOMAIN 1 17 EXTRACELLULAR.
FT TRANSMEM 18 43 1 (POTENTIAL).
FT DOMAIN 44 53 CYTOPLASMIC.
FT TRANSMEM 56 81 2 (POTENTIAL).
FT DOMAIN 82 95 EXTRACELLULAR.
FT TRANSMEM 96 115 3 (POTENTIAL).
FT DOMAIN 116 134 CYTOPLASMIC.
FT TRANSMEM 135 158 4 (POTENTIAL).
FT DOMAIN 159 182 EXTRACELLULAR.
FT TRANSMEM 183 210 5 (POTENTIAL).
FT DOMAIN 211 240 CYTOPLASMIC.
FT TRANSMEM 241 263 6 (POTENTIAL).
FT DOMAIN 264 271 EXTRACELLULAR.
FT TRANSMEM 272 295 7 (POTENTIAL).
FT DOMAIN 296 399 CYTOPLASMIC.
FT DISULFID 92 169 BY SIMILARITY.
FT BINDING 282 282 RETINAL CHROMOPHORE.
FT CARBOHYD 6 6 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 399 AA; 45096 MW; 5AA6857ABC912100 CRC64;

Query Match 54.3%; Score 69; DB 1; Length 399;
Best Local Similarity 50.0%; Pred. No. 0.019;
Matches 11; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

Oy 4 IAYSILCVLGLGNILVITFA 25
| : : : : | : : : : | : : : : | : : : : |
Db 24 IFISICCIIGVGLNGLIIIVFA 45

RESULT 10
ID CCR5_MOUSE STANDARD; PRT; 374 AA.
AC Q04683;

DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE C-X-C CHEMOKINE RECEPTOR TYPE 5 (CXCR-5) (CXCR-5) (BURKITT'S LYMPHOMA
 DE RECEPTOR 1 HOMOLOG).
 GN BLR1 OR CXCR5 OR GPCR6.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALE/C; TISSUE=Liver;
 RX MEDLINE=94009211; PubMed=8405054;
 RA Kaiser E., Foerster R., Wolf I., Epeensperger C., Kuehl W.M., Lipp M.;
 RT "The G protein-coupled receptor BLR1 is involved in murine B cell
 RT differentiation and is also expressed in neuronal tissues.";
 RL Eur. J. Immunol. 23:2532-2539(1993).
 RN [2]
 RP SEQUENCE OF 151-269 FROM N.A.
 RC TISSUE=Testis;
 RX MEDLINE=94116980; PubMed=8288218;
 RA Wilkie T.M., Chen Y., Gilbert D.J., Moore K.J., Yu L., Simon M.I.,
 RA Copeland N.G., Jenkins N.A.;
 RT "Identification, chromosomal location, and genome organization of
 RT mammalian G-protein-coupled receptors.";
 RL Genomics 18:175-184(1993).
 RN [3]
 RP CHARACTERIZATION.
 RX MEDLINE=97133211; PubMed=8978608;
 RA Foerster R., Mattis A.E., Kremmer E., Wolf E., Brem G., Lipp M.;
 RT "A putative chemokine receptor, BLR1, directs B cell migration to
 RT defined lymphoid organs and specific anatomic compartments of the
 RT spleen.";
 RL Cell 87:1037-1047(1996).
 RN [4]
 RP LIGAND BINDING.
 RX MEDLINE=98146056; PubMed=9486651;
 RA Gunn M.D., Ngo V.N., Ansel K.M., Eklund E.H., Cyster J.G.,
 RA Williams L.T.;
 RT "A B-cell-homing chemokine made in lymphoid follicles activates
 RT Burkitt's lymphoma receptor-1.";
 RL Nature 391:799-803(1998).
 CC -!- FUNCTION: CYTOKINE RECEPTOR THAT BINDS TO B LYMPHOCYTE
 CC CHEMOATTRACTANT (BLC). INVOLVED IN B-CELL MIGRATION INTO B-CELL
 CC FOLLICLES OF SPLEEN AND PEYER'S PATCHES, BUT NOT IN THOSE OF
 CC MESENTERIC OR PERIPHERAL LYMPH NODES.
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -!- TISSUE SPECIFICITY: MAINLY IN SPLEEN, IN RESTING B-CELLS.
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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 CC -----
 DR EMBL; X71788; CAA50673.1; -;
 DR EMBL; L20332; AAA16852.1; -;
 DR PIR; S42628; S42628.
 DR GCRdb; GCR_0809; -;
 DR GCRdb; GCR_0832; -;
 DR MGD; MGI:103567; Brl.
 DR InterPro; IPR000276; -;
 DR InterPro; IPR001053; -;
 DR Pfam; PF00001; 7tm.1; 1.
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PRINTS; PR00564; BURKITTSLYMR.
 DR PROSITE; PS00237; G-PROTEIN_RECEPTOR.F1.1; 1.
 DR PROSITE; PS0262; G-PROTEIN_RECEPTOR.F1.2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; B-cell.

FT DOMAIN 1 57 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 58 78 1 (POTENTIAL).
 FT DOMAIN 79 90 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 91 111 2 (POTENTIAL).
 FT DOMAIN 112 126 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 127 147 3 (POTENTIAL).
 FT DOMAIN 148 169 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 170 190 4 (POTENTIAL).
 FT DOMAIN 191 221 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 222 242 5 (POTENTIAL).
 FT DOMAIN 243 261 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 262 282 6 (POTENTIAL).
 FT DOMAIN 283 306 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 307 327 7 (POTENTIAL).
 FT DOMAIN 328 374 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 28 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 198 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT DISULFID 124 204 POTENTIAL.
 SQ SEQUENCE 374 AA; 42100 MW; 385258420C1EDE30 CRC64;

 Query Match 52.8%; Score 67; DB 1; Length 374;
 Best Local Similarity 63.2%; Pred. NO. 0.034;
 Matches 12; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

 QY 4 IAYSLICVGLGLGNILVVI 22
 Db 58 VAYSLLIFLLGMGNILVLV 76

 RESULT 11
 CCR5_RAT
 ID CCR5_RAT STANDARD; PRT; 374 AA.
 AC P34997;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE C-X-C CHEMOKINE RECEPTOR TYPE 5 (CXCR-5) (CXCR-5) (BURKITT'S LYMPHOMA
 DE RECEPTOR 1 HOMOLOG) (NEUROLYMPHATIC RECEPTOR) (NLR).
 GN BLR1 OR CXCR5.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RX MEDLINE=93238948; PubMed=8386678;
 RA Koubou M., Vanetti M., Wang X., Schaefer M., Hoelltt V.;
 RT "Cloning of a novel putative G-protein-coupled receptor (NLR) which
 RT is expressed in neuronal and lymphatic tissue.";
 RL FEBS Lett. 321:173-178(1993).
 CC -!- FUNCTION: CYTOKINE RECEPTOR THAT BINDS TO B LYMPHOCYTE
 CC CHEMOATTRACTANT (BLC) (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN NEURONAL AND LYMPHATIC TISSUE.
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; X71463; CAA50582.1; -;
 DR PIR; S32785; S32785.
 DR GCRdb; GCR_0648; -;
 DR InterPro; IPR000276; -;
 DR InterPro; IPR001053; -;
 DR Pfam; PF00001; 7tm.1; 1.
 DR PRINTS; PR00237; GPCRHHODPSN.

DR PRINTS: PR00564; BURKITTSLYMR.
 DR PROSITE; PS00237; G-PROTEIN_RECEP_FL_1; 1.
 DR PROSITE; PS0262; G-PROTEIN_RECEP_FL_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; B-cell.
 FT DOMAIN 1 57 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 58 78 1 (POTENTIAL).
 FT DOMAIN 79 90 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 91 111 2 (POTENTIAL).
 FT DOMAIN 112 126 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 127 147 3 (POTENTIAL).
 FT DOMAIN 148 169 4 (POTENTIAL).
 FT TRANSMEM 170 190 4 (POTENTIAL).
 FT DOMAIN 191 221 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 222 242 5 (POTENTIAL).
 FT DOMAIN 243 261 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 262 282 6 (POTENTIAL).
 FT DOMAIN 283 306 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 307 327 7 (POTENTIAL).
 FT DOMAIN 328 374 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 28 28 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT DISULFID 124 204 POTENTIAL.
 SQ SEQUENCE 374 AA; 42012 MW; D87A3AC816207319 CRC64;
 Query Match 52.8%; Score 67; DB 1; Length 374;
 Best Local Similarity 63.2%; Pred. No. 0.034;
 Matches 12; Conservative 6; Mismatches 1; Indels 0; Gaps 0;
 QY 4 IAYSILCVLGLGNILVVI 22
 DB 58 VAYSILFLGLMGNIPLV 76
 RESULT 12
 CCR5_HUMAN STANDARD; PRT; 372 AA.
 ID CCR5_HUMAN
 AC P32302; Q14811;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE C-X-C CHEMOKINE RECEPTOR TYPE 5 (CXCR-5) (CXCR-5) (BURKITT'S LYMPHOMA
 DE RECEPTOR 1) (MONOCYTE-DERIVED RECEPTOR 15) (MDR15).
 GN BLR1 OR CXCR5.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (LONG FORM).
 RC TISSUE=Lymphocytes;
 RX MEDLINE=93049615; PubMed=1425907;
 RA Dobner T., Wolf I., Enrich T., Lipp M.;
 RT "Differentiation-specific expression of a novel G protein-coupled
 RT receptor from Burkitt's lymphoma.";
 RL Eur. J. Immunol. 22:2795-2799(1992).
 RN [2]
 RP SEQUENCE FROM N.A. (SHORT FORM).
 RC TISSUE=Blood;
 RX MEDLINE=95366951; PubMed=7639692;
 RA Barella L., Loetscher M., Tobler A., Baggiolini M., Moser B.;
 RT "Sequence variation of a novel heptahelical leucocyte receptor
 RT through alternative transcript formation.";
 RL Biochem. J. 309:773-779(1995).
 RN [3]
 RP LIGAND BINDING.
 RX MEDLINE=98130629; PubMed=9463416;
 RA Legler D.F., Loetscher M., Stuber Roos R., Clark-Lewis I.,
 RA Baggiolini M., Moser B.;
 RT "B cell-attracting chemokine 1, a human CXC chemokine expressed in
 RT lymphoid tissues, selectively attracts B lymphocytes via
 RT BLR1/CXCR5.";
 RL J. Exp. Med. 187:655-660(1998).

CC -!- FUNCTION: CYTOKINE RECEPTOR THAT BINDS TO BLC. BLR1 EXERTS
 CC POSSIBLY A REGULATORY FUNCTION IN BURKITT LYMPHOMA (BL)
 CC LYMPHOMAGENESIS AND/OR B-CELL DIFFERENTIATION. IT IS A POTENTIAL
 CC CANDIDATE FOR CELL-CELL INTERACTION, AND ACTIVATION OF MATURE B-
 CC LYMPHOCYTES IN LYMPHATIC TISSUES.
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A
 CC SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -!- TISSUE SPECIFICITY: EXPRESSION IN MATURE B-CELLS AND BURKITT
 CC LYMPHOMA CELLS.
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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 CC -----
 CC EMBL; X68149; CAA48252.1; -;
 CC EMBL; X68829; CAA48723.1; -;
 CC PIR; S26667; S26667.
 CC GCRDB; GCR_0453; -;
 CC GCRDB; GCR_2072; -;
 CC GCRDB; GCR_2612; -;
 CC MIN; 601613; -;
 CC InterPro; IPR000276; -;
 CC InterPro; IPR001053; -;
 CC Pfam; PF00001; 7tm_1; 1.
 CC PRINTS; PR00237; GPCRHHODOPSN.
 CC PRINTS; PR00564; BURKITTSLYMR.
 CC PROSITE; PS00237; G-PROTEIN_RECEP_FL_1; 1.
 CC PROSITE; PS0262; G-PROTEIN_RECEP_FL_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; B-cell;
 KW Alternative splicing.
 FT DOMAIN 1 55 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 56 76 1 (POTENTIAL).
 FT DOMAIN 77 88 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 89 109 2 (POTENTIAL).
 FT DOMAIN 110 124 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 125 145 3 (POTENTIAL).
 FT DOMAIN 146 167 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 168 188 4 (POTENTIAL).
 FT DOMAIN 189 219 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 220 240 5 (POTENTIAL).
 FT DOMAIN 241 259 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 260 280 6 (POTENTIAL).
 FT DOMAIN 281 304 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 305 325 7 (POTENTIAL).
 FT DOMAIN 326 372 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 28 28 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 196 196 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT DISULFID 122 202 POTENTIAL.
 FT VARSPLIC 1 45 MISSING (IN SHORT ISOFORM).
 FT CONFLICT 344 344 G -> S (IN REF. 2).
 SQ SEQUENCE 372 AA; 41955 MW; 60F84C839492ACCF CRC64;
 Query Match 51.2%; Score 65; DB 1; Length 372;
 Best Local Similarity 57.9%; Pred. No. 0.063;
 Matches 11; Conservative 7; Mismatches 1; Indels 0; Gaps 0;
 QY 4 IAYSILCVLGLGNILVVI 22
 DB 56 VAYSILFLGLVGNVPLV 74
 RESULT 13
 CKR1_HUMAN STANDARD; PRT; 355 AA.
 ID CKR1_HUMAN
 AC P32246;
 DT 01-OCT-1993 (Rel. 27, Created)

01-OCT-1993 (Rel. 27, Last sequence update)
 01-OCT-2000 (Rel. 40, Last annotation update)
 C-C CHEMOKINE RECEPTOR TYPE 1 (C-C CKR-1) (CC-CKR-1) (CCR-1) (CCR1)
 (MACROPHAGE INFLAMMATORY PROTEIN-1 ALPHA RECEPTOR) (MIP-1ALPHA-R)
 (RANTES-R) (HM145) (LD78 RECEPTOR).
 GN CCR1 OR CCR1B1 OR CCR1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93161416; PubMed=7679328;
 RA Neote K., Digregorio D., Mak J.Y., Horuk R., Schall T.J.;
 RT "Molecular cloning, functional expression, and signalling
 RT characteristics of a C-C chemokine receptor.";
 RL Cell 72:415-425(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93240122; PubMed=7683036;
 RA Gao J.-L., Kuhns D., Tiffany H.L., McDermott D., Li X., Francke U.,
 RA Murphy P.M.;
 RT "Structure and functional expression of the human macrophage
 RT inflammatory protein 1 alpha/RANTES receptor.";
 RL J. Exp. Med. 177:1421-1427(1993).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX TISSUE=Monocytes;
 RA MEDLINE=94092629; PubMed=7505609;
 RA Nomura H., Nielsen B.W., Matsushima K.;
 RT "Molecular cloning of cDNAs encoding a LD78 receptor and putative
 RT leukocyte chemotactic peptide receptors.";
 RL Int. Immunol. 5:1239-1249(1993).
 CC -1- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
 CC MIP-1 DELTA, RANTES, AND MCP-3 AND, LESS EFFICIENTLY, TO MIP-1-
 CC BETA OR MCP-1 AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING
 CC THE INTRACELLULAR CALCIUM IONS LEVEL. RESPONSIBLE FOR AFFECTING
 CC STEM CELL PROLIFERATION.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED IN DIFFERENT HEMATOPOIETIC
 CC CELLS.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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 CC -----
 CC EMBL; L09230; AAA58408.1; -;
 CC EMBL; L10918; AAA36543.1; -;
 CC EMBL; D10925; BAA01723.1; -;
 CC PIR; A45177; A45177.
 CC GCRdb; GCR_0498; -;
 CC GCRdb; GCR_0557; -;
 CC GCRdb; GCR_0573; -;
 CC MIM; 601159; -;
 CC InterPro; IPR000276; -;
 CC InterPro; IPR000355; -;
 CC InterPro; IPR002236; -;
 CC Pfam; PF00001; 7tm_1; 1.
 CC PRINTS; PR00237; GPCRHHODOPSN.
 CC PRINTS; PR00657; CCHEMOKINER.
 CC PRINTS; PR01106; CHEMOKINER1.
 CC PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.
 CC PROSITE; PS0262; G-PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 34
 FT TRANSMEM 35 60
 FT DOMAIN 61 64
 FT DOMAIN 65 91
 FT TRANSMEM 91 91

FT DOMAIN 92 107
 FT TRANSMEM 108 129
 FT DOMAIN 130 146
 FT TRANSMEM 147 171
 FT DOMAIN 172 197
 FT TRANSMEM 198 223
 FT DOMAIN 224 239
 FT TRANSMEM 240 264
 FT DOMAIN 265 281
 FT TRANSMEM 282 305
 FT DOMAIN 306 355
 FT CARBOHYD 5 5
 FT DISULFID 106 183
 FT CONFLICT 337 337
 SQ SEQUENCE 355 AA; 41172 MW; B2C100FFED275985 CRC64;
 Query Match 49.6%; Score 63; DB 1; Length 355;
 Best Local Similarity 70.6%; Pred. No. 0.11;
 Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
 QY 6 YSLICVLGLGNILWVI 22
 DB 41 YSLVFVIGLVGNILWVL 57
 RESULT 14
 SSR3_MOUSE STANDARD; PRT; 428 AA.
 ID SSR3_MOUSE
 AC P30935;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 01-FEB-1996 (Rel. 33, Last annotation update)
 DE SOMATOSTATIN RECEPTOR TYPE 3 (SSR) (SSR-28).
 GN SSR3 OR SMSTR3.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93015924; PubMed=1328199;
 RA Yasuda K., Rens-Domiano S., Breder C.D., Law S.F., Saper C.B.,
 RA Reisine T., Bell G.I.;
 RT "Cloning of a novel somatostatin receptor, SSR3, coupled to
 RT adenylyl cyclase.";
 RL J. Biol. Chem. 267:20422-20428(1992).
 CC -1- FUNCTION: RECEPTOR FOR SOMATOSTATINS-14 AND -28. THIS RECEPTOR IS
 CC COUPLED VIA PERTUSSIS TOXIN SENSITIVE G PROTEINS TO INHIBITION OF
 CC ADENYLYL CYCLASE.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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 CC -----
 CC EMBL; M91000; AAA40144.1; -;
 CC PIR; A44021; A44021.
 CC HSSP; P34996; 1DDO.
 CC GCRdb; GCR_0470; -;
 CC MGD; MGI:98329; Smstr3.
 CC InterPro; IPR000276; -;
 CC InterPro; IPR000586; -;
 CC InterPro; IPR001856; -;
 CC Pfam; PF00001; 7tm_1; 1.
 CC PRINTS; PR00237; GPCRHHODOPSN.
 CC PRINTS; PR00246; SOMATOSTATNR.
 CC PRINTS; PR00589; SOMATOSTATNR3.

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OM protein - protein search, using sw model

Run on: May 23, 2001, 15:35:12 ; Search time 189.03 Seconds
(without alignments)
16.121 Million cell updates/sec

Title: US-08-887-977-10_COPY_39_64

Perfect score: 127

Sequence: 1 LYRIAYSLICVLGLGNILVVITFAF 26

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL15:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rodent:*

12: sp_unclassified:*

13: sp_vertebrate:*

14: sp_virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	102	80.3	367	11 Q9R1V0	Q9R1V0 mus musculus
2	69	54.3	373	13 Q57585	O57585 brachydanio
3	65	51.2	383	13 Q42324	O42324 catostomus
4	64	50.4	355	6 Q9MYJ8	Q9MYJ8 callithrix
5	64	50.4	393	5 Q9VVO0	Q9VVO0 drosophila
6	62	48.8	339	6 Q9TUS4	Q9TUS4 lemur varie
7	62	48.8	339	6 Q9TUS3	Q9TUS3 lemur catia
8	62	48.8	339	6 Q9TUS2	Q9TUS2 lemur catia
9	62	48.8	339	6 Q9TUS1	Q9TUS1 lemur varie
10	62	48.8	339	6 Q9TUS0	Q9TUS0 lemur varie
11	62	48.8	339	6 Q9TQU3	Q9TQU3 lemur catia
12	62	48.8	351	6 Q9MYJ9	Q9MYJ9 oryctolagus
13	61	48.0	393	11 Q9R1M0	Q9R1M0 mus musculus
14	61	48.0	400	6 Q9MYW9	Q9MYW9 macaca mula
15	61	48.0	401	11 Q9R1L9	Q9R1L9 mus musculus
16	61	48.0	438	11 Q9R0D1	Q9R0D1 mus musculus
17	61	48.0	444	11 Q9J1Y1	Q9J1Y1 mus musculus
18	60	47.2	353	13 Q93247	O93247 cyprinus ca
19	60	47.2	358	6 Q9N0M0	Q9N0M0 ovis aries

20	60	47.2	359	6 Q9N0U1	Q9N0U1 ovis aries
21	60	47.2	378	11 Q08707	Q08707 mus musculus
22	60	47.2	382	11 Q09027	Q09027 rattus norv
23	59	46.5	377	13 Q73733	Q73733 brachydanio
24	59	46.5	388	4 Q9UIV1	Q9UIV1 homo sapien
25	58	45.7	352	6 Q9TV47	Q9TV47 cercopithec
26	58	45.7	352	6 Q9TV45	Q9TV45 cercopithec
27	58	45.7	352	6 Q9TSQ7	Q9TSQ7 cercopithec
28	58	45.7	451	5 Q9VVO1	Q9VVO1 drosophila
29	58	45.7	469	4 Q9NSD7	Q9NSD7 homo sapien
30	57	44.9	344	6 Q77833	Q77833 cercocebus
31	57	44.9	352	6 Q77776	Q77776 cercocebus
32	57	44.9	353	13 Q9PTF7	Q9PTF7 brachydanio
33	57	44.9	370	4 Q75194	Q75194 homo sapien
34	57	44.9	380	5 Q9NFV3	Q9NFV3 lymnaea sta
35	57	44.9	380	5 Q9NFV1	Q9NFV1 lymnaea sta
36	57	44.9	380	5 Q9NFV0	Q9NFV0 lymnaea sta
37	57	44.9	383	14 Q89609	Q89609 equine herp
38	56	44.1	308	11 Q9R0K3	Q9R0K3 mus musculu
39	56	44.1	334	6 Q9TU07	Q9TU07 erythrocebu
40	56	44.1	339	6 Q9TUJ9	Q9TUJ9 cercopithec
41	56	44.1	339	6 Q9TU08	Q9TU08 cercopithec
42	56	44.1	339	6 Q9TU07	Q9TU07 macaca fusc
43	56	44.1	339	6 Q9TU06	Q9TU06 macaca fusc
44	56	44.1	339	6 Q9TU05	Q9TU05 macaca fusc
45	56	44.1	339	6 Q9TU04	Q9TU04 macaca mula

ALIGNMENTS

RESULT 1

Q9R1V0

ID Q9R1V0

AC Q9R1V0;

DT 01-MAY-2000 (Tremblrel. 13, Created)

DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)

DT 01-JUN-2000 (Tremblrel. 14, Last annotation update)

DE CC CHEMOKINE LARC SPECIFIC RECEPTOR.

GN MCCR6.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RA Tanaka Y.;

RT "Molecular Cloning of Murine Homologue of CCR6, the Specific Receptor for CC Chemokine LARC";

RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.

DR EMBL; AB016031; BAA82443.1;

DR INTERPRO; IPR000190;

DR INTERPRO; IPR000276;

DR INTERPRO; IPR000355;

DR PFAM; PF000001; 7tm.1.1;

DR PRINTS; PR00237; GPCRHHODOPSN.

DR PRINTS; PR00635; ANGIOTENSINR.

DR PRINTS; PR00657; CCHEMOKINR.

DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.

KW Receptor.

SQ SEQUENCE 367 AA; 42082 MW; 207FD98B2F7A6DD3 CRC64;

Query Match 80.3%; Score 102; DB 11; Length 367;

Best Local Similarity 87.0%; Pred. No. 2.4e-06;

Matches 20; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 IAYSLICVLGLGNILVVITFAF 26

||||| ||||||| |||||||

Db 43 IAYSLICVFGILGNIMVMTFAF 65

RESULT 2

```

057585
ID O57585 PRELIMINARY; PRT; 373 AA.
AC O57585;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE OPIOID RECEPTOR HOMOLOG.
GN OPRD1.
OS Brachydanio rerio (zebrafish) (zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Rasbora; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99141513; PubMed=9987040;
RA Barralio A., Gonzalez-Sarmiento R., Porteros A., Garcia-Isidoro F.,
RA Rodriguez R.E.;
RT Cloning, molecular characterization, and distribution of a gene
RT homologous to delta opioid receptor from zebrafish (Danio rerio).;
RL Biochem. Biophys. Res. Commun. 245:544-548(1998).
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; AJ001596; CAA04862.1; -
DR ZFIN; ZDB-GENE-990415-199; oprd1.
DR INTERPRO; IPR000276; -
DR PFAM; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G-PROTEIN RECEPTOR; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
SQ SEQUENCE 373 AA; 42520 MW; FF15794192DAB934 CRC64;

Query Match 54.3%; Score 69; DB 13; Length 373;
Best Local Similarity 81.2%; Pred. No. 0.077; 0; Indels 0; Gaps 0;
Matches 13; Conservative 3; Mismatches 0;

OY 6 YSLICVGLGNILVV 21
DB 59 YSVICVGLGNILVM 74

RESULT 3
O42324
ID O42324 PRELIMINARY; PRT; 383 AA.
AC O42324;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE MU-OPIOID RECEPTOR.
OS Catostomus commersoni (White sucker).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Catostomidae; Catostomus.
OX NCBI_TaxID=7971;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=CNs.
RA Darlison M.G., Harvey R.J., Greten F.R., Kreienkamp H.J., Zwieters H.,
RA Stthmer T., Lederis K., Richter D.;
RA Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; Y10904; CAA71843.1; -
DR INTERPRO; IPR000276; -
DR INTERPRO; IPR001418; -
DR PFAM; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PR00384; OPIOIDR.
DR PROSITE; PS00237; G-PROTEIN RECEPTOR; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
SQ SEQUENCE 383 AA; 43232 MW; F58838B57A107305 CRC64;

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Query Match 51.2%; Score 65; DB 13; Length 383;
Best Local Similarity 62.5%; Pred. No. 0.28;
Matches 10; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

OY 6 YSLICVGLGNILVV 21
DB 64 YSVICVGLGNILVM 79

RESULT 4
O9MYJ8
ID O9MYJ8 PRELIMINARY; PRT; 355 AA.
AC O9MYJ8;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE CHEMOKINE RECEPTOR.
GN CCRI.
OS Callithrix jacchus (Common marmoset).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Callithrix.
OX NCBI_TaxID=9483;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20153429; PubMed=10686294;
RA Liang M., Rosser M.P., Ng H.P., May K., Bauman J.G., Islam I.,
RA Hannam A., Kretschmer P.J., Pu H., Dunning L., Snider R.M.,
RA Morrissey M.M., Hesselgesser J., Perez H.D., Horuk R.;
RT "Species selectivity of a small molecule antagonist for the CCRI
RT chemokine receptor.";
RL Eur. J. Pharmacol. 389:41-49(2000).
DR EMBL; AF127528; AAF36453.1; -
KW Receptor.
SQ SEQUENCE 355 AA; 40928 MW; 2B01C47E9874A2C1 CRC64;

Query Match 50.4%; Score 64; DB 6; Length 355;
Best Local Similarity 70.6%; Pred. No. 0.35;
Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 6 YSLICVGLGNILVV 22
DB 41 YSLVEVGLGNILVV 57

RESULT 5
O9VVQ0
ID O9VVQ0 PRELIMINARY; PRT; 393 AA.
AC O9VVQ0;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE CGI3702 PROTEIN.
GN CGI3702.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blaise R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

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RT species.^a;
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF162014; AAD47769.1; -.
 DR INTERPRO: IPR000248; -
 DR INTERPRO: IPR00376; -
 DR INTERPRO: IPR00355; -
 DR INTERPRO: IPR01277; -
 DR INTERPRO: IPR022336; -
 DR INTERPRO: IPR002337; -
 DR INTERPRO: IPR002238; -
 DR INTERPRO: IPR002240; -

DR PFAM; PF00001; 7tm.1; 1.
 DR PRINTS; PRO0237; GPCRHHODOPSN.
 DR PRINTS; PRO0241; ANGIOTENSINR.
 DR PRINTS; PRO0645; LCRIORPHANR.
 DR PRINTS; PRO0657; CCHEMOKINER.
 DR PRINTS; PRO1106; CHEMOKINER1.
 DR PRINTS; PRO1107; CHEMOKINER2.
 DR PRINTS; PRO1108; CHEMOKINER3.
 DR PRINTS; PRO1110; CHEMOKINER5.
 DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; UNKNOWN1.
 KW Receptor.
 FT NON_TER 1 1
 FT NON_TER 339 339
 SQ SEQUENCE 339 AA; 38713 MW; 77DCE451AA3A4CB6 CRC64;

Query Match 48.8%; Score 62; DB 6; Length 339;
 Best Local Similarity 61.1%; Pred. No. 0.64;
 Matches 11; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 6 YSLICVLGLGNILVWIT 23
 |||: : ||: ||: ||: ||:
 Db 30 YSLVFIPLGNMLVLT 47

RESULT 11

ID Q9TQ03 PRELIMINARY; PRT; 339 AA.
 AC Q9TQ03;
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)
 DE C-C CHEMOKINE RECEPTOR 5 (FRAGMENT).
 GN CCR5.
 OS Lemur catta (Ring-tailed lemur).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Strepsirhini; Lemnidae; Lemur.
 OX NCBI_TaxID=9447;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
 RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wollinsky S.;
 RT "Sequences of the CCR5 genes from diverse simian and prosimian
 species";
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF162011; AAD47766.1; -;
 DR EMBL; AF162008; AAD47763.1; -;
 DR INTERPRO; IPR000248; -;
 DR INTERPRO; IPR000276; -;
 DR INTERPRO; IPR000355; -;
 DR INTERPRO; IPR001277; -;
 DR INTERPRO; IPR002236; -;
 DR INTERPRO; IPR002237; -;
 DR INTERPRO; IPR002238; -;
 DR INTERPRO; IPR002240; -;
 DR PFAM; PF00001; 7tm.1; 1.
 DR PRINTS; PRO0237; GPCRHHODOPSN.
 DR PRINTS; PRO0241; ANGIOTENSINR.
 DR PRINTS; PRO0645; LCRIORPHANR.
 DR PRINTS; PRO0657; CCHEMOKINER.
 DR PRINTS; PRO1106; CHEMOKINER1.
 DR PRINTS; PRO1107; CHEMOKINER2.
 DR PRINTS; PRO1108; CHEMOKINER3.
 DR PRINTS; PRO1110; CHEMOKINER5.
 DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; UNKNOWN1.
 KW Receptor.
 FT NON_TER 1 1
 FT NON_TER 339 339
 SQ SEQUENCE 339 AA; 38712 MW; 8A2D0D74093A56AE CRC64;

Query Match 48.8%; Score 62; DB 6; Length 339;
 Best Local Similarity 61.1%; Pred. No. 0.64;

Matches 11; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
 QY 6 YSLICVLGLGNILVWIT 23
 |||: : ||: ||: ||: ||:
 Db 30 YSLVFIPLGNMLVLT 47

RESULT 12

ID Q9MYJ9 PRELIMINARY; PRT; 351 AA.
 AC Q9MYJ9;
 DT 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
 DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)
 DE CHEMOKINE RECEPTOR.
 GN CCR1.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20153429; PubMed=10686294;
 RA Liang M., Rosser M.P., Ng H.P., May K., Bauman J.G., Islam I.,
 RA Ghanam A., Kretschmer P.J., Pu H., Dunning L., Snider R.M.,
 RA Morrissey M.M., Hesselgeser J., Perez H.D., Horuk R.;
 RT "Species selectivity of a small molecule antagonist for the CCR1
 chemokine receptor";
 RL Eur. J. Pharmacol. 389:41-49(2000).
 DR EMBL; AF127527; AAF36452.1; -;
 KW Receptor.
 SQ SEQUENCE 351 AA; 40534 MW; B3FED6117A141552 CRC64;

Query Match 48.8%; Score 62; DB 6; Length 351;
 Best Local Similarity 64.7%; Pred. No. 0.66;
 Matches 11; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 6 YSLICVLGLGNILVWI 22
 |||: : ||: ||: ||: ||:
 Db 41 YSLVFIPLGNMLVWL 57

RESULT 13

ID Q9R1M0 PRELIMINARY; PRT; 393 AA.
 AC Q9R1M0;
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-JUN-2000 (Tremblrel. 14, Last annotation update)
 DE MU OPIOID RECEPTOR MORID.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J;
 RX MEDLINE=99348417; PubMed=10419560;
 RA Pan Y.X., Xu J., Bolan E., Abbadi C., Chang A., Zuckerman A.,
 RA Rossi G., Pasternak G.W.;
 RT "Identification and characterization of three new alternatively
 spliced mu-opioid receptor isoforms";
 RL Mol. Pharmacol. 56:396-403(1999).
 DR EMBL; AF074973; AAD51861.1; -;
 DR INTERPRO; IPR000105; -;
 DR INTERPRO; IPR000276; -;
 DR INTERPRO; IPR000586; -;
 DR INTERPRO; IPR000611; -;
 DR INTERPRO; IPR000826; -;
 DR INTERPRO; IPR001418; -;
 DR PFAM; PF00001; 7tm.1; 1.
 DR PRINTS; PRO0237; GPCRHHODOPSN.

DR PRINTS; PR00246; SOMATOSTATNPR.
DR PRINTS; PR00384; OPIOIDR.
DR PRINTS; PR00526; FMETLEUPHER.
DR PRINTS; PR00537; MUOPIOIDR.
DR PRINTS; PR01012; NRPEPTIDEYR.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; 1.
KW Receptor.
SQ SEQUENCE 393 AA; 43942 MW; 44A102A98DA09EAC CRC64;

Query Match 48.0%; Score 61; DB 11; Length 393;
Best Local Similarity 62.5%; Pred. No. 1;
Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 6 YSLICVGLGLGNILV 21
||:||||| || ||:
Db 75 YSIVCVVGLFGNFLVM 90

RESULT 14

ID Q9MYW9 PRELIMINARY; PRT; 400 AA.
AC Q9MYW9:
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)
DE MU OPIOID RECEPTOR.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-STRIATUM;
RA Miller G.M., Madras B.K.;
RT "Cloning of the Macaca mulatta mu opioid receptor.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF286024; AAF97249.1; -
KW Receptor.
SQ SEQUENCE 400 AA; 44922 MW; C6EAE7847179DD3 CRC64;

Query Match 48.0%; Score 61; DB 6; Length 400;
Best Local Similarity 62.5%; Pred. No. 1;
Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 6 YSLICVGLGLGNILV 21
||:||||| || ||:
Db 77 YSIVCVVGLFGNFLVM 92

RESULT 15

ID Q9RIL9 PRELIMINARY; PRT; 401 AA.
AC Q9RIL9:
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2000 (Tremblrel. 14, Last annotation update)
DE MU OPIOID RECEPTOR MORIE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RX MEDLINE=99348417; PubMed=10419560;
RA Pan Y.X., Xu J., Bolan E., Abbadie C., Chang A., Zuckerman A.,
RA Rossi G., Pasternak G.W.;
RT "Identification and characterization of three new alternatively
spliced mu-opioid receptor isoforms.";
RL Mol. Pharmacol. 56:396-403(1999).

DR EMBL; AF074974; AAD51862.1; -
DR INTERPRO; IPR000105; -
DR INTERPRO; IPR000276; -
DR INTERPRO; IPR000586; -
DR INTERPRO; IPR000611; -
DR INTERPRO; IPR000826; -
DR INTERPRO; IPR001418; -
DR PFAM; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PRINTS; PR00246; SOMATOSTATNPR.
DR PRINTS; PR00384; OPIOIDR.
DR PRINTS; PR00526; FMETLEUPHER.
DR PRINTS; PR00537; MUOPIOIDR.
DR PRINTS; PR01012; NRPEPTIDEYR.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; 1.
KW Receptor.
SQ SEQUENCE 401 AA; 44847 MW; 2C72C33B40623D9C CRC64;

Query Match 48.0%; Score 61; DB 11; Length 401;
Best Local Similarity 62.5%; Pred. No. 1;
Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 6 YSLICVGLGLGNILV 21
||:||||| || ||:
Db 75 YSIVCVVGLFGNFLVM 90

Search completed: May 23, 2001, 15:35:12
Job time: 618 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 23, 2001, 15:28:26 ; Search time 184.73 Seconds
(without alignments)
3.404 Million cell updates/sec

Title: US-08-887-977-10_COPY_65_75

Perfect score: 57

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 390729 seqs, 57163235 residues

Total number of hits satisfying chosen parameters: 390729

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 1: /SID56/gcgdata/geneseq/geneseq/AA1980.DAT.*
 - 2: /SID56/gcgdata/geneseq/geneseq/AA1981.DAT.*
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 - 4: /SID56/gcgdata/geneseq/geneseq/AA1983.DAT.*
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 - 21: /SID56/gcgdata/geneseq/geneseq/AA2000.DAT.*
 - 22: /SID56/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	57	100.0	365	19	W48086 Human dendritic ce
2	57	100.0	365	21	Y97077 Primate (human) ch
3	49	86.0	360	17	R99274 Chemokine receptor
4	49	86.0	360	21	B07498 A human CCR4 chemo
5	43	75.4	159	21	R41786 Human ORFX ORF1550
6	43	75.4	246	20	Y57292 Human BGCKr protei
7	43	75.4	333	20	Y57289 Human BGCKr partia
8	43	75.4	349	20	W93170 Human HFA041 prot
9	43	75.4	350	20	Y57290 Human BGCKr protei
10	43	75.4	350	20	Y57291 Mouse BGCKr protei
11	43	75.4	350	20	Y30125 A human seven-pass

12	43	75.4	350	20	Y17435 Human signal pepti
13	43	75.4	350	20	W93169 Human HFA041 prot
14	43	75.4	350	21	B37788 Human TSC7. Homo
15	43	75.4	350	21	Y71301 Human orphan G pro
16	43	75.4	350	21	B02835 Human G protein co
17	43	75.4	350	21	Y94325 Human seven transm
18	41	71.9	355	18	W07618 Human G-protein re
19	41	71.9	355	19	W49807 Human G-protein ch
20	41	71.9	355	19	W56689 Human MCP-4 recept
21	41	71.9	355	20	W97868 Human CC chemokine
22	39	68.4	92	20	W97363 A partial CXCR4B p
23	39	68.4	116	21	G01911 Human secreted pro
24	39	68.4	337	15	R53753 Seven transmembran
25	39	68.4	337	19	W48734 Human RM3 seven tr
26	39	68.4	337	21	B21698 Human 7TM receptor
27	39	68.4	352	13	R27792 New platelet facto
28	39	68.4	352	16	R68812 Human monocyte pF4
29	39	68.4	352	16	R80757 Chemokine superfam
30	39	68.4	352	20	Y39993 Human CXCR4 protei
31	39	68.4	352	21	Y52507 Human CXC-chemokin
32	39	68.4	356	20	W97362 G-protein coupled
33	39	68.4	359	19	W64778 A murine CXC chemo
34	39	68.4	359	20	Y39994 Mouse CXCR4 protei
35	38	66.7	100	20	W88231 HIV-1 co-receptor
36	38	66.7	184	18	W27406 Inactive human CCR
37	38	66.7	193	19	W70000 Rodent chemokine r
38	38	66.7	215	18	W27408 Inactive human CCR
39	38	66.7	215	20	W82338 HIV-1 co-receptor
40	38	66.7	302	19	W70001 Rodent chemokine r
41	38	66.7	332	18	W26766 Human chemokine re
42	38	66.7	351	20	Y23825 A7 times membrane
43	38	66.7	352	18	W27407 Human CCR5. Homo
44	38	66.7	352	18	W27123 Human chemokine re
45	38	66.7	352	18	W27125 Macaque chemokine

ALIGNMENTS

RESULT	1
W48086	
ID	W48086 standard; Protein; 365 AA.
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AC	W48086;
XX	
DT	11-JUN-1998 (first entry)
XX	
DE	Human dendritic cell chemokine receptor.
XX	
KW	Human; thymus expressed chemokine; TECK; MIP-3alpha; MIP-3beta;
KW	receptor; dendritic cell; macrophage; inflammation; asthma.
XX	
OS	Homo sapiens.
XX	
EH	Key Location/Qualifiers
FT	Misc-difference 193
FT	/note= "encoded by CAN"
XX	
PN	W09801557-A2.
XX	
PD	15-JAN-1998.
XX	
PF	02-JUL-1997; 97WO-US10819.
XX	
PR	04-JUN-1997; 97US-0048593.
PR	05-JUL-1996; 96US-0675814.
PR	11-OCT-1996; 96US-0028329.
XX	
PA	(SCHE) SCHERING CORP.
XX	
PI	Gish KC, Schall TJ, Vicari A, Wang W, Zlotnik A;
XX	
DR	WPI; 1998-101054/09.

DR N-PSDB; V15418.
XX Novel chemokines, e.g. thymus expressed chemokine - used for
PT treating inflammatory conditions including asthma.
XX
XX
PS Claim 3; Page 94-95; 202pp; English.
XX
CC The present sequence represents human dendritic cell chemokine receptor.
CC Antibodies which bind to the protein can be used in detecting or
CC diagnosing various immunological conditions related to expression
CC of the protein. The nucleic acid can be used for screening and
CC isolating DNA clones for the chemokines, especially from other
CC species. The chemokine can be used in the treatment of conditions
CC associated with abnormal physiology or development, including
CC inflammatory conditions such as asthma.
XX
XX
SQ Sequence 365 AA;

Query Match 100.0%; Score 57; DB 19; Length 365;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YKKARSMTDVIY 11
Db 65 ykkarsmtdv 75
|||||

RESULT 2
Y97077
ID Y97077 standard; Protein; 365 AA.
XX Y97077;
XX
XX
XX 04-DEC-2000 (first entry)
XX
XX Primate (human) chemokine receptor CCR6.
XX
XX MIP-3-alpha; chemokine; CCR6 receptor; ligand; cytostatic; agonist;
KW antagonist; anti-psoriatic; dermatological; immunosuppressive;
KW anti-inflammatory.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FT Misc-difference 193
FT /note= "Encoded by CAN#"
XX
XX WO2000046248-A1.
XX
XX 10-AUG-2000.
XX
XX 02-FEB-2000; 2000WO-US00511.
XX
XX 03-FEB-1999; 99US-0244281.
XX
XX (SCHE) SCHERING CORP.
XX
XX Oldham ER, Homey B, Dieu-Nosjean M, Caux C, Zlotnik A;
XX
XX WPI; 2000-543477/49.
XX N-PSDB; A51971.
XX
XX Novel methods for modulating the migration of cells within or to the
PT skin using MIP-3-alpha or CCR6 agonists or antagonists, useful for
PT treating skin disorders, e.g. cancer
XX
XX Disclosure; Page 53-54; 61pp; English.
XX
XX The MIP-3-alpha chemokine is expressed in inflamed skin cells. This
CC chemokine is the ligand for the CCR6 receptor. MIP-3-alpha or CCR6
CC agonists or antagonists can be used to modulate the migration of a cell
CC within or to the skin of a mammal. MIP-3-alpha can be used to purify a

CC population of cells expressing a MIP-3-alpha receptor. The methods are
CC useful for treating a mammalian subject with a skin disease or condition,
CC e.g. cancer, metastasis, psoriasis, atopic or contact dermatitis,
CC systemic lupus erythematosus and lichen ruber planus, or for treating
CC skin transplants or grafts.
XX
XX
SQ Sequence 365 AA;

Query Match 100.0%; Score 57; DB 21; Length 365;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YKKARSMTDVIY 11
Db 65 ykkarsmtdv 75
|||||

RESULT 3
R99274
ID R99274 standard; Protein; 360 AA.
XX
XX R99274;
XX
XX 09-DEC-1996 (first entry)
XX
XX Chemokine receptor K5.5.
XX
XX Chemokine receptor K5.5; MIP-1-alpha; RANTES; MCP-1; allergy;
KW atheroma; HIV; AIDS; graft rejection; stem cell.
XX
XX Homo sapiens.
XX
XX WO9623068-A1.
XX
XX 01-AUG-1996.
XX
XX 24-JAN-1996; 96WO-GB00143.
XX
XX 27-JAN-1995; 95GB-0001683.
XX
XX (GLAX) GLAXO GROUP LTD.
XX
XX Power CA, Wells TNC;
XX
XX WPI; 1996-362692/36.
XX N-PSDB; T35277.
XX
XX Chemokine receptor which binds MIP-1-alpha, RANTES and/or MCP-1 -
PT useful in screening for agents to treat asthma, hay fever, eczema,
PT allergies, atopic dermatitis, rhinitis or conjunctivits.
XX
XX Claim 1; Fig 3; 47pp; English.
XX
XX Human chemokine receptor K5.5 (R99274) binds MIP-1-alpha, RANTES
CC and/or MCP-1. Its amino acid sequence was deduced from a cDNA
CC clone (r35277) obtd. from a human spleen lambda gt11 cDNA
CC library. Recombinant chemokine receptor K5.5 can be expressed
CC in transformed host cells. It can be used to screen for agents
CC which act as antagonists to MCP-1, MIP-1-alpha and/or RANTES.
CC Such agents may be useful in treating allergies, atheromas and
CC diseases mediated by viruses, such as AIDS. They can also be
CC used to prevent graft rejection or to protect stem cells from
CC the effects of chemotherapy.
XX
XX
SQ Sequence 360 AA;

Query Match 86.08; Score 49; DB 17; Length 360;
Best Local Similarity 81.88; Pred. No. 0.047;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YKKARSMTDVIY 11

Db 67 ykrlrsmtdiv 77
 ||: |||||

RESULT 4
 B07498
 ID B07498 standard; Protein; 360 AA.

XX AC B07498;
 XX DT 20-OCT-2000 (first entry)

XX DE A human CCR4 chemokine receptor polypeptide.

XX KW Systemic memory T cell; CCR4; TARC; integrin dependent arrest;
 KW thymus and activation-regulated chemokine; vascular receptor;
 KW MDC; monokine derived chemokine; adhesion trigger; inflammation.

XX OS Homo sapiens.
 XX PN WO200041724-A1.

XX PD 20-JUL-2000.

XX PF 14-JAN-2000; 2000WO-US00953.

XX PR 15-JAN-1999; 99US-0232878.

XX PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PA (LEUK-) LEUKOSITE INC.

XX PI Butcher EC, Campbell JJ, Wu L, Rottman JB;

XX DR WPI; 2000-475957/41.
 DR N-PSDB; A58872.

XX PT Modulating the trafficking of systemic memory T cells in mammals by
 PT administering a CCR4 modulating agent, useful for the treatment of
 PT inflammation -

XX PS Disclosure; Page 35-36; 39pp; English.

XX CC The specification describes a method of modulating the trafficking of
 CC systemic memory T cells in a mammalian host. The method comprises
 CC administering a CCR4 modulating agent. It has been found that systemic
 CC T cells such as express high levels of CCR4. Ligands of CCR4 such as
 CC TARC (thymus and activation-regulated chemokine) and MDC (monokine
 CC derived chemokine) act as an adhesion trigger and, upon CCR4 binding,
 CC these cells undergo integrin dependent arrest to the appropriate
 CC vascular receptors. This arrest acts to localize the cells at the
 CC target site. The method modulates this triggering and CCR4 mediated
 CC chemotaxis to affect the localization of T cells in targeted tissues.
 CC The active agent may be a CCR4 agonist that acts to enhance T cell
 CC localization. Alternatively, it may be an antagonist that blocks CCR4
 CC biological activity. A CCR4 antagonist may be administered for the
 CC treatment of inflammation. The present sequence represents a human CCR4.

XX SQ Sequence 360 AA;

Query Match 86.0%; Score 49; DB 21; Length 360;
 Best Local Similarity 81.8%; Pred. No. 0.047; Indels 0; Gaps 0;
 Matches 9; Conservative 1; Mismatches 1;

QY 1 YKARSMTDIV 11
 ||: |||||

Db 67 ykrlrsmtdiv 77

RESULT 5
 B41786
 ID B41786 standard; Protein; 159 AA.

AC B41786;

XX DT 08-FEB-2001 (first entry)

XX DE Human ORFX ORF1550 polypeptide sequence SEQ ID NO:3100.

XX KW Human; open reading frame; ORFX; detection; cytotostatic; hepatotropic;
 KW vulnary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective;
 KW anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;
 KW immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
 KW hypotensive; dermatological; immunosuppressive; antinflammatory;
 KW antiviral; antibacterial; antifungal; cancer; proliferative disorder; hypertensive;
 KW antianaemic; gene therapy; cancer; proliferative disorder; hypertensive;
 KW neurodegenerative disorder; osteoarthritis; graft vs host disease;
 KW cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
 KW cholesterol ester storage; systemic lupus erythematosus; infection;
 KW severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
 KW allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
 KW bone damage; cartilage damage; antinflammatory disease; coagulation;
 KW thrombosis; contraceptive.

XX OS Homo sapiens.

XX PN WO200058473-A2.

XX PD 05-OCT-2000.

XX PF 31-MAR-2000; 2000WO-US08621.

XX PR 31-MAR-1999; 99US-0127607.

XX PR 02-APR-1999; 99US-0127636.

XX PR 05-APR-1999; 99US-0127728.

XX PR 30-MAR-2000; 2000US-0540763.

XX PA (CURA-) CURAGEN CORP.

XX PI Shimkets RA, Leach M;

XX DR WPI; 2000-602362/57.

XX DR N-PSDB; C75995.

XX PT Novel nucleic acids and peptides derived from open reading frame X,
 PT useful for treating e.g. cancers, proliferative disorders,
 PT neurodegenerative disorders and cardiovascular disease -

XX PS Claim 11; Page 2318-2319; 5507pp; English.

XX CC C74446 to C77606 encode the proteins given in B40237 to B43397, which
 CC represent the human ORFX open reading frames 1 to 3161. The ORFX
 CC sequences have activities such as: cytotostatic; hepatotropic; vulnary;
 CC antipsoriatic; antiparkinsonian; nootropic; neuroprotective; osteopathic;
 CC anticonvulsant; antiarthritic; immunosuppressant; immunostimulant;
 CC cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive;
 CC dermatological; immunosuppressive; antinflammatory; antibacterial;
 CC antiviral; antifungal; antirheumatic; antithyroid; and antianaemic. The
 CC sequences can be used for determining the presence of or predisposition
 CC to, or preventing or treating pathological conditions associated with an
 CC ORFX-associated disorder. The nucleic acids can be used to express ORFX
 CC proteins in gene therapy vectors. The proteins and nucleic acids may be
 CC used to treat cancers, proliferative disorders, neurodegenerative
 CC disorders, osteoarthritis, graft vs host disease, cardiovascular disease,
 CC diabetes mellitus, hypertension, hypothyroidism, cholesterol ester
 CC storage, systemic lupus erythematosus, severe combined immunodeficiency
 CC (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune
 CC disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and
 CC cartilage damage, nocturnal haemoglobinuria, antinflammatory disease; to
 CC enhance coagulation; to inhibit thrombosis; and as a contraceptive.

XX SQ Sequence 159 AA;

Query Match 75.4%; Score 43; DB 21; Length 159;
 Best Local Similarity 72.7%; Pred. No. 0.31;

Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YKARSMTDVI 11
||| |:
Db 10 ykkqrkttdvy 20

RESULT 6
Y57292
ID Y57292 standard; Protein; 246 AA.
AC Y57292;
XX
XX
DT 05-JUN-2000 (first entry)
XX
DE Human BGCKr protein fragment (residues 58-303).
XX
KW BGCKr protein; G-protein coupled receptor; human; chemokine; exocytosis;
KW cell proliferation; anti-inflammatory; anti-angiogenic; antitumor; HIV;
KW anti-allergic; antiviral.
XX
XX Homo sapiens.
XX
XX WO9952945-A2.
XX
XX 21-OCT-1999.
XX
XX 16-APR-1999; 99WO-US08395.
XX
XX 16-APR-1998; 98US-0061753.
XX
XX 16-APR-1999; 99US-0061753.
XX
XX (MILL-) MILLENIUM PHARM INC.
XX
XX Gonzalo JA, Gutierrez-Ramos JC;
XX
XX WPI; 1999-620375/53.
XX
XX New nucleic acid encoding human BGCKr receptor, used e.g. for
XX modulating inflammation and tumor growth
XX
XX Disclosure; Fig 10; 123pp; English.
XX
XX The invention relates to a human BGCKr protein, a G-protein coupled
XX receptor. The BGCKr protein can be expressed by standard recombinant
XX methodology. BGCKr are receptor proteins possibly involved in modulation
XX of proinflammatory or stimulatory functions of chemokines; cell
XX proliferation, migration, adhesion and targeting, and exocytosis. The
XX BGCKr nucleic acids and derived proteins (or their variants), antibodies
XX and modulators are potentially useful for modulating inflammation;
XX chemoattractant activity of leucocytes; angiogenesis; cell proliferation;
XX tumour growth; allergic reactions and entry of human immune deficiency
XX virus into cells, for therapeutic or prophylactic purposes. They are also
XX used for diagnosis and in drug-screening assays. The present sequence
XX represents a human BGCKr protein fragment.

QY 1 YKARSMTDVI 11
||| |:
Db 12 ykkqrkttdvy 22

RESULT 7
Y57289
ID Y57289 standard; Protein; 333 AA.
XX
XX
AC Y57289;

XX
DT 05-JUN-2000 (first entry)
XX
DE Human BGCKr partial amino acid sequence.
XX
KW BGCKr protein; G-protein coupled receptor; human; chemokine; exocytosis;
KW cell proliferation; anti-inflammatory; anti-angiogenic; antitumor; HIV;
KW anti-allergic; antiviral.
XX
XX Homo sapiens.
XX
XX WO9952945-A2.
XX
XX 21-OCT-1999.
XX
XX 16-APR-1999; 99WO-US08395.
XX
XX 16-APR-1998; 98US-0061753.
XX
XX 16-APR-1999; 99US-0061753.
XX
XX (MILL-) MILLENIUM PHARM INC.
XX
XX Gonzalo JA, Gutierrez-Ramos JC;
XX
XX WPI; 1999-620375/53.
XX
XX N-PSDB; 290527.
XX
XX New nucleic acid encoding human BGCKr receptor, used e.g. for
XX modulating inflammation and tumor growth
XX
XX Claim 1; Fig 1A-B; 123pp; English.
XX
XX The invention relates to a human BGCKr protein, a G-protein coupled
XX receptor. The BGCKr protein can be expressed by standard recombinant
XX methodology. BGCKr are receptor proteins possibly involved in modulation
XX of proinflammatory or stimulatory functions of chemokines; cell
XX proliferation, migration, adhesion and targeting, and exocytosis. The
XX BGCKr nucleic acids and derived proteins (or their variants), antibodies
XX and modulators are potentially useful for modulating inflammation;
XX chemoattractant activity of leucocytes; angiogenesis; cell proliferation;
XX tumour growth; allergic reactions and entry of human immune deficiency
XX virus into cells, for therapeutic or prophylactic purposes. They are also
XX used for diagnosis and in drug-screening assays. The present sequence
XX represents the sequence of a partial human BGCKr protein.

QY 1 YKARSMTDVI 11
||| |:
Db 52 ykkqrkttdvy 62

Query Match 75.4%; Score 43; DB 20; Length 333;
Best Local Similarity 72.7%; Pred. No. 0.73;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YKARSMTDVI 11
||| |:
Db 52 ykkqrkttdvy 62

RESULT 8
W93170
ID W93170 standard; Protein; 349 AA.
XX
XX W93170;
XX
XX 24-MAY-1999 (first entry)
XX
XX Human HFIAO41 protein.
XX
XX HFIAO41; G-coupled receptor; disease susceptibility; diagnosis; immunise;
KW treatment; FIAO41 protein; gene therapy; immune response; vaccine; HIV-2;
KW inoculate; bacterial; fungal; protozoan; viral; infection; HIV-1; cancer;
KW diabetes; anorexia; bulimia; Parkinson's disease; acute heart failure;
KW hypotension; hypertension; urinary retention; osteoporosis; allergy;
KW angina pectoris; myocardial infarction; ulcer; asthma; schizophrenia;

benign prostatic hypertrophy; psychotic disorder; neurological disorder;
anxiety; manic depression; delirium; dementia; severe mental retardation;
dyskinesia; Huntington's disease; Gilles de la Tourette's syndrome;
linkage analysis; gene mapping; human; ss.

Homo sapiens.
EP899332-A2.
03-MAR-1999.
17-FEB-1998; 98EP-0301170.
27-OCT-1997; 97US-0962922.
15-AUG-1997; 97US-0055895.
(SMK) SMITHKLINE BEECHAM CORP.
Ellis CE;
WPI: 1999-144803/13.
N-PSDB; X22558.
New G-coupled receptor (HFIA041) polypeptide and polynucleotide -
useful as diagnostic reagents and for prevention and treatment of
cancer, HIV infections and Parkinson's disease
Disclosure; Page 25-26; 27pp; English.
This sequence encodes a G-coupled receptor, HFIA041 which is useful for
diagnosing susceptibility to diseases by detecting mutations in the
HFIA041 gene, and can diagnose diseases associated with HFIA041 protein
imbalance by determining HFIA041 polypeptide expression levels. Agonists
and antagonists of the protein can be used in treatment to activate
(agonist) or inhibit (antagonist) HFIA041 activity, in addition to direct
administration of antisense sequences to prevent expression, or HFIA041
polynucleotides to treat conditions associated with a lack of HFIA041
protein. Gene therapy may also be used to affect endogenous HFIA041
polypeptide expression. HFIA041 antibodies are useful for inducing an
immune response to immunise and prevent disease, and for isolating
HFIA041 clones or purifying the polypeptides by affinity chromatography.
HFIA041 polypeptides can be administered directly or as a vaccine to
inoculate against disease. Diseases diagnosed, prevented and treated
include bacterial, fungal, protozoan and viral infections, particularly
HIV-1 or -2 infections; cancer; diabetes; anorexia; bulimia; Parkinson's
disease; acute heart failure; hypotension; hypertension; urinary
retention; osteoporosis; angina pectoris; myocardial infarction; ulcers;
asthma; allergies; benign prostatic hypertrophy; and psychotic and
neurological disorders, including anxiety, schizophrania, manic
depression, delirium, dementia, severe mental retardation and dyskinesias
such as Huntington's disease or Gilles de la Tourette's syndrome. The
HFIA041 polypeptide is also useful for mapping the gene to a chromosome,
allowing gene inheritance to be studied through linkage analysis.

Sequence 349 AA;

Query Match 75.4%; Score 43; DB 20; Length 349;
Best Local Similarity 72.7%; Pred. No. 0.77;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YKKARSMTDVY 11
||| | : ||||
Db 68 ykkqrkttdvy 78

RESULT 9
Y57290
ID Y57290 standard; Protein; 350 AA.
AC Y57290;
XX
XX 05-JUN-2000 (first entry)

Human BGCKr protein.

BGCKr protein; G-protein coupled receptor; human; chemokine; exocytosis;
cell proliferation; anti-inflammatory; anti-angiogenic; antitumor; HIV;
anti-allergic; antiviral.

Homo sapiens.

WO9952945-A2.

21-OCT-1999.

16-APR-1999; 99WO-US08395.

16-APR-1998; 98US-0061753.

16-APR-1999; 99US-0061753.

(MILL-) MILLENIUM PHARM INC.

Gonzalo JA, Gutierrez-Ramos JC;

WPI; 1999-620375/53.

N-PSDB; Z90528.

New nucleic acid encoding human BGCKr receptor, used e.g. for
modulating inflammation and tumor growth

Claim 8; Fig 2A-B; 123pp; English.

The invention relates to a human BGCKr protein, a G-protein coupled
receptor. The BGCKr protein can be expressed by standard recombinant
methodology. BGCKr are receptor proteins possibly involved in modulation
of proinflammatory or stimulatory functions of chemokines; cell
proliferation, migration, adhesion and targeting, and exocytosis. The
BGCKr nucleic acids and derived proteins (or their variants), antibodies
and modulators are potentially useful for modulating inflammation;
chemotactant activity of leucocytes; angiogenesis; cell proliferation;
tumor growth; allergic reactions and entry of human immune deficiency
virus into cells, for therapeutic or prophylactic purposes. They are also
used for diagnosis and in drug-screening assays. The present sequence
represents the full-length human BGCKr protein.

Sequence 350 AA;

Query Match 75.4%; Score 43; DB 20; Length 350;
Best Local Similarity 72.7%; Pred. No. 0.77;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YKKARSMTDVY 11
||| | : ||||
Db 69 ykkqrkttdvy 79

RESULT 10
Y57291
ID Y57291 standard; Protein; 350 AA.
XX
AC Y57291;

XX 05-JUN-2000 (first entry)
XX Mouse BGCKr protein.
XX BGCKr protein; G-protein coupled receptor; human; chemokine; exocytosis;
cell proliferation; anti-inflammatory; anti-angiogenic; antitumor; HIV;
anti-allergic; antiviral.

OS Mus sp.
XX
XX
FH Key Location/Qualifiers
FT Misc-difference 170

/note= "encoded by ATN"

FT XX
 PN XX W09952945-A2.
 XX XX
 XX XX 21-OCT-1999.
 PD XX
 XX XX
 XX XX 16-APR-1999; 99WO-US08395.
 PF XX
 XX XX 16-APR-1998; 98US-0061753.
 PR XX
 XX XX 16-APR-1999; 99US-0061753.
 XX XX
 XX XX (MILL-) MILLENIUM PHARM INC.
 XX XX
 XX XX Gonzalo JA, Gutierrez-Ramos JC;
 PI XX
 XX XX WPI: 1999-620375/53.
 DR XX
 DR XX N-PSDB; 290529.
 XX XX

PT New nucleic acid encoding human BGCKr receptor, used e.g. for
 PT modulating inflammation and tumor growth
 XX
 XX Disclosure; Fig 3; 123pp; English.

CC The invention relates to a human BGCKr protein, a G-protein coupled
 CC receptor. The BGCKr protein can be expressed by standard recombinant
 CC methodology. BGCKr are receptor proteins possibly involved in modulation
 CC of proinflammatory or stimulatory functions of chemokines; cell
 CC proliferation, migration, adhesion and targeting, and exocytosis. The
 CC BGCKr nucleic acids and derived proteins (or their variants), antibodies
 CC and modulators are potentially useful for modulating inflammation;
 CC chemoattractant activity of leucocytes; angiogenesis; cell proliferation;
 CC tumour growth; allergic reactions and entry of human immune deficiency
 CC virus into cells, for therapeutic or prophylactic purposes. They are also
 CC used for diagnosis and in drug-screening assays. The present sequence
 CC represents the mouse BGCKr protein.

XX Sequence 350 AA;

Query Match 75.4%; Score 43; DB 20; Length 350;
 Best Local Similarity 72.7%; Pred. No. 0.77;
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 YKARSMTDYY 11
 III I: IIII
 Db 69 ykkqrkttdy 79

RESULT 11
 Y30125
 ID Y30125 standard; Protein; 350 AA.

AC AC Y30125;

XX 14-OCT-1999 (first entry)

XX A human seven-pass transmembrane receptor protein.

XX Seven-pass transmembrane receptor; autoimmune disease;
 KW white blood cell dysfunction.

XX Homo sapiens.

XX W09933876-A1.

XX 08-JUL-1999.

XX 24-DEC-1998; 98WO-JP05886.

XX 24-DEC-1997; 97JP-0354537.

XX (ASAH) ASAH KOGYO KK.

XX

PI Ishimaru H, Koshio T, Ohno T;
 XX
 DR WPI: 1999-493806/41.
 DR N-PSDB; X86674.

XX New seven-pass transmembrane receptor protein useful for treating,
 PT preventing or diagnosing autoimmune diseases

XX Claim 1; Page 101-103; 118pp; Japanese.

XX The present sequence represents a seven-pass transmembrane receptor
 CC protein. The protein and its DNA can be used to screen substances
 CC for the diagnosis, prevention and treatment of autoimmune diseases,
 CC particularly those due to white blood cell dysfunction.

XX Sequence 350 AA;

Query Match 75.4%; Score 43; DB 20; Length 350;
 Best Local Similarity 72.7%; Pred. No. 0.77;
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 YKARSMTDYY 11
 III I: IIII
 Db 69 ykkqrkttdy 79

RESULT 12

Y17435
 ID Y17435 standard; Protein; 350 AA.

XX AC Y17435;

XX 29-JUL-1999 (first entry)

XX Human signal peptide-containing protein SP-16.

XX Human; signal peptide-containing protein; SP; cell proliferation;
 KW cancer; neuronal disorder; immune response; detection.

XX Homo sapiens.

XX W09924463-A2.

XX 20-MAY-1999.

XX 04-NOV-1998; 98WO-US23578.

XX 07-NOV-1997; 97US-0966316.

XX (INCY-) INCYTE PHARM INC.

XX Au-Young J, Lal P, Mathur P, Murry LE, Reddy R;

XX WPI: 1999-337694/28.

XX N-PSDB; X61288.

XX cDNA clones encoding signal peptide-containing proteins

XX Claim 1; Fig 1; 83pp; English.

XX The present sequence represents a human signal peptide-containing
 CC protein (SP), designated SP-16. SP proteins can be used to stimulate
 CC cell proliferation or to treat or prevent cancer. SP antagonists are
 CC also used to treat or prevent cancer, and also for treating or
 CC preventing neuronal disorders or immune responses. Polynucleotide
 CC sequences complementary to the SP-encoding polynucleotides are useful
 CC for the detection of SP-encoding nucleic acid molecules in biological
 CC samples.

XX Sequence 350 AA;

XX

Query Match 75.4%; Score 43; DB 20; Length 350;
 Best Local Similarity 72.7%; Pred. NO. 0.77;
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YKARSMTDVI 11
 III I: IIII
 Db 69 ykkqtktdvy 79

RESULT 13

W93169
 ID W93169 standard; Protein; 350 AA.

XX AC W93169;

XX DT 24-MAY-1999 (first entry)

XX DE Human HFIAO41 protein.

XX HFIAO41; G-coupled receptor; disease susceptibility; diagnosis; immunise;
 KW treatment; FIAO41 protein; gene therapy; immune response; vaccine; HIV-2;
 KW inoculates; bacterial; fungal; protozoan; viral; infection; HIV-1; cancer;
 KW diabetes; anorexia; bulimia; Parkinson's disease; acute heart failure;
 KW hypotension; hypertension; urinary retention; osteoporosis; allergy;
 KW angina pectoris; myocardial infarction; ulcer; asthma; schizophrenia;
 KW benign prostatic hypertrophy; psychotic disorder; neurological disorder;
 KW anxiety; manic depression; delirium; dementia; severe mental retardation;
 KW dyskinesia; Huntington's disease; Gilles de la Tourette's syndrome;
 KW linkage analysis; gene mapping; human.

XX OS Homo sapiens.

XX PN EP899332-A2.

XX PD 03-MAR-1999.

XX PF 17-FEB-1998; 98EP-0301170.

XX PR 27-OCT-1997; 97US-0962922.

XX PR 15-AUG-1997; 97US-0055895.

XX PA (SMIK) SMITHKLINE BEECHAM CORP.

XX PI Ellis CE;

XX PR WPI; 1999-144803/13.

XX DR N-PSDB; X22557.

XX PT New G-coupled receptor (HFIAO41) polypeptide and polynucleotide -
 PT useful as diagnostic reagents and for prevention and treatment of
 PT cancer, HIV infections and Parkinson's disease

XX PS Claim 1; Page 22-23; 27pp; English.

XX This sequence represents a G-coupled receptor, HFIAO41 which is useful
 CC for diagnosing susceptibility to diseases by detecting mutations in the
 CC HFIAO41 gene, and can diagnose diseases associated with HFIAO41 protein
 CC imbalance by determining HFIAO41 polypeptide expression levels. Agonists
 CC and antagonists of the protein can be used in treatment to activate
 CC (agonist) or inhibit (antagonist) HFIAO41 activity. In addition to direct
 CC administration of antisense sequences to prevent expression, or HFIAO41
 CC polynucleotides to treat conditions associated with a lack of FIAO41
 CC protein. Gene therapy may also be used to affect endogenous HFIAO41
 CC polypeptide expression. HFIAO41 antibodies are useful for inducing an
 CC immune response to immunise and prevent disease, and for isolating
 CC HFIAO41 clones or purifying the polypeptides by affinity chromatography.
 CC HFIAO41 polypeptides can be administered directly or as a vaccine to
 CC inoculate against disease. Diseases diagnosed, prevented and treated
 CC include bacterial, fungal, protozoan and viral infections, particularly
 CC HIV-1 or -2 infections; cancer; diabetes; anorexia; bulimia; Parkinson's
 CC disease; acute heart failure; hypotension; hypertension; urinary
 CC retention; osteoporosis; angina pectoris; myocardial infarction; ulcers;
 CC asthma; allergies; benign prostatic hypertrophy; and psychotic and

CC neurological disorders, including anxiety, schizophrenia, manic
 CC depression, delirium, dementia, severe mental retardation and dyskinesias
 CC such as Huntington's disease or Gilles de la Tourette's syndrome. The
 CC HFIAO41 polypeptide is also useful for mapping the gene to a chromosome,
 CC allowing gene inheritance to be studied through linkage analysis.

XX SQ Sequence 350 AA;

Query Match 75.4%; Score 43; DB 20; Length 350;
 Best Local Similarity 72.7%; Pred. NO. 0.77;
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YKARSMTDVI 11
 III I: IIII
 Db 69 ykkqtktdvy 79

RESULT 14

B37788
 ID B37788 standard; Protein; 350 AA.

XX AC B37788;

XX DT 23-FEB-2001 (first entry)

XX DE Human TSC7.

XX KW Human; TSC; tuberous sclerosis complex; cytostatic; antimicrobial;
 KW osteopathic; antiulcer; antiasthmatic; antiallergic; neuroprotective;
 KW cardiant; hypotensive; hypertensive; nootropic; anticonvulsant;
 KW analgesic; tranquiliser; immunosuppressive; antiinflammatory;
 KW gene therapy; TSC7; infection; cancer; autoimmune disorder;
 KW Parkinson's disease; osteoporosis; neurological disorder.

XX OS Homo sapiens.

XX PN WO2000064941-A2.

XX PD 02-NOV-2000.

XX PF 21-APR-2000; 2000WO-US10979.

XX PR 23-APR-1999; 99US-0130817.

XX PR 20-APR-2000; 2000US-0556002.

XX PA (CURA-) CURAGEN CORP.

XX PI Gould-Rothberg BE;

XX DR WPI; 2000-679670/66.

XX DR N-PSDB; C68722.

XX PT Novel nucleic acid encoding G-protein coupled receptor for diagnosis
 PT and treatment of conditions associated with disorder in a G-protein
 PT mediated pathway such as cancer, neurological disorders and infections

XX PS Claim 12; Page 8; 132pp; English.

XX The present sequence is human tuberous sclerosis complex 7 (TSC7).
 CC TSC7 polynucleotides and polypeptides are useful for determining the
 CC presence or predisposition to a disease associated with altered levels of
 CC TSC7. TSC7 polynucleotides, polypeptides and antibodies specific for the
 CC polypeptide are useful for treating or preventing pathological conditions
 CC associated with the disorder in a G-protein mediated pathway. They are
 CC useful for diagnosing a hyperproliferative condition such as a neoplasm
 CC or dermatological condition. TSC7 nucleic acids and polypeptides are
 CC useful in the treatment of microbial infections, pain, cancer, anorexia,
 CC asthma, autoimmune disorders, Parkinson's disease, acute heart failure,
 CC hypo/hypertension, osteoporosis, multiple sclerosis, angina pectoris,
 CC myocardial infarction, ulcers, allergies, benign prostatic hypertrophy
 CC and psychotic and neurological disorders, including schizophrenia.

CC dementia, severe mental retardation and dyskinesias, such as
 CC Huntington's disease and/or other pathologies and disorders. TSC7
 CC polypeptides are also useful as immunogens to produce antibodies and as
 CC vaccines.

XX Sequence 350 AA;

Query Match 75.4%; Score 43; DB 21; Length 350;

Best Local Similarity 72.7%; Pred. No. 0.77; Mismatches 2; Indels 0; Gaps 0;

Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YKARSMTDVY 11

Db 69 ykkqrktkdv 79

RESULT 15

Y71301

ID Y71301 standard; Protein; 350 AA.

XX AC Y71301;

XX DT 02-NOV-2000 (first entry)

XX DE Human orphan G protein-coupled receptor hppr1.

XX KW Human; orphan G protein-coupled receptor; GPCR; hppr1; drug screening;

XX KM transmembrane receptor; expressed sequence tag; EST; signal cascade.

XX OS Homo sapiens.

XX PN WO200031258-A2.

XX PD 02-JUN-2000.

XX PF 13-OCT-1999; 99WO-US23687.

XX PR 20-NOV-1998; 98US-0109213.

XX PR 16-FEB-1999; 99US-0120416.

XX PR 26-FEB-1999; 99US-0121852.

XX PR 12-MAR-1999; 99US-0123946.

XX PR 12-MAR-1999; 99US-0123949.

XX PR 28-MAY-1999; 99US-0136436.

XX PR 28-MAY-1999; 99US-0136437.

XX PR 28-MAY-1999; 99US-0136439.

XX PR 28-MAY-1999; 99US-0136567.

XX PR 28-MAY-1999; 99US-0137127.

XX PR 28-MAY-1999; 99US-0137131.

XX PR 29-JUN-1999; 99US-0141448.

XX PR 29-SEP-1999; 99US-0156555.

XX PR 29-SEP-1999; 99US-0156633.

XX PR 29-SEP-1999; 99US-0156634.

XX PR 29-SEP-1999; 99US-0156653.

XX PR 01-OCT-1999; 99US-0157280.

XX PR 01-OCT-1999; 99US-0157281.

XX PR 01-OCT-1999; 99US-0157282.

XX PR 01-OCT-1999; 99US-0157293.

XX PR 01-OCT-1999; 99US-0157294.

XX PR 12-OCT-1999; 99US-0416760.

XX PR 12-OCT-1999; 99US-0417044.

XX PA (AREN-) ARENA PHARM INC.

XX PI Chen R, Dang HT, Liaw CW, Lin I;

XX DR WPI; 2000-400068/34.

XX DR N-PSDB; D01128.

XX PT Novel human orphan G protein-coupled receptors and the encoding cDNAs

XX PT for use in the identification of G protein-coupled receptor agonists -

XX PS Claim 42; Page 69-70; 102pp; English.

XX

CC The present amino acid sequence is the hppr1, an endogenous human
 CC orphan G protein-coupled receptor (GPCR), expressed in the pituitary
 CC gland, heart, salivary gland, small intestine and testis. The hppr1 cDNA
 CC was identified using EST (expressed sequence tag) AA359504 and 238667 as
 CC a probe. The orphan GPCR of the invention, like all GPCRs has seven
 CC transmembrane alpha helices with an extracellular N-terminus and an
 CC intracellular C-terminus. However, no endogenous ligands has yet been
 CC identified for the proteins of the invention. The orphan GPCRs may be
 CC used in the identification of their endogenous ligands, and to screen
 CC potential GPCR agonists and antagonists for use as pharmaceutical agents.
 CC The proteins may also be used in the study of GPCR-mediated signalling
 CC cascades, and to elucidate their precise role in normal and diseased
 CC human conditions. Nucleic acid encoding human orphan GPCRs may be used
 CC for tissue localisation expression analysis to provide information about
 CC their function in healthy and pathological states.

XX SQ Sequence 350 AA;

Query Match 75.4%; Score 43; DB 21; Length 350;

Best Local Similarity 72.7%; Pred. No. 0.77; Mismatches 2; Indels 0; Gaps 0;

Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YKARSMTDVY 11

Db 69 ykkqrktkdv 79

Search completed: May 23, 2001, 15:28:27

Job time: 404 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 23, 2001, 15:30:05 ; Search time 95.91 Seconds
(without alignments)
2.203 Million cell updates/sec

Title: US-08-887-977-10_COPY_65_75

Perfect score: 57

Sequence: 1 YRKARSMWDVY 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 185757 seqs, 19210857 residues

Total number of hits satisfying chosen parameters: 185757

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued_Patents_AA.*
- 1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
 - 2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
 - 3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
 - 4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
 - 5: /cgn2_6/ptodata/2/iaa/PT05_COMB.pep.*
 - 6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	49	86.0	360	4	US-08-875-573-20
2	43	75.4	350	2	US-08-966-316-16
3	43	75.4	350	2	US-08-966-316-18
4	41	71.9	355	1	US-08-461-244-2
5	39	68.4	337	1	US-08-153-848-46
6	39	68.4	337	3	US-09-299-843A-46
7	39	68.4	337	5	PCT-US93-11153-46
8	39	68.4	352	1	US-08-202-056-3
9	39	68.4	352	1	US-08-076-093A-4
10	39	68.4	352	1	US-08-450-393A-6
11	39	68.4	352	1	US-08-701-265-4
12	39	68.4	352	2	US-08-284-586-4
13	39	68.4	352	2	US-08-805-478-4
14	39	68.4	352	2	US-08-802-627A-4
15	39	68.4	352	2	US-08-801-238-4
16	39	68.4	352	2	US-08-801-228-4
17	39	68.4	352	3	US-09-104-296-4
18	39	68.4	352	4	US-08-446-669-6
19	39	68.4	352	5	PCT-US95-00476-6
20	38	66.7	87	4	US-09-087-232A-18
21	38	66.7	100	4	US-09-087-232A-15
22	38	66.7	215	4	US-09-087-232A-17
23	38	66.7	352	4	US-09-087-232A-13
24	38	66.7	727	1	US-08-424-424B-2
25	38	66.7	727	5	PCT-US94-05363A-2
26	37	64.9	355	1	US-08-153-848-28
27	37	64.9	355	1	US-08-153-848-32

28	37	64.9	355	3	US-09-299-843A-28	Sequence 28, Appl
29	37	64.9	355	3	US-09-299-843A-32	Sequence 32, Appl
30	37	64.9	355	5	PCT-US93-11153-28	Sequence 28, Appl
31	37	64.9	355	5	PCT-US93-11153-32	Sequence 32, Appl
32	36	63.2	355	1	US-08-012-988A-2	Sequence 2, Appl
33	36	63.2	355	1	US-08-450-393A-5	Sequence 5, Appl
34	36	63.2	355	4	US-08-446-669-5	Sequence 5, Appl
35	36	63.2	355	5	PCT-US95-00476-5	Sequence 5, Appl
36	35	61.4	40	1	US-08-383-751A-3	Sequence 3, Appl
37	35	61.4	342	2	US-08-742-011-2	Sequence 2, Appl
38	35	61.4	358	1	US-08-153-848-19	Sequence 19, Appl
39	35	61.4	358	3	US-09-299-843A-19	Sequence 19, Appl
40	35	61.4	358	5	PCT-US93-11153-19	Sequence 19, Appl
41	35	61.4	359	1	US-08-153-848-24	Sequence 24, Appl
42	35	61.4	359	3	US-09-299-843A-24	Sequence 24, Appl
43	35	61.4	359	5	PCT-US93-11153-24	Sequence 24, Appl
44	35	61.4	361	2	US-08-902-294-2	Sequence 2, Appl
45	35	61.4	361	3	US-09-178-637-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-08-875-573-20
; Sequence 20, Application US/08875573
; Patent No. 6150132
; GENERAL INFORMATION:
; APPLICANT: Wells, Timothy N.C.
; APPLICANT: Power, Christine A.
; TITLE OF INVENTION: A CHEMOKINE RECEPTOR ABLE TO BIND TO
; TITLE OF INVENTION: MCP-1, MIP-1 ALPHA AND/OR RANTES. ITS USES
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 No. 6150132th Glebe Rd. 8th floor
; CITY: Arlington
; STATE: VA
; COUNTRY: USA
; ZIP: 22201-4741
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,573
; FILING DATE: 31-OCT-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB96/00143
; FILING DATE: 24-JAN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9501683.8
; FILING DATE: 27-JAN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilson, Mary J.
; REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 1430-172
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4000
; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 360 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-875-573-20

Query Match 86.0%; Score 49; DB 4; Length 360;
Best Local Similarity 81.8%; Pred. No. 0.056;

Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YKARSMTDVI 11
||: |||||
Db 67 YKRLRSMTDVI 77

RESULT 2

US-08-966-316-16
; Sequence 16, Application US/08966316
; Patent No. 5932445

GENERAL INFORMATION:

; APPLICANT: Lal, Preeti
; APPLICANT: Au-Young, Janice
; APPLICANT: Reddy, Roopa
; APPLICANT: Murty, Lynn E.
; APPLICANT: Mathur, Preete
; TITLE OF INVENTION: SIGNAL PEPTIDE - CONTAINING PROTEINS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304

COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/966,316
; FILING DATE: Herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER:
; FILING DATE:

ATTORNEY/AGENT INFORMATION:

; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0424 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:

INFORMATION FOR SEQ ID NO: 16:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 350 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

IMMEDIATE SOURCE:

; LIBRARY: UTRSN011
; CLONE: 2547002
US-08-966-316-16

Query Match 75.4%; Score 43; DB 2; Length 350;

Best Local Similarity 72.7%; Pred. No. 0.75;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YKARSMTDVI 11
||: |||||
Db 69 YKQRTKTDVI 79

RESULT 3

US-08-966-316-18
; Sequence 18, Application US/08966316
; Patent No. 5932445

GENERAL INFORMATION:

; APPLICANT: Lal, Preeti

; APPLICANT: Au-Young, Janice
; APPLICANT: Reddy, Roopa
; APPLICANT: Murty, Lynn E.
; APPLICANT: Mathur, Preete
; TITLE OF INVENTION: SIGNAL PEPTIDE - CONTAINING PROTEINS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304

COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/966,316
; FILING DATE: Herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER:
; FILING DATE:

ATTORNEY/AGENT INFORMATION:

; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0424 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:

INFORMATION FOR SEQ ID NO: 18:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 350 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

IMMEDIATE SOURCE:

; LIBRARY: GenBank
; CLONE: 399711
US-08-966-316-18

Query Match 75.4%; Score 43; DB 2; Length 350;

Best Local Similarity 72.7%; Pred. No. 0.75;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YKARSMTDVI 11
||: |||||
Db 69 YKRTKTDVI 79

RESULT 4

US-08-461-244-2
; Sequence 2, Application US/08461244
; Patent No. 5776729

GENERAL INFORMATION:

; APPLICANT: Soppet, Daniel R.
; APPLICANT: Yi, Li
; APPLICANT: Ruben, Steven M.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: HUMAN G-PROTEIN RECEPTOR HGBR32
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07068

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,244
FILING DATE: 05-JUN-1995
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Ferraro, Gregory D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-445
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-461-244-2

Query Match 71.9%; Score 41; DB 1; Length 355;
Best Local Similarity 80.0%; Pred. No. 1.8;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 KKRSMTDXY 11
Db 64 KKLRSITDXY 73

RESULT 5
US-08-153-848-46
Sequence 46, Application US/08153848
Patent No. 5759804
GENERAL INFORMATION:
APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schweikart, Vicki L.
TITLE OF INVENTION: No. 5759804el Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Bicknell
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/153,848
FILING DATE: 17-NOV-1992
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 5759804and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31794
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 46:

SEQUENCE CHARACTERISTICS:
LENGTH: 337 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-153-848-46

Query Match 68.4%; Score 39; DB 1; Length 337;
Best Local Similarity 80.0%; Pred. No. 4.2;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 KKRSMTDXY 11
Db 52 KKLRSMTDKY 61

RESULT 6
US-09-299-843A-46
Sequence 46, Application US/09299843A
Patent No. 6107475
GENERAL INFORMATION:
APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schweikart, Vicki L.
TITLE OF INVENTION: No. 6107475el Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/299,843A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/088,337
FILING DATE: 01-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/153,848
FILING DATE: 17-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Jill E. Uhl
REGISTRATION NUMBER: 43,213
REFERENCE/DOCKET NUMBER: 27866/32059B
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX:
INFORMATION FOR SEQ ID NO: 46:

SEQUENCE CHARACTERISTICS:
LENGTH: 337 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-299-843A-46

Query Match 68.4%; Score 39; DB 3; Length 337;
Best Local Similarity 80.0%; Pred. No. 4.2;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 KKARSMTDVY 11
 II IIIII I
 Db 52 KKLRSMTDKY 61

RESULT 7

PCT-US93-11153-46
 ; Sequence 46, Application PC/TUS9311153
 ; GENERAL INFORMATION:
 ; APPLICANT: Godiska, Ronald
 ; APPLICANT: Gray, Patrick W.
 ; APPLICANT: Schwellkart, Vicki L.
 ; TITLE OF INVENTION: Novel Seven Transmembrane Receptors
 ; NUMBER OF SEQUENCES: 64
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
 ; ADDRESSEE: Bicknell
 ; STREET: 6300 Sears Tower, 233 South Wacker Drive
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: USA
 ; ZIP: 60606
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; FILING DATE: PCT/US93/11153
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/977,452
 ; FILING DATE: 17-NOV-1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Noland, Greta E.
 ; REGISTRATION NUMBER: 35,302
 ; REFERENCE/DOCKET NUMBER: 31794
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (312) 474-6300
 ; TELEFAX: (312) 474-0448
 ; TELEX: 25-3856
 ; INFORMATION FOR SEQ ID NO: 46:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 337 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 PCT-US93-11153-46

Query Match 68.4%; Score 39; DB 5; Length 337;
 Best Local Similarity 80.0%; Pred. No. 4.2;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 KKARSMTDVY 11
 II IIIII I
 Db 52 KKLRSMTDKY 61

RESULT 8

US-08-202-056-3
 ; Sequence 3, Application US/08202056
 ; Patent No. 5440021
 ; GENERAL INFORMATION:
 ; APPLICANT: Chuntharapai, Anan
 ; APPLICANT: Hebert, Caroline
 ; APPLICANT: Kim, Kyung Jin
 ; APPLICANT: Lee, James
 ; TITLE OF INVENTION: Antibodies to Human IL-8 Type B Receptor
 ; NUMBER OF SEQUENCES: 8
 ; CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.
 STREET: 460 Point San Bruno Blvd
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 5.25 inch, 360 kb floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: patin (Genentech)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/202,056
 ; FILING DATE: 25-FEB-1994
 ; CLASSIFICATION: 436
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/677211
 ; FILING DATE: 29-MAR-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Love, Richard B.
 ; REGISTRATION NUMBER: 34,659
 ; REFERENCE/DOCKET NUMBER: 706P3
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415/952-5530
 ; TELEFAX: 415/952-9881
 ; TELEX: 910/371-7168
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 352 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 US-08-202-056-3

Query Match 68.4%; Score 39; DB 1; Length 352;
 Best Local Similarity 80.0%; Pred. No. 4.4;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 KKARSMTDVY 11
 II IIIII I
 Db 67 KKLRSMTDKY 76

RESULT 9

US-08-076-093A-4
 ; Sequence 4, Application US/08076093A
 ; Patent No. 5543503
 ; GENERAL INFORMATION:
 ; APPLICANT: Chuntharapai, Anan
 ; APPLICANT: Lee, James
 ; APPLICANT: Hebert, Caroline
 ; APPLICANT: Jin Kim, K.
 ; TITLE OF INVENTION: Antibodies to Human PF4A Receptors
 ; NUMBER OF SEQUENCES: 6
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genentech, Inc.
 ; STREET: 460 Point San Bruno Blvd
 ; CITY: South San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94080
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: WinPatin (Genentech)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/076,093A
 ; FILING DATE: 11-Jun-1993
 ; CLASSIFICATION: 530
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/810782
 ; FILING DATE: 19-DEC-1991

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/677211
;; FILING DATE: 29-MAR-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Love, Richard B
;; REGISTRATION NUMBER: 34,659
;; REFERENCE/DOCKET NUMBER: 706P2
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 415/225-5530
;; TELEFAX: 415/952-9881
;; TELEX: 910/371-7168
;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 352 amino acids
;; TYPE: Amino Acid
;; TOPOLOGY: Linear
US-08-076-093A-4

Query Match 68.4%; Score 39; DB 1; Length 352;
Best Local Similarity 80.0%; Pred. No. 4.4;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 KKARSMTDVY 11
|| ||||| |
Db 67 KKLRSMTDKY 76

RESULT 10
US-08-450-393A-6
;; Sequence 6, Application US/08450393A
;; Patent No. 5707815
;; GENERAL INFORMATION:
;; APPLICANT: Charo, Israel
;; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
;; TITLE OF INVENTION: PROTEIN RECEPTORS
;; NUMBER OF SEQUENCES: 14
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
;; STREET: 5 Palo Alto Square
;; CITY: Palo Alto
;; STATE: California
;; COUNTRY: USA
;; ZIP: 94306-2155
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/450,393A
;; FILING DATE: May 25, 1995
;; CLASSIFICATION: 424
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Cseir, Luann
;; REGISTRATION NUMBER: 31,822
;; REFERENCE/DOCKET NUMBER: UCAL-237/0205
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 415-843-5165
;; TELEFAX: 415-8857-0663
;; TELEX: 380816COOLEYPA
;; INFORMATION FOR SEQ ID NO: 6:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 352 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; HYPOTHETICAL: NO
US-08-450-393A-6

Query Match 68.4%; Score 39; DB 1; Length 352;

Best Local Similarity 80.0%; Pred. No. 4.4;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2 KKARSMTDVY 11
|| ||||| |
Db 67 KKLRSMTDKY 76

RESULT 11
US-08-701-265-4
;; Sequence 4, Application US/08701265
;; Patent No. 5776457
;; GENERAL INFORMATION:
;; APPLICANT: Chuntharapai, Anan
;; APPLICANT: Lee, James
;; APPLICANT: Hebert, Caroline
;; APPLICANT: Jin Kim, K.
;; TITLE OF INVENTION: Antibodies to Human PF4A Receptors
;; NUMBER OF SEQUENCES: 6
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Genentech, Inc.
;; STREET: 460 Point San Bruno Blvd
;; CITY: South San Francisco
;; STATE: California
;; COUNTRY: USA
;; ZIP: 94080
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: WinPatIn (Genentech)
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/701,265
;; FILING DATE: 22-AUG-1996
;; CLASSIFICATION: 424
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/076093
;; FILING DATE: 11-Jun-1993
;; APPLICATION NUMBER: 07/810782
;; FILING DATE: 19-DEC-1991
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/677211
;; FILING DATE: 29-MAR-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Love, Richard B
;; REGISTRATION NUMBER: 34,659
;; REFERENCE/DOCKET NUMBER: 706P2
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 415/225-5530
;; TELEFAX: 415/952-9881
;; TELEX: 910/371-7168
;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 352 amino acids
;; TYPE: Amino Acid
;; TOPOLOGY: Linear
US-08-701-265-4

Query Match 68.4%; Score 39; DB 1; Length 352;
Best Local Similarity 80.0%; Pred. No. 4.4;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2 KKARSMTDVY 11
|| ||||| |
Db 67 KKLRSMTDKY 76

RESULT 12
US-08-284-586-4
;; Sequence 4, Application US/08284586
;; Patent No. 5840856
;; GENERAL INFORMATION:

APPLICANT: Chuntharapai, Anan
APPLICANT: Lee, James
APPLICANT: Hebert, Caroline
APPLICANT: Jin Kim, K.
TITLE OF INVENTION: Antibodies to Human PF4A Receptors
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/284,586
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/076,093A
FILING DATE: 11-Jun-1993
APPLICATION NUMBER: 07/810782
FILING DATE: 19-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/677211
FILING DATE: 29-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: 706P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-284-586-4

Query Match 68.4%; Score 39; DB 2; Length 352;
Best Local Similarity 80.0%; Pred. No. 4.4;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 KKARSMTDXY 11
||| ||||| |
Db 67 KKLRSMTDXY 76

RESULT 13
US-08-805-478-4
; Sequence 4, Application US/08805478
; Patent No. 5874543
; GENERAL INFORMATION:
; APPLICANT: Chuntharapai, Anan
; APPLICANT: Lee, James
; APPLICANT: Hebert, Caroline
; APPLICANT: Jin Kim, K.
; TITLE OF INVENTION: ANTIBODIES TO PF4A RECEPTOR
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/805,478
FILING DATE: 25-Feb-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/284586
FILING DATE: 10-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/076093
FILING DATE: 11-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/810782
FILING DATE: 19-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P0706P2PIC1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-805-478-4

Query Match 68.4%; Score 39; DB 2; Length 352;
Best Local Similarity 80.0%; Pred. No. 4.4;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 KKARSMTDXY 11
||| ||||| |
Db 67 KKLRSMTDXY 76

RESULT 14
US-08-802-627A-4
; Sequence 4, Application US/08802627A
; Patent No. 5892017
; GENERAL INFORMATION:
; APPLICANT: Lee, James
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: NUCLEIC ACID ENCODING PF4A RECEPTOR
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/802,627A
FILING DATE: 19-Feb-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/284586
FILING DATE: 10-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/076093

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; FILING DATE: 11-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/810782
; FILING DATE: 19-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P0706P2PID2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5530
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-802-627A-4

Query Match 68.4%; Score 39; DB 2; Length 352;
Best Local Similarity 80.0%; Pred. No. 4.4;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 KKARSMTDXY 11
Db 67 KKLRSMTDKY 76

RESULT 15
US-08-801-238-4
; Sequence 4, Application US/08801238
; Patent No. 5919896
; GENERAL INFORMATION:
; APPLICANT: Lee, James
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: PF4A RECEPTOR
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/801,238
; FILING DATE: 19-Feb-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/284586
; FILING DATE: 10-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/076093
; FILING DATE: 11-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/810782
; FILING DATE: 19-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P0706P2PID1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5530
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:

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; LENGTH: 352 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-801-238-4

Query Match 68.4%; Score 39; DB 2; Length 352;
Best Local Similarity 80.0%; Pred. No. 4.4;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 KKARSMTDXY 11
Db 67 KKLRSMTDKY 76

Search completed: May 23, 2001, 15:30:05
Job time: 412 sec

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GenCore version 4.5
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OM protein - protein search, using sw model
Run on: May 23, 2001, 15:31:58 ; Search time 110.15 Seconds
(without alignments)
6.863 Million cell updates/sec

Title: US-08-887-977-10_COPY_65_75
Perfect score: 57
Sequence: 1 YKKARSMTDVY 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 198801 seqs, 68722935 residues
Total number of hits satisfying chosen parameters: 198801

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_67:*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	57	100.0	369	JC5068	G protein-coupled
2	49	86.0	360	A57160	chemokine (C-C) re
3	46	80.7	360	JC4587	chemokine (C-C) re
4	43	75.4	350	JN0621	G protein-coupled
5	41	71.9	355	JC5067	G protein-coupled
6	39	68.4	352	G00048	fusin (LESTRA) - C
7	39	68.4	352	A45747	neuropeptide Y/pep
8	39	68.4	353	S28787	neuropeptide Y/pep
9	38	66.7	352	A43113	chemokine (C-C) re
10	37	64.9	273	F71605	hypothetical prote
11	37	64.9	355	JC4304	orphan G protein-c
12	36	63.2	292	B70385	hypothetical prote
13	36	63.2	354	F58186	probable G protein
14	36	63.2	355	A45177	chemokine (C-C) re
15	36	63.2	719	T47727	hypothetical prote
16	36	63.2	916	S22864	DNA topoisomerase
17	35	61.4	186	H75106	hypothetical prote
18	35	61.4	378	A45680	G protein-coupled
19	35	61.4	378	B55735	lymphocyte-specifi
20	35	61.4	378	A55735	G protein-coupled
21	35	61.4	502	T48560	hypothetical prote
22	35	61.4	510	D70009	probable ABC trans
23	35	61.4	544	S42723	matricin - mouse
24	35	61.4	545	S43082	CCR (chaperonin co
25	35	61.4	953	T46227	hypothetical prote
26	35	61.4	1208	T23222	hypothetical prote
27	35	61.4	2810	T22298	hypothetical prote
28	34	59.6	198	S60923	hypothetical prote
29	34	59.6	306	T05605	hypothetical prote

chemokine (C-C) re
MIP-1 alpha recept
cellular tumor ant
cellular tumor ant
cellular tumor ant
tumor suppressor p
DNA primase (EC 2
neurotransmitter t
Na+/Cl(-)-dependen
hypothetical prote
hypothetical prote
hypothetical prote
lysophospholipase
tungsten formylmet
MIP-1 alpha recept
chemokine (C-C) re

30	34	59.6	355	2	G02436
31	34	59.6	356	2	I49340
32	34	59.6	381	2	S38824
33	34	59.6	390	1	DNMS53
34	34	59.6	391	1	S02192
35	34	59.6	391	2	JC6193
36	34	59.6	409	2	S48352
37	34	59.6	727	2	S27043
38	34	59.6	727	2	I56506
39	34	59.6	1047	2	T21306
40	34	59.6	1805	1	A64224
41	33	57.9	223	2	D75040
42	33	57.9	259	2	D69998
43	33	57.9	306	2	F69129
44	33	57.9	359	2	I49341
45	33	57.9	360	2	JC2443

ALIGNMENTS

RESULT 1
JC5068
G protein-coupled receptor CKR-L3 - human
C:Species: Homo sapiens (man)
C:Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 21-Jul-2000
C:Accession: JC5068
R:Zaballos, A.; Varona, R.; Gutierrez, J.; Lind, P.; Marquez, G.
Biochem. Biophys. Res. Commun. 227, 846-853, 1996
A:Title: Molecular cloning and RNA expression of two new human chemokine receptor-lik
A:Reference number: JC5067; MUID:97040707
A:Accession: JC5068
A:Molecule type: DNA
A:Residues: 1-369 <ZAB>
A:Cross-references: EMBL:Z79784; NID:gl668737; PIDN:CAB02144.1; PID:gl668738
C:Comment: This protein belongs to the family of alpha chemokine receptors.
C:Genetics:
A:Gene: GDB:CMKBR6; STRL22; GPR29; CCR6; CKR-L3; GPR-CY4
A:Cross-references: GDB:5370639; OMIM:601835
A:Map position: 6q27-6q27
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; transmembrane protein
F:42-68/Domain: transmembrane #status predicted <TM1>
F:79-99/Domain: transmembrane #status predicted <TM2>
F:115-136/Domain: transmembrane #status predicted <TM3>
F:160-180/Domain: transmembrane #status predicted <TM4>
F:212-233/Domain: transmembrane #status predicted <TM5>
F:250-271/Domain: transmembrane #status predicted <TM6>
F:292-315/Domain: transmembrane #status predicted <TM7>

Query Match 100.0%; Score 57; DB 2; Length 369;
Best Local Similarity 100.0%; Pred. No. 0.00074;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YKKARSMTDVY 11
| | | | | | | | | |
DB 69 YKKARSMTDVY 79

RESULT 2
A57160
chemokine (C-C) receptor 4 - human
N:Alternate names: C-C CKR-4
C:Species: Homo sapiens (man)
C:Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 21-Jul-2000
C:Accession: A57160
J:Power, C.A.; Meyer, A.; Nemeth, K.; Bacon, K.B.; Hoogewerf, A.J.; Proudfoot, A.E.I.
J. Biol. Chem. 270, 19495-19500, 1995
A:Title: Molecular cloning and functional expression of a novel CC chemokine receptor
A:Reference number: A57160; MUID:95370289
A:Accession: A57160
A>Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA
 A:Residues: 1-360 <POW>
 A:Cross-references: GB:X85740; NID:gl370103; PIDN:CAA59743.1; PID:g971452
 A:Note: source clone K5-5
 C:Genetics:
 A:Gene: GDB:CMKBR4
 A:Cross-references: GDB:677463
 A:Map position: 3p21-3p21
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane protein
 F:40-65/Domain: transmembrane #status predicted <TM1>
 F:76-97/Domain: transmembrane #status predicted <TM2>
 F:112-133/Domain: transmembrane #status predicted <TM3>
 F:151-175/Domain: transmembrane #status predicted <TM4>
 F:208-226/Domain: transmembrane #status predicted <TM5>
 F:243-264/Domain: transmembrane #status predicted <TM6>
 F:291-308/Domain: transmembrane #status predicted <TM7>
 F:29-276.110-187/Disulfide bonds: #status predicted
 F:72.350/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted
 F:145/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
 F:183,194/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted

Query Match 86.0%; Score 49; DB 2; Length 360;
 Best Local Similarity 81.8%; Pred. No. 0.031;
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YKKARSMTDVY 11
 ||: |||||
 Db 67 YKRLRSMTDVY 77

RESULT 3

JC4587
 Chemokine (C-C) receptor 4 - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 08-Mar-1996 #sequence_revision 19-Apr-1996 #text_change 20-Jun-2000
 C:Accession: JC4587
 R:Hoogwerf, A.J.; Black, D.; Proudfoot, A.E.I.; Wells, T.N.C.; Power, C.A.
 Biochem. Biophys. Res. Commun. 218, 337-343, 1996
 A:Title: Molecular cloning of murine CC CKR-4 and high affinity binding of chemokines to
 A:Reference number: JC4587; MUID:96136324
 A:Accession: JC4587
 A:Molecule type: mRNA
 A:Residues: 1-360 <HO>
 A:Cross-references: EMBL:X90862; NID:gl167851; PIDN:CAA62372.1; PID:gl167852
 A:Experimental source: thymus
 C:Genetics:
 A:Gene: cc ckr-4
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: glycoprotein; phosphoprotein; receptor; thymus
 F:2183.194/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:72.202,350/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status pred
 F:145/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
 F:321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted

Query Match 80.7%; Score 46; DB 2; Length 360;
 Best Local Similarity 72.7%; Pred. No. 0.13;
 Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YKKARSMTDVY 11
 ||: |||||
 Db 67 YKRLKSMTDVY 77

RESULT 4

JN0621
 G protein-coupled receptor type B - bovine
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 19-May-2000
 C:Accession: JN0621

R:Matsuoka, I.; Mori, T.; Aoki, J.; Sato, T.; Kurihara, K.
 Biochem. Biophys. Res. Commun. 194, 504-511, 1993
 A:Title: Identification of novel members of G-protein coupled receptor superfamily ex
 A:Reference number: JN0621; MUID:93326166
 A:Accession: JN0621
 A:Molecule type: mRNA
 A:Residues: 1-350 <MAT>
 A:Cross-references: GB:S63848; NID:g399710; PIDN:AA827547.1; PID:g399711
 A:Experimental source: tongue taste papillae
 C:Comment: This protein is involved in modulating taste sensitivity or regeneration o
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: G protein-coupled receptor; glycoprotein; receptor; transmembrane protein
 F:42-66/Domain: transmembrane #status predicted <TM1>
 F:80-99/Domain: transmembrane #status predicted <TM2>
 F:114-135/Domain: transmembrane #status predicted <TM3>
 F:154-175/Domain: transmembrane #status predicted <TM4>
 F:200-222/Domain: transmembrane #status predicted <TM5>
 F:242-265/Domain: transmembrane #status predicted <TM6>
 F:284-306/Domain: transmembrane #status predicted <TM7>
 F:6.19/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 75.4%; Score 43; DB 2; Length 350;
 Best Local Similarity 72.7%; Pred. No. 0.51;
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YKKARSMTDVY 11
 ||: |||||
 Db 69 YKRRKTKTDVY 79

RESULT 5

JC5067
 G protein-coupled receptor CKR-L1 - human
 N:Alternate names: chemokine receptor-like protein TER1; GPR-CY6
 C:Species: Homo sapiens (man)
 C:Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 21-Jul-2000
 C:Accession: JC5067; G02776; G02387
 R:Zaballos, A.; Varona, R.; Gutierrez, J.; Lind, P.; Marquez, G.
 Biochem. Biophys. Res. Commun. 227, 846-853, 1996
 A:Title: Molecular cloning and RNA expression of two new human chemokine receptor-lik
 A:Reference number: JC5067; MUID:97040707
 A:Accession: JC5067
 A:Molecule type: DNA
 A:Residues: 1-355 <ZAB>
 A:Cross-references: EMBL:Z79782; NID:gl668735; PIDN:CAB02142.1; PID:gl668736
 R:Napolitano, M.; Zingoni, A.; Bernardini, G.; Spinetti, G.; Rocchi, M.; Santoni, A.
 submitted to the EMBL Data Library, June 1996
 A:Reference number: H01714
 A:Accession: G02776
 A:Status: translated from GB/EMBL/DBDJ
 A:Molecule type: DNA
 A:Residues: 1-355 <NAP>
 A:Cross-references: EMBL:U62556; NID:gl468978; PID:gl468979
 R:Bonner, T.I.
 submitted to the EMBL Data Library, January 1996
 A:Reference number: H01154
 A:Accession: G02387
 A:Status: preliminary; translated from GB/EMBL/DBDJ
 A:Molecule type: DNA
 A:Residues: 1-355 <BON>
 A:Cross-references: EMBL:U45983; NID:gl245056; PID:gl245057
 C:Comment: This protein belongs to the family of beta chemokine receptors.

Qy 1 YKKARSMTDVY 11
 ||: |||||
 Db 69 YKRRKTKTDVY 79

Qy 1 YKKARSMTDVY 11
 ||: |||||
 Db 69 YKRRKTKTDVY 79

Qy 1 YKKARSMTDVY 11
 ||: |||||
 Db 69 YKRRKTKTDVY 79

Qy 1 YKKARSMTDVY 11
 ||: |||||
 Db 69 YKRRKTKTDVY 79

Qy 1 YKKARSMTDVY 11
 ||: |||||
 Db 69 YKRRKTKTDVY 79

Qy 1 YKKARSMTDVY 11
 ||: |||||
 Db 69 YKRRKTKTDVY 79

A:Molecule type: mRNA
A:Residues: 1-352 <SAM1>
A:Cross-references: GB:G91492; NID:gl1262810; PIDN:CAA62796.1; PID:gl1262811
R:Samson, M.; Libert, F.; Doranz, B.J.; Rucker, J.; Liesnard, C.; Farber, C.M.; Saragost
M.; Imal, T.; Rana, S.; Yi, Y.; Smyth, R.J.; Collman, R.G.; Doms, R.W.; Vassart, G.; Pa
Nature 382, 722-725, 1996
A:Title: Resistance to HIV-1 infection in caucasian individuals bearing mutant alleles o
A:Reference number: S71808; MUID:96345670
A:Accession: S71808
A:Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 182-206;207-230 <SAM2>
A:Accession: A58834
A:Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-184, 'IKSHLGAGPAACHGHLGNPKNSVSK' <SAM3>
A:Cross-references: GB:X93933; NID:gl1524062; PIDN:CAA67767.1; PID:gl1524063
A:Note: this frameshift mutation results in a non-functional receptor but confers a degra
nd may have had a selective advantage by conferring resistance to Yersinia plague infect
R:Combadiere, C.; Ahuja, S.K.; Tiffany, H.L.; Murphy, P.M.
J. Leukoc. Biol. 60, 147-152, 1996
A:Title: Cloning and functional expression of CC CKR5, a human monocyte CC chemokine rec
A:Reference number: A58832; MUID:96295970
A:Accession: A58832
A:Molecule type: mRNA
A:Residues: 1-352 <COM1>
A:Cross-references: GB:U57840; NID:gl1502408; PIDN:AA817071.1; PID:gl1502409
A:Experimental source: clone 8, endotoxin-stimulated peripheral blood monocytes
R:Combadiere, C.
submitted to the EMBL Data Library, May 1996
A:Reference number: H01541
A:Accession: G02653
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-89, 'L', '91-352 <COM2>
A:Cross-references: EMBL:U57840
R:Raport, C.J.; Gosling, J.; Schweickart, V.L.; Gray, P.W.; Charo, I.F.
J. Biol. Chem. 271, 17161-17166, 1996
A:Title: Molecular cloning and functional characterization of a novel human CC chemokine
A:Reference number: A58833; MUID:96291862
A:Accession: A58833
A:Molecule type: mRNA
A:Residues: 1-352 <RAP>
A:Cross-references: GB:U45994; NID:gl157945; PIDN:AAC50598.1; PID:gl1457946
C:Comment: This is a receptor for chemokines MIP-1alpha (see PIR:A30574), MIP-1beta (see
C:Comment: Macrophage- and dual-tropic strains of HIV-1 bind to a complex of chemokine C
C:Genetics:
A:Gene: GDB:CMKBR5; CCR5; CCR-5; CC-CCR-5; CCR5; ChemR13
A:Cross-references: GDB:1230510; OMIM:601373
A:Map position: 3p21-3p21
C:Function:
A:Description: G protein-coupled receptor for chemokines MIP-1alpha, MIP-1beta and RANTR
A:Note: probably acts to control granulocyte proliferation and differentiation
C:Superfamily: vertebrate rhodopsin
C:Keywords: AIDS; G protein-coupled receptor; glycoprotein; phosphoprotein; transmembran
F:32-56/Domain: transmembrane #status predicted <TM1>
F:67-87/Domain: transmembrane #status predicted <TM2>
F:103-124/Domain: transmembrane #status predicted <TM3>
F:142-166/Domain: transmembrane #status predicted <TM4>
F:193-218/Domain: transmembrane #status predicted <TM5>
F:236-257/Domain: transmembrane #status predicted <TM6>
F:285-300/Domain: transmembrane #status predicted <TM7>
F:20-269, 101-178/disulfide bonds: #status predicted
F:268/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:336,337,342/Binding site: phosphate (Ser) (covalent) #status predicted
F:340,343/Binding site: phosphate (Thr) (covalent) #status predicted

Query Match 66.7%; Score 38; DB 2; Length 352;
Best Local Similarity 60.0%; Pred. No. 5.4;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 2 KKARSMTDVY 11

Db 59 KRLKSWTDIY 68
I: :||||:|

RESULT 10

F71605

hypothetical protein PF0820c - malaria parasite (Plasmodium falciparum)

C:Species: Plasmodium falciparum

C>Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 21-Jul-2000

C:Accession: F71605

R:Gardner, M.J.; Rettel, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.

; Perlea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H

Science 282, 1126-1132, 1998

A:Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.

A:Reference number: A71600; MUID:99021743

A:Accession: F71605

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-273 <GAR>

A:Cross-references: GB:AE001419; GB:AE001362; NID:g3845281; PIDN:AACT1953.1; PID:g384

A:Experimental source: clone 3D7

C:Genetics:

A:Gene: PF0820c

Query Match 64.9%; Score 37; DB 2; Length 273;

Best Local Similarity 63.6%; Pred. No. 6.6;

Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 YKARSMTDVY 11

||| |||

Db 188 KYASSTTDIY 198

RESULT 11

JC4304

orphan G protein-coupled receptor - human

C:Alternate names: V28 protein

C:Species: Homo sapiens (man)

C>Date: 16-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 19-May-2000

C:Accession: JC4304

R:Raport, C.J.; Schweickart, V.L.; Eddy Jr., R.L.; Shows, T.B.; Gray, P.W.

Gene 163, 295-299, 1995

A:Title: The orphan G-protein-coupled receptor-encoding gene V28 is closely related t

A:Reference number: JC4304; MUID:96011651

A:Accession: JC4304

A:Molecule type: mRNA

A:Residues: 1-355 <RAP>

A:Cross-references: GB:U20350; NID:g665580; PIDN:AAA91783.1; PID:g665581

A:Experimental source: peripheral blood mononuclear cell

C:Comment: This protein is a cell-surface receptor which recognizes extracellular sig

C:Comment: This protein is a key regulator of many immune and homeostatic responses,

C:Genetics:

A:Gene: V28

A:Map position: 3pter-p21

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor; lymphokine; transmembrane protein

F:33-57/Domain: transmembrane #status predicted <TM1>

F:66-88/Domain: transmembrane #status predicted <TM2>

F:104-125/Domain: transmembrane #status predicted <TM3>

F:146-165/Domain: transmembrane #status predicted <TM4>

F:197-217/Domain: transmembrane #status predicted <TM5>

F:230-254/Domain: transmembrane #status predicted <TM6>

F:275-296/Domain: transmembrane #status predicted <TM7>

Query Match 64.9%; Score 37; DB 2; Length 355;

Best Local Similarity 60.0%; Pred. No. 8.7;

Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 KKARSMTDVY 11

||| |||

Db 60 KKPSTVDIY 69

RESULT 12

B70385 hypothetical protein aq_983 - Aquifex aeolicus

C:Species: Aquifex aeolicus

C:Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 18-Aug-2000

C:Accession: B70385

R:Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; O'V.

V. Nature 392, 353-358, 1998

A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.

A:Reference number: A70300; MUID:98196666

A:Accession: B70385

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-292 <AOP>

A:Cross-references: GB:AE000717; NID:g2983492; PIDN:AAC07075.1; PID:g2983497; GB:AE00065

A:Experimental source: strain VF5

C:Genetics:

C:Superfamily: Aquifex aeolicus hypothetical protein aq_983

Query Match

Best Local Similarity 63.2%; Score 36; DB 2; Length 292;

Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 YKARSMTDVI 11

I : I : I : I : I

Db 223 YRKEKSLHDVI 233

RESULT 13

I58186

probable G protein-coupled receptor - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 21-Jul-2000

C:Accession: I58186

R:Harrison, J.K.; Barber, C.M.; Lynch, K.R.

Neurosci. Lett. 169, 85-89, 1994

A:Title: cDNA cloning of a G-protein-coupled receptor expressed in rat spinal cord and b

A:Reference number: I58186; MUID:94323113

A:Accession: I58186

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-354 <RES>

A:Cross-references: EMBL:U04808; NID:g2558635; PIDN:AAB87093.1; PID:g439861

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor

Query Match

Best Local Similarity 63.2%; Score 36; DB 2; Length 354;

Matches 5; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 2 KKARSMTDVI 11

I : I : I : I : I

Db 61 RKSKSITDIY 70

RESULT 14

A45177

chemokine (C-C) receptor 1 - human

N:Alternate names: C-C CKR-1; macrophage inflammatory protein-1-alpha receptor

C:Species: Homo sapiens (man)

C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 13-Aug-1999

C:Accession: A45177; I55671

R:Neote, K.; DiGregorio, D.; Mak, J.Y.; Horuk, R.; Schall, T.J.

Cell 72, 415-425, 1993

A:Title: Molecular cloning, functional expression, and signaling characteristics of a C-

A:Reference number: A45177; MUID:93161416

A:Accession: A45177

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-355 <NEO>

A:Cross-references: GB:L10918; NID:g292416; PIDN:AAA36543.1; PID:g292417

A:Experimental source: HL60 cells

A:Note: sequence extracted from NCBI backbone (NCBIP:124876)

R:Gao, J.

J. Exp. Med. 177, 1421-1427, 1993

A:Title: Structure and functional expression of the human macrophage inflammatory 1 a

A:Reference number: I55671; MUID:93240122

A:Accession: I55671

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-355 <RES>

A:Cross-references: GB:L10918; NID:g292416; PIDN:AAA36543.1; PID:g292417

C:Genetics:

A:Gene: GDB:CMKRL1; CMKR-1

A:Cross-references: GDB:I38446; OMIM:601159

A:Map position: 3p21-3p21

C:Superfamily: vertebrate rhodopsin

C:Keywords: disulfide bond; G protein-coupled receptor; glycoprotein; phosphoprotein;

F:36-60/Domain: transmembrane #status predicted <TM1>

F:71-91/Domain: transmembrane #status predicted <TM2>

F:108-129/Domain: transmembrane #status predicted <TM3>

F:147-171/Domain: transmembrane #status predicted <TM4>

F:205-223/Domain: transmembrane #status predicted <TM5>

F:240-264/Domain: transmembrane #status predicted <TM6>

F:288-305/Domain: transmembrane #status predicted <TM7>

F:5/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:24-273,106-183/Disulfide bonds: #status predicted

F:345/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted

Query Match

Best Local Similarity 63.2%; Score 36; DB 2; Length 355;

Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 YKARSMTDVI 11

I : I : I : I : I

Db 62 YKRLKNMTSIY 72

RESULT 15

T47727

hypothetical protein F18021.60 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 02-Sep-2000

C:Accession: T47727

R:Benes, V.; Wurmbach, E.; Drzonek, H.; Ansorge, W.; Mewes, H.W.; Rudd, S.; Lemcke, K

submitted to the Protein Sequence Database, April 2000

A:Reference number: Z24474

A:Accession: T47727

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-719 <BEN>

A:Cross-references: EMBL:ATF18021

A:Experimental source: cultivar Columbia; BAC clone F18021

C:Genetics:

A:Map position: 3

A:Introns: 244/2; 491/1; 511/1

A:Note: F18021.60

C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hom

Query Match

Best Local Similarity 63.2%; Score 36; DB 2; Length 719;

Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 KKARSMTDVI 11

I : I : I : I : I

Db 598 KKANTKTDVI 607

Search completed: May 23, 2001, 15:31:59
Job time: 506 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 23, 2001, 15:36:17 ; Search time 62.39 Seconds
(without alignments)
6.040 Million cell updates/sec

Title: US-08-887-977-10_COPY_65_75
Perfect score: 57
Sequence: 1 YKARSMTDVI 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	57	100.0	367	1	CCR6_MOUSE
2	57	100.0	374	1	CCR6_MOUSE
3	49	86.0	360	1	CCR4_MOUSE
4	46	80.7	360	1	CCR4_MOUSE
5	43	75.4	350	1	GUSB_BOVIN
6	41	71.9	354	1	CCR5_RAT
7	41	71.9	355	1	CCR8_HUMAN
8	41	71.9	373	1	CCR2_MOUSE
9	41	71.9	373	1	CCR2_RAT
10	40	70.2	353	1	CCR8_MOUSE
11	39	68.4	192	1	CCR4_SHEEP
12	39	68.4	349	1	CCR4_RAT
13	39	68.4	352	1	CCR4_CERTO
14	39	68.4	352	1	CCR4_HUMAN
15	39	68.4	352	1	CCR4_MACFA
16	39	68.4	352	1	CCR4_MACMU
17	39	68.4	352	1	CCR4_PAPAN
18	39	68.4	353	1	CCR4_BOVIN
19	39	68.4	353	1	CCR4_FELCA
20	39	68.4	359	1	CCR4_MOUSE
21	38	66.7	352	1	CCR5_CERAE
22	38	66.7	352	1	CCR5_CERTO
23	38	66.7	352	1	CCR5_GORGO
24	38	66.7	352	1	CCR5_HUMAN
25	38	66.7	352	1	CCR5_HYLLE
26	38	66.7	352	1	CCR5_MACMU
27	38	66.7	352	1	CCR5_PANTR
28	38	66.7	352	1	CCR5_PAPHA
29	38	66.7	352	1	CCR5_PONPY
30	38	66.7	352	1	CCR5_PYGBI
31	38	66.7	352	1	CCR5_PYGNE
32	38	66.7	352	1	CCR5_TAFRA
33	38	66.7	352	1	CCR5_TRAPH

34	37	64.9	354	1	CCR5_MOUSE	P51682	mus musculus
35	37	64.9	355	1	C3X1_HUMAN	P49238	homo sapien
36	37	64.9	355	1	CCR1_HUMAN	P56482	macaca mula
37	37	64.9	356	1	CCR8_MACMU	O97665	macaca mula
38	36	63.2	349	1	IL8A_RAT	P70612	rattus norv
39	36	63.2	354	1	C3X1_RAT	P35411	rattus norv
40	36	63.2	355	1	CCR1_HUMAN	P32246	homo sapien
41	36	63.2	370	1	VK02_SPVKA	Q08520	swinepox vi
42	36	63.2	636	1	P73_HUMAN	O15350	homo sapien
43	36	63.2	916	1	TOP1_ARATH	P30181	arabidopsis
44	35	61.4	342	1	BONZ_CERAE	O18983	cercopithec
45	35	61.4	342	1	BONZ_HUMAN	O00574	homo sapien

ALIGNMENTS

RESULT 1

ID	CCR6_MOUSE	STANDARD;	PRT;	367 AA.
AC	O54689;			
DT	30-MAY-2000 (Rel. 39, Created)			
DT	30-MAY-2000 (Rel. 39, Last sequence update)			
DE	01-OCT-2000 (Rel. 40, Last annotation update)			
DE	C-C CHEMOKINE RECEPTOR TYPE 6 (C-C CCR-6) (CCR-6) (KY411).			
GN	CCR6 OR CMKBR6.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Yanagihara S., Komura E., Yamaguchi Y.;			
RT	"Mouse G protein-coupled receptor KY411.";			
RL	Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=99077268; PubMed=9862452;			
RA	Varona R., Zaballos A., Gutierrez J., Martin P., Roncal F.,			
RA	Albar J.P., Ardavin C., Marquez G.;			
RT	"Molecular cloning, functional characterization and mRNA expression			
RT	analysis of the murine chemokine receptor CCR6 and its specific ligand			
RL	MIP-3alpha.";			
FEBS	Lett. 440:188-194(1998).			
CC	-!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-3-			
CC	INTRACELLULAR AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE			
CC	-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.			
CC	-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.			
CC	THIS SWISS-PROT entry is copyright. It is produced through a collaboration			
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CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	EMBL; AB009369; BAA23776.1;			
DR	EMBL; AJ222714; CAA10956.1;			
DR	MGI; MGI:1333797; Cmkbr6.			
DR	InterPro: IPR000276;			
DR	Pfam; PF00001; 7tm_1; 1.			
DR	PRINTS; PR00237; GPCRHOOPS.			
DR	PROSITE; PS00237; G_PROTEIN_RECP_FL_1; 1.			
DR	PROSITE; PS00267; G_PROTEIN_RECP_FL_2; 1.			
KW	G-protein coupled receptor; Transmembrane; Glycoprotein.			
FT	DOMAIN 1 39			
FT	TRANSMEM 40 66			
FT	DOMAIN 67 75			
FT	TRANSMEM 76 96			
FT	DOMAIN 97 111			
FT	TRANSMEM 112 133			


```
RESULT 3
CKR4_HUMAN
ID CKR4_HUMAN STANDARD; PRT; 360 AA.
AC P51679;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE C-C CHEMOKINE RECEPTOR TYPE 4 (C-CR-4) (CCR-4) (CCR4)
DE (K5-5).
GN CCR4 OR CMKBR4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95370289; PubMed=7642634;
RA Power C.A., Meyer A., Nemeth K., Bacon K.B., Hoogewerf A.J.,
RA Proudfoot A.E.I., Wells T.N.C.;
RT "Molecular cloning and functional expression of a novel CC chemokine
RT receptor cDNA from a human basophilic cell line.";
RL J. Biol. Chem. 270:19495-19500(1995).
RN [2]
RP FUNCTION.
RX MEDLINE=97313486; PubMed=9169480;
RA Inai T., Baba M., Nishimura M., Kakizaki M., Takagi S., Yoshie O.;
RT "The T cell-directed CC chemokine TARC is a highly specific
RT biological ligand for CC chemokine receptor 4.";
RL J. Biol. Chem. 272:15036-15042(1997).
CC -1- FUNCTION: RECEPTOR FOR C-C TYPE CHEMOKINE. BINDS TO TARC, MIP-1-
CC ALPHA, RANTES, AND MCP-1. SUBSEQUENTLY TRANSDUCES A SIGNAL BY
CC INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: EXPRESSED STRONGLY IN PERIPHERAL BLOOD T CELLS
CC BUT NOT IN B CELLS, NATURAL KILLER CELLS, MONOCYTES, OR
CC GRANULOCYTES.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC
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CC
CC EMBL; X85740; CAA59743.1; -
CC MIM; 604836; -
CC GCRDB; GCR_2115; -
CC InterPro; IPR000276; -
CC InterPro; IPR000355; -
CC InterPro; IPR002239; -
CC Pfam; PF00001; 7tm_1; 1.
CC PRINTS; PR00237; GPCRHHODOPSN.
CC PRINTS; PR00657; CCHEMOKINER4.
CC PROSITE; PS00237; G-PROTEIN_RECEPTOR_F1_1; 1.
CC PROSITE; PS00262; G-PROTEIN_RECEPTOR_F1_2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein.
KW DOMAIN 1 39 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 1 39 1 (POTENTIAL)
FT TRANSMEM 40 67
FT DOMAIN 68 77 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 78 98 2 (POTENTIAL).
FT DOMAIN 99 111 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 112 133 3 (POTENTIAL).
FT DOMAIN 134 150 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 151 175 4 (POTENTIAL).
FT DOMAIN 176 206 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 207 226 5 (POTENTIAL).
FT DOMAIN 227 242 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 243 267 6 (POTENTIAL).
FT DOMAIN 268 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 284

FT TRANSMEM 285 308 7 (POTENTIAL).
FT DOMAIN 309 360 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 183 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 194 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 110 187 BY SIMILARITY.
SQ SEQUENCE 360 AA; 41402; 51EBE12AD1FAFBF CRC64;

Query Match 86.0%; Score 49; DB 1; Length 360;
Best Local Similarity 81.8%; Pred. No. 0.016;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YKARSMTDYY 11
DB 67 YKRLRSMTDYY 77

RESULT 4
CKR4_MOUSE
ID CKR4_MOUSE STANDARD; PRT; 360 AA.
AC P51680;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE C-C CHEMOKINE RECEPTOR TYPE 4 (C-CR-4) (CCR-4) (CCR4).
GN CCR4 OR CMKBR4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6 X CBA; TISSUE=Thymus;
RX MEDLINE=96136324; PubMed=8573157;
RA Hoogewerf A.J., Black D., Proudfoot A.E.I., Wells T.N.C., Power C.A.;
RT "Molecular cloning of murine CC CRK-4 and high affinity binding of
RT chemokines to murine and human CC CRK-4.";
RL Biochem. Biophys. Res. Commun. 218:337-343(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6 X CBA; TISSUE=Thymus;
RX MEDLINE=96136324; PubMed=8573157;
RA Hoogewerf A.J., Black D., Proudfoot A.E.I., Wells T.N.C., Power C.A.;
RT "Molecular cloning of murine CC CRK-4 and high affinity binding of
RT chemokines to murine and human CC CRK-4.";
RL Biochem. Biophys. Res. Commun. 218:337-343(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6; TISSUE=Spleen;
RX MEDLINE=97335974; PubMed=9192769;
RA YOUNG B.-S., Kim S.-H., Lyu M.-S., Kozak C.A., Taub D.D., Kwon B.-S.;
RT "Molecular cloning and characterization of a cDNA, CHEM1, encoding a
RT chemokine receptor with a homology to the human C-C chemokine
RT receptor, CCR-4.";
RL Blood 89:4448-4460(1997).
CC -1- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO TARC AND
CC SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR
CC CALCIUM IONS LEVEL (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: DETECTED IN THE THYMUS AND T-CELLS.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; X90862; CAA62372.1; -
CC EMBL; U15208; AAA92582.1; -
CC GCRDB; GCR_1714; -
CC MGD; MGI:107824; Cmkbr4.
CC InterPro; IPR000276; -
CC InterPro; IPR000355; -
CC InterPro; IPR002239; -
CC Pfam; PF00001; 7tm_1; 1.
CC PRINTS; PR00237; GPCRHHODOPSN.
CC PRINTS; PR00657; CCHEMOKINER.
CC PRINTS; PR01109; CHEMOKINER4.
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DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 KW PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
 FT DOMAIN 39
 FT TRANSMEM 40
 FT DOMAIN 67
 FT TRANSMEM 77
 FT TRANSMEM 78
 FT TRANSMEM 98
 FT TRANSMEM 99
 FT TRANSMEM 111
 FT TRANSMEM 112
 FT TRANSMEM 113
 FT TRANSMEM 134
 FT TRANSMEM 151
 FT TRANSMEM 175
 FT TRANSMEM 176
 FT TRANSMEM 206
 FT TRANSMEM 207
 FT TRANSMEM 227
 FT TRANSMEM 243
 FT TRANSMEM 267
 FT TRANSMEM 284
 FT TRANSMEM 285
 FT TRANSMEM 309
 FT TRANSMEM 360
 FT CARBOHYD 2
 FT CARBOHYD 183
 FT CARBOHYD 194
 FT DISULFID 194
 FT DISULFID 110
 FT CONFLICT 4
 FT CONFLICT 145
 FT CONFLICT 181
 FT CONFLICT 205
 FT CONFLICT 221
 FT CONFLICT 241
 FT CONFLICT 246
 FT CONFLICT 293
 FT CONFLICT 311
 FT CONFLICT 311
 SQ SEQUENCE 360 AA; 41462 MW; 97BDB8C96D259AE3 CRC64;

Query Match 80.7%; Score 46; DB 1; Length 360;
 Best Local Similarity 72.7%; Pred. No. 0.066;
 Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YKARSMTDVI 11
 |||:|||||

Db 67 YKRLKSMTDVI 77

RESULT 5
 GUSB_BOVIN STANDARD; PRT; 350 AA.
 ID GUSB_BOVIN STANDARD; PRT; 350 AA.
 AC P35350;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 01-JUN-1994 (Rel. 29, Last annotation update)
 DE POSSIBLE GUSTATORY RECEPTOR TYPE B (PPRI PROTEIN).
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Tongue;
 RX MEDLINE=93326166; PubMed=8392843;
 RA Matsuoka I., Mori T., Aoki J., Sato T., Kurihara K.;
 RT "Identification of novel members of G-protein coupled receptor
 superfamily expressed in bovine taste tissue";
 RL Biochem. Biophys. Res. Commun. 194:504-511(1993).
 CC -!- FUNCTION: POSSIBLE TASTE RECEPTOR. MAY ALSO BE A RECEPTOR FOR
 PEPTIDE LIGANDS.
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN CIRCUMVALLATE AND FUNGIFORM
 CC PAPILLAE, OLFACTORY EPITHELIUM AND LUNG. LOWER EXPRESSION IN
 CC LIVER, KIDNEY AND TONGUE EPITHELIUM BEARING NO TASTE PAPILLAE.
 CC VERY LOW EXPRESSION IN THE CEREBRAL CORTEX OF THE BRAIN.
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -!- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-18 IS THE INITIATOR.

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 CC or send an email to license@isb-sib.ch).

DR EMBL; S63848; AAB27547.1; -
 DR PIR; JN0621; JN0621.
 DR GCRdb; GCR_0757; -
 DR InterPro; IPR000276; -
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Phosphorylation.
 FT DOMAIN 1 41 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 42 66 1 (POTENTIAL).
 FT TRANSMEM 67 79 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 80 99 2 (POTENTIAL).
 FT TRANSMEM 100 113 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 114 135 3 (POTENTIAL).
 FT TRANSMEM 136 153 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 154 175 4 (POTENTIAL).
 FT TRANSMEM 176 199 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 200 222 5 (POTENTIAL).
 FT TRANSMEM 223 241 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 242 265 6 (POTENTIAL).
 FT TRANSMEM 266 283 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 284 306 7 (POTENTIAL).
 FT TRANSMEM 307 350 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 6 6 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 19 19 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT DISULFID 112 184 BY SIMILARITY.
 SQ SEQUENCE 350 AA; 40008 MW; E46BF942F3919C82 CRC64;

Query Match 75.4%; Score 43; DB 1; Length 350;
 Best Local Similarity 72.7%; Pred. No. 0.26;
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YKARSMTDVI 11
 |||:|||||

Db 69 YKRRRTKTDVI 79

RESULT 6
 CKR5_RAT STANDARD; PRT; 354 AA.
 ID CKR5_RAT STANDARD; PRT; 354 AA.
 AC O08556;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE C-C CHEMOKINE RECEPTOR TYPE 5 (C-C CKR-5) (CCR-5) (MIP-1
 DE ALPHA RECEPTOR).
 GN CCR5 OR CMKBR5.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Wistar; Tissue=Brain;
 RX MEDLINE=98334064; PubMed=9670989;
 RA Spleiss O., Gourmala N., Boddeke H.W.G.M., Sauter A., Fiebich B.L.,
 RA Berger M., Gebicke-Haerter P.J.;
 RT "Cloning of rat HIV-1-chemokine coreceptor CKR5 from microglia and
 RT upregulation of its mRNA in ischemic and endotoxemic rat brain";
 RL J. Neurosci. Res. 53:16-28(1998).
 RN [2]

```

RP SEQUENCE FROM N.A.
RC STRAIN-SPRAGUE-DAWLEY;
RX MEDLINE=98318173; PubMed=9655467;
RA Jiang Y., Salafra M.N., Adhikari S., Xia Y., Feng L., Sonntag M.K.,
RA Defebvre C.M., Pennell N.A., Streit W.J., Harrison J.K.;
RT "Chemokine receptor expression in cultured glia and rat experimental
RL allergic encephalomyelitis.";
RL J. Neuroimmunol. 86:1-12(1998).
CC -1- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
CC MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
CC INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; Y12009; CAA72737.1; -
CC GCRDB; GCR_1470; -
CC InterPro; IPR000276; -
CC InterPro; IPR000355; -
CC InterPro; IPR002240; -
CC Pfam; PF00001; 7cml; 1.
CC PRINTS; PR00237; GPCRHDOPSN.
CC PRINTS; PR00657; CCHEMOKINER.
CC PRINTS; PR01110; CHEMOKINER5.
CC PROSITE; PS00237; G-PROTEIN_RECP_FL_1; 1.
CC PROSITE; PS0262; G-PROTEIN_RECP_FL_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 32
FT TRANSMEM 33 60
FT DOMAIN 61 70
FT TRANSMEM 71 91
FT DOMAIN 92 104
FT TRANSMEM 105 126
FT DOMAIN 127 143
FT TRANSMEM 144 168
FT DOMAIN 169 200
FT TRANSMEM 201 220
FT TRANSMEM 221 237
FT DOMAIN 238 262
FT TRANSMEM 263 279
FT DOMAIN 280 303
FT TRANSMEM 304 354
FT DISULFID 103 180
FT CARBOHYD 270 270
FT SEQUENCE 354 AA; 41030 MW; 77EDB368AA4C868D CRC64;

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Query Match 71.9%; Score 41; DB 1; Length 354;
 Best Local Similarity 70.0%; Pred. No. 0.67;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 KKARSMTDVIY 11
 II:IIII:I
 DB 61 KKLKLSMTDIY 70

RESULT 7
 CKR8_HUMAN
 ID CKR8_HUMAN STANDARD; PRT; 355 AA.
 AC P51685;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE C-C CHEMOKINE RECEPTOR TYPE 8 (C-C CKR-8) (CC-CKR-8) (CCR-8) (GPR-CY6)
 DE (GPCY6) (CHEMOKINE RECEPTOR-LIKE 1) (CCR-L1) (TER1) (CMKRL2) (CC-

DE CHEMOKINE RECEPTOR CHEMRL1).
 GN CCR8 OR CMKRB8 OR CKRL1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97351133; PubMed=9207005;
 RA Tiffany H.L., Lautens L.L., Gao J.-L., Pease J., Locati M.,
 RA Combadiere C., Modi W., Bonner T.I., Murphy P.M.;
 RT "Identification of CCR8: a human monocyte and thymus receptor for the
 RT CC chemokine I-309.";
 RL J. Exp. Med. 186:165-170(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98129363; PubMed=9469461;
 RA Goya I., Gutierrez J., Varona R., Kremer L., Zaballos A., Marquez G.;
 RT "Identification of CCR8 as the specific receptor for the human beta-
 RT chemokine I-309: cloning and molecular characterization of murine
 RT CCR8 as the receptor for TCA-3.";
 RL J. Immunol. 160:1975-1981(1998).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97040707; PubMed=8886020;
 RA Zaballos A., Varona R., Gutierrez J., Lind P., Marquez G.;
 RT "Molecular cloning and RNA expression of two new human chemokine
 RT receptor-like genes.";
 RL Biochem. Biophys. Res. Commun. 227:846-853(1996).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97131825; PubMed=8977299;
 RA Samson M., Stordeur P., Labbe O., Soularue P., Vassart G.,
 RA Parmentier M.;
 RT "Molecular cloning and chromosomal mapping of a novel human gene,
 RT Chemrl, expressed in T lymphocytes and polymorphonuclear cells and
 RT encoding a putative chemokine receptor.";
 RL Eur. J. Immunol. 26:3021-3028(1996).
 RN [5]
 RP SEQUENCE FROM N.A.
 RX Nakajima T., Yoshida R., Harada S.;
 RA Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP LIGAND BINDING.
 RX MEDLINE=98180363; PubMed=9521068;
 RA Bernardini G., Hedrick J., Sozzani S., Luini W., Spinetti G.,
 RA Weiss M., Menon S., Zlotnik A., Mantovani A., Santoni A.,
 RA Napolitano M.;
 RT "Identification of the CC chemokines TARC and macrophage inflammatory
 RT protein-1 beta as novel functional ligands for the CCR8 receptor.";
 RL Eur. J. Immunol. 28:582-588(1998).
 CC -1- FUNCTION: RECEPTOR FOR THE CHEMOKINES SCYAL/I-309, SCY44/MIP-1-
 CC BETA AND SCY41/TARC. MAY REGULATE MONOCYTE CHEMOTAXIS AND THYMIC
 CC CELL LINE APOPTOSIS.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC
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 CC
 CC EMBL; U45983; AAB61962.1; -
 CC EMBL; U62556; AAB05542.1; -
 CC EMBL; Z79782; CAB02142.1; -
 CC EMBL; Y08456; CAA69712.1; -
 CC EMBL; D49919; BAA23387.1; -
 CC EMBL; AF005210; AAB62547.1; -
 CC GCRDB; GCR_1333; -
 CC GCRDB; GCR_1915; -

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DR GCRDb; GCR_2111; -
DR GCRDb; GCR_2611; -
DR GCRDb; GCR_2619; -
DR MIM: 601834; -
DR InterPro; IPR000276; -
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECF_FL1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECF_FL2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 35
FT TRANSMEM 36 63
FT DOMAIN 64 73
FT TRANSMEM 74 93
FT DOMAIN 94 107
FT TRANSMEM 108 129
FT DOMAIN 130 146
FT TRANSMEM 147 171
FT DOMAIN 172 202
FT TRANSMEM 203 222
FT DOMAIN 223 238
FT TRANSMEM 239 263
FT DOMAIN 264 280
FT TRANSMEM 281 304
FT DOMAIN 305 355
FT DISULFID 106 183
SQ SEQUENCE 355 AA; 40844 MW; BC14A153CF695361 CRC64;

Query Match 71.9%; Score 41; DB 1; Length 355;
Best Local Similarity 80.0%; Pred. No. 0.67;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 2 KKARSMTDVIY 11
Db 64 KKLRSITDVIY 73

RESULT 8
ID CKR2_MOUSE STANDARD; PRT; 373 AA.
AC PS1683; Q611172;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE C-C CHEMOKINE RECEPTOR TYPE 2 (C-C CKR-2) (CCR-2) (CCR2)
DE (JE/FIC RECEPTOR) (MCP-1 RECEPTOR).
GN CKR2 OR CMKBR2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96205938; PubMed=8631787;
RA Boring L., Gosling J., Monteclaro F.S., Lusis A.J., Tsou C.-L.,
RA Charo I.F.;
RT "Molecular cloning and functional expression of murine JE (monocyte
RT chemoattractant protein 1) and murine macrophage inflammatory protein
RT alpha receptors: evidence for two closely linked C-C chemokine
RT receptors on chromosome 9."
RL J. Biol. Chem. 271:7551-7558(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=BALB/C;
RA Kurihara T., Bravo R.;
RT "Cloning and functional expression of mCCR2, a murine receptor for
RT the C-C chemokines JE and FIC."
RL J. Biol. Chem. 271:11603-11606(1996).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=97026720; PubMed=8872898;

```

Heesen M., Tanabe S., Berman M.A., Yoshizawa I., Luo Y., Kim R.,
Post T.W., Gerard C., Dorf M.E.;
"Mouse astrocytes respond to the chemokines MCP-1 and KC, but reverse
transcriptase-polymerase chain reaction does not detect mRNA for the
KC or new MCP-1 receptor.";
J. Neurosci. Res. 45:382-391(1996).
-!- FUNCTION: RECEPTOR FOR THE MCP-1 (JE), MCP-3 (FIC) AND MCP-5
CHEMOKINES. TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR
CALCIUM IONS LEVEL.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-!- TISSUE SPECIFICITY: DETECTED IN MONOCYTE/MACROPHAGE CELL LINES,
BUT NOT IN NONHEMATOPOIETIC CELL LINES.
-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

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EMBL; U47035; AAC52453.1; -
EMBL; U51717; AAC52557.1; -
EMBL; U56819; AAC52784.1; -
GCRDb; GCR_1649; -
GCRDb; GCR_1651; -
GCRDb; GCR_1657; -
MGD; MGI:106185; Cmkbr2.
InterPro; IPR000276; -
InterPro; IPR000355; -
InterPro; IPR002237; -
Pfam; PF00001; 7tm.1; 1.
PRINTS; PR00237; GPCRHHODOPSN.
PRINTS; PR00657; GPCHEMOKINER.
PRINTS; PR01107; CHEMOKINER2.
PROSITE; PS00237; G_PROTEIN_RECF_FL1; 1.
PROSITE; PS0262; G_PROTEIN_RECF_FL2; 1.
G-protein coupled receptor; Transmembrane.
DOMAIN 1 55
TRANSMEM 56 83
DOMAIN 84 93
TRANSMEM 94 114
DOMAIN 115 127
TRANSMEM 128 149
DOMAIN 150 166
TRANSMEM 167 191
DOMAIN 192 219
TRANSMEM 220 239
DOMAIN 240 256
TRANSMEM 257 281
DOMAIN 282 298
TRANSMEM 299 322
DOMAIN 323 373
DISULFID 126 203
CONFLICT 39 39
CONFLICT 184 184
CONFLICT 264 264
SEQUENCE 373 AA; 42782 MW; FA012C10F4C9325A CRC64;
Query Match 71.9%; Score 41; DB 1; Length 373;
Best Local Similarity 70.0%; Pred. No. 0.7;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 2 KKARSMTDVIY 11
Db 84 KKLKSMTDVIY 93
II:IIII:II
II:IIII:II

RESULT 9
CKR2_RAT
ID CKR2_RAT STANDARD; PRT; 373 AA.

AC 05193;
 DT 01-OCT-2000 (Rel. 40, Created)
 DT 01-OCT-2000 (Rel. 40, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE C-C CHEMOKINE RECEPTOR TYPE 2 (C-C CKR-2) (CCR-2) (CCR2).
 GN CCR2 OR CMKR2.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SPRAGUE DAWLEY;
 RX MEDLINE=98318173; PubMed=9655467;
 RA Jiang Y., Salafraanca M.N., Adhikari S., Xia Y., Peng L., Sonntag M.K.,
 RA defiebre C.M., Pennell N.A., Streit W.J., Harrison J.K.;
 RT "Chemokine receptor expression in cultured glia and rat experimental
 RT allergic encephalomyelitis";
 RL J. Neuroimmunol. 86:1-12(1998).
 CC -!- FUNCTION: RECEPTOR FOR THE MCP-1 (JE), MCP-3 (FIC) AND MCP-5
 CC CHEMOKINES. TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR
 CC CALCIUM IONS LEVEL (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN LUNG, SPLEEN, KIDNEY, THYMUS AND
 CC MACROPHAGES.
 CC -!- INDUCTION: IN ANIMALS IN WHICH EXPERIMENTAL ALLERGIC
 CC ENCEPHALOMYELITIS (EAE) HAS BEEN INDUCED.
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC
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 CC
 CC EMBL: U77349; AAC03242.1; -;
 DR InterPro: IPR000276; -;
 DR InterPro: IPR000355; -;
 DR InterPro: IPR002237; -;
 DR Pfam: PF00001; 7tm.1; 1.
 DR PRINTS: PR00237; GPCRHOOPS.
 DR PRINTS: PR00657; CCHEMOKINER.
 DR PRINTS: PR01107; CHEMOKINER2.
 DR PROSITE; PS00237; G_PROTEIN_RECEPT_F1_1; 1.
 DR PROSITE; PS00262; G_PROTEIN_RECEPT_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane.
 FT DOMAIN 1 60
 FT EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 61 81
 FT POTENTIAL.
 FT CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 82 91
 FT POTENTIAL.
 FT TRANSMEM 92 112
 FT POTENTIAL.
 FT DOMAIN 113 128
 FT EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 129 149
 FT POTENTIAL.
 FT DOMAIN 150 170
 FT CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 171 191
 FT POTENTIAL.
 FT DOMAIN 192 220
 FT EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 221 241
 FT POTENTIAL.
 FT DOMAIN 242 256
 FT CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 257 277
 FT POTENTIAL.
 FT DOMAIN 278 301
 FT EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 302 322
 FT POTENTIAL.
 FT DOMAIN 323 373
 FT CYTOPLASMIC (POTENTIAL).
 FT DISULFID 126 203
 FT BY SIMILARITY.
 FT CARBOHYD 126 203
 SQ SEQUENCE 373 AA; 42763 MW; 2E7BB012F5D6FD09 CRC64;

Query Match 71.9%; Score 41; DB 1; Length 373;
 Best Local Similarity 70.0%; Pred. No. 0.7;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 KKASMTDVI 11
 || :|||||

Db 84 KKLKSMTDVI 93

RESULT 10
 CCR8_MOUSE STANDARD; PRT; 353 AA.
 ID CCR8_MOUSE
 AC P56484;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE C-C CHEMOKINE RECEPTOR TYPE 8 (C-C CKR-8) (CC-CKR-8) (CCR-8).
 GN CCR8 OR CMKR8.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC Mus musculus (Mouse).
 RX Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 RA Zaballos A., Goya I.I., Gutierrez J., Varona R., Marquez G.;
 CC -!- FUNCTION: RECEPTOR FOR THE TCA-3 CHEMOKINE.
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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 CC
 CC EMBL: Z98206; CAB10896.1; -;
 DR EMBL: Z98205; CAB10895.1; -;
 DR GCD; GCR_2595; -;
 DR MGD; MGI:1201402; Cmkbr8.
 DR InterPro: IPR000276; -;
 DR Pfam: PF00001; 7tm.1; 1.
 DR PROSITE; PS00237; G_PROTEIN_RECEPT_F1_1; 1.
 DR PROSITE; PS00262; G_PROTEIN_RECEPT_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 33
 FT EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 34 61
 FT 1 (POTENTIAL).
 FT CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 62 71
 FT 2 (POTENTIAL).
 FT TRANSMEM 72 91
 FT 3 (POTENTIAL).
 FT DOMAIN 92 105
 FT EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 106 127
 FT 4 (POTENTIAL).
 FT DOMAIN 128 144
 FT CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 145 169
 FT 5 (POTENTIAL).
 FT DOMAIN 170 200
 FT EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 201 220
 FT 6 (POTENTIAL).
 FT DOMAIN 221 236
 FT CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 237 261
 FT 7 (POTENTIAL).
 FT DOMAIN 262 278
 FT EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 279 302
 FT 8 (POTENTIAL).
 FT DOMAIN 303 333
 FT CYTOPLASMIC (POTENTIAL).
 FT DISULFID 104 181
 FT BY SIMILARITY.
 FT CARBOHYD 8 8
 FT N-LINKED (GLCNAC... (POTENTIAL).
 SQ SEQUENCE 353 AA; 40045 MW; 31EC4B642CDB9AE5 CRC64;

Query Match 70.2%; Score 40; DB 1; Length 353;
 Best Local Similarity 70.0%; Pred. No. 1.1;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 KKASMTDVI 11
 || |||:|:|

Db 62 KKLKSMTDVI 71

RESULT 11
 CCR4_SHEEP STANDARD; PRT; 192 AA.
 ID CCR4_SHEEP

AC Q28553;
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DE 15-JUL-1998 (Rel. 36, Last annotation update)
 DE 15-JUL-1998 (Rel. 36, Last annotation update)
 DE C-X-C CHEMOKINE RECEPTOR TYPE 4 (CXCR-4) (SDF-1 RECEPTOR)
 DE STROMAL CELL-DERIVED FACTOR 1 RECEPTOR (FUSIN) (LEUKOCYTE-DERIVED
 DE SEVEN TRANSMEMBRANE DOMAIN RECEPTOR) (LESTR) (FRAGMENT).
 GN CXCR4 OR LESTR.
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Ovis.
 OX NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Hypothalamus;
 RA Dyer C.J., Matteri R.L., Keisler D.H.;
 RT "Development of an ovine Y3 cDNA and expression of the Y3 receptor
 RT mRNA in the ovine hypothalamus and pituitary.";
 RL Abstr. - Soc. Neurosci. 21:1890-1890(1995).
 CC -1- FUNCTION: RECEPTOR FOR THE C-X-C CHEMOKINE SDF-1. TRANSDUCES A
 CC SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -1- CAUTION: WAS ORIGINALLY THOUGHT TO BE A RECEPTOR FOR NEUROPEPTIDE
 CC Y, TYPE 3 (NPY3-R).
 CC -----
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 CC -----
 CC EMBL; U38942; AAA81347.1;
 DR GCRDB; GCR_1581;
 DR InterPro; IPR000276;
 DR Pfam; PF00001; 7tm.1; 1.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1;
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT NON_TER 1
 FT DOMAIN <1 29
 FT TRANSMEM 30 53
 FT DOMAIN 54 69
 FT TRANSMEM 70 89
 FT DOMAIN 90 100
 FT TRANSMEM 101 122
 FT DOMAIN 123 144
 FT TRANSMEM 145 165
 FT DOMAIN 166 190
 FT TRANSMEM 191 >192
 FT DISULFID 199 176
 FT NON_TER 192 192
 SQ SEQUENCE 192 AA; 22178 MW; A8BCFE303C52BD98 CRC64;

Query Match 68.4%; Score 39; DB 1; Length 192;
 Best Local Similarity 80.0%; Pred. No. 0.89;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 KKARSMTDVY 11
 || |||||
 DB 57 KKLRSMTDKY 66

RESULT 12
 CCR4_RAT
 ID CCR4_RAT STANDARD; PRT; 349 AA.
 AC O08565;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE C-X-C CHEMOKINE RECEPTOR TYPE 4 (CXCR-4) (SDF-1 RECEPTOR)
 DE STROMAL CELL-DERIVED FACTOR 1 RECEPTOR (FUSIN) (LEUKOCYTE-DERIVED
 DE SEVEN TRANSMEMBRANE DOMAIN RECEPTOR) (LESTR).
 GN CXCR4 OR CXKRA.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Wistar; TISSUE-Spleen;
 RA Harrison J.K., Salafranca M.N.;
 RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: RECEPTOR FOR THE C-X-C CHEMOKINE SDF-1. TRANSDUCES A
 CC SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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 CC -----
 CC EMBL; U50610; AAB50408.1;
 DR GCRDB; GCR_1401;
 DR InterPro; IPR000276;
 DR InterPro; IPR001277;
 DR Pfam; PF00001; 7tm.1; 1.
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PRINTS; PR00645; LCRLOPHANR.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 36
 FT TRANSMEM 37 60
 FT DOMAIN 61 76
 FT TRANSMEM 77 96
 FT DOMAIN 97 107
 FT TRANSMEM 108 129
 FT DOMAIN 130 151
 FT TRANSMEM 152 172
 FT DOMAIN 173 197
 FT TRANSMEM 198 217
 FT DOMAIN 218 237
 FT TRANSMEM 238 258
 FT DOMAIN 259 282
 FT TRANSMEM 283 302
 FT DOMAIN 303 349
 FT DISULFID 106 183
 FT CARBOHYD 8 8
 SQ SEQUENCE 349 AA; 7E0789A605C60C09 CRC64;

Query Match 68.4%; Score 39; DB 1; Length 349;
 Best Local Similarity 80.0%; Pred. No. 1.7;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 KKARSMTDVY 11
 || |||||
 DB 64 KKLRSMTDKY 73

RESULT 13
 CCR4_CERTO
 ID CCR4_CERTO STANDARD; PRT; 352 AA.
 AC O62747;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)

DE C-X-C CHEMOKINE RECEPTOR TYPE 4 (CXC-R4) (CXCR-4) (SDF-1 RECEPTOR)
DE (STROMAL CELL-DERIVED FACTOR 1 RECEPTOR) (FUSIN) (LESTR).
GN CXCR4.
OS Cercopithecus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9531;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98321155; PubMed=9565999;
RA Chen Z., Gettie A., Ho D.D., Marx P.A.;
RT "Primary SIVsm isolates use the CCR5 coreceptor from sooty mangabeys
naturally infected in west Africa: a comparison of coreceptor usage
of primary SIVsm, HIV-2, and SIVmac.";
RL Virology 246:113-124(1998).
CC -!- FUNCTION: RECEPTOR FOR THE C-X-C CHEMOKINE SDF-1. TRANSDUCES A
CC SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CC -----
DR EMBL; AF051906; AAC39834.1;
DR InterPro; IPR000276;
DR InterPro; IPR001277;
DR Pfam; PF00001; 7tm.1.1;
DR PRINTS; PR00237; GPCRHHODPSN.
DR PRINTS; PR00645; LCRHORHANK.
DR PROSITE; PS00237; G-PROTEIN_RECEP_FL1; 1.
DR PROSITE; PS00262; G-PROTEIN_RECEP_FL2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 39
FT TRANSMEM 40 63
FT DOMAIN 64 79
FT TRANSMEM 80 99
FT DOMAIN 100 110
FT TRANSMEM 111 132
FT DOMAIN 133 154
FT TRANSMEM 155 175
FT DOMAIN 176 200
FT TRANSMEM 201 220
FT DOMAIN 221 240
FT TRANSMEM 241 261
FT DOMAIN 262 285
FT TRANSMEM 286 305
FT DOMAIN 306 352
FT CARBOHYD 11 11
FT DISULFID 109 186
SQ SEQUENCE 352 AA; 39648 MW; 4027432B8032F87E CRC64;
Query Match 68.4%; Score 39; DB 1; Length 352;
Best Local Similarity 80.0%; Pred. No. 1.7;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 KKARSMTDVI 11
Db 67 KKLRSMTDKY 76
|||
RESULT 14
CCR4_HUMAN STANDARD; PRT; 352 AA.
ID CCR4_HUMAN P56438;
AC P30991; P56438;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)

DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE C-X-C CHEMOKINE RECEPTOR TYPE 4 (CXC-R4) (CXCR-4) (SDF-1 RECEPTOR)
DE (STROMAL CELL-DERIVED FACTOR 1 RECEPTOR) (FUSIN) (LEUKOCYTE-DERIVED
DE SEVEN TRANSMEMBRANE DOMAIN RECEPTOR) (LESTR) (LCR1) (FB22) (NPYRL)
DE (HM89).
GN CXCR4.
OS Homo sapiens (Human), and Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606, 9598;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93319629; PubMed=8329116;
RA Herzog H., Hort Y.J., Shine J., Selbie L.A.;
RT "Molecular cloning, characterization, and localization of the human
RT homolog to the reported bovine NPY Y3 receptor: lack of NPY binding
RT and activation.";
RL DNA Cell Biol. 12:465-471(1993).
RN [2]
RP SEQUENCE FROM N.A.
RX SPECIES=Human; TISSUE=Brain;
RX MEDLINE=94052833; PubMed=8234909;
RA Jazin E.E., Yoo H., Blomqvist G., Yee F., Weng G., Walker M.W.,
RA Salon J., Larhammar D., Wahlestedt C.R.;
RT "A proposed bovine neuropeptide Y (NPY) receptor cDNA clone, or its
RT human homologue, confers neither NPY binding sites nor NPY
RT responsiveness on transfected cells.";
RL Regul. Pept. 47:247-258(1993).
RN [3]
RP SEQUENCE FROM N.A.
RX SPECIES=Human; TISSUE=Spleen;
RX MEDLINE=93315164; PubMed=8325644;
RA Federspiel B., Delaney A.D., Clark-Lewis I., Jirik F., Duncan A.M.,
RA Schappert K.T., Melhado I.;
RT "Molecular cloning of the cDNA and chromosomal localization of the
RT gene for a putative seven-transmembrane segment (7-TMS) receptor
RT isolated from human spleen.";
RL Genomics 16:707-712(1993).
RN [4]
RP SEQUENCE FROM N.A.
RX SPECIES=Human; TISSUE=Leukocyte;
RX MEDLINE=94103215; PubMed=8276799;
RA Loetscher M., Geiser T., O'Reilly T., Zwaalen R., Baggiolini M.,
RA Moser B.;
RT "Cloning of a human seven-transmembrane domain receptor, LESTR, that
RT is highly expressed in leukocytes.";
RL J. Biol. Chem. 269:232-237(1994).
RN [5]
RP SEQUENCE FROM N.A.
RX SPECIES=Human; TISSUE=Monocytes;
RX MEDLINE=94092629; PubMed=7505609;
RA Nomura H., Nielsen B.W., Matsushima K.;
RT "Molecular cloning of cDNAs encoding a LD78 receptor and putative
RT leukocyte chemotactic peptide receptors.";
RL Int. Immunol. 5:1239-1249(1993).
RN [6]
RP SEQUENCE FROM N.A.
RX SPECIES=Human;
RX Wegner S.A., Ehrenberg P.K., Chang G., Dayhoff D.E., Michael N.L.;
RA Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE FROM N.A.
RX SPECIES=Human;
RX MEDLINE=98258970; PubMed=9599023;
RA Caruz A., Samsom M., Alonso J.M., Alcamí J., Baluev F.,
RA Virelizier J.L., Parmentier M., Arenzana-Seisdedos F.;
RT "Genomic organization and promoter characterization of human CXCR4
RT gene.";
RL FEBS Lett. 426:271-278(1998).
RN [8]
RP SEQUENCE FROM N.A.
RX SPECIES=Human;

RA Xiao L., Weiss S., Qari S., Rudolph D., Hodge T., Lal R.;
RT "Partial resistance to infection by syncytium-inducing primary HIV-1
in exposed uninfected individuals homozygous for CCR5 32bp
deletion.";
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
RN [9]
RP SEQUENCE FROM N.A.
RC SPECIES=Human; TISSUE=Blood;
RA Frodl R., Moepf B., Gierschik P.;
RT "Genomic organization and expression pattern of the human chemokine
receptor CXCR4.";
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
RN [10]
RP SEQUENCE FROM N.A.
RC SPECIES=P.troglodytes;
RA Pretet J.-L., Zerbib A., Girard M., Guillet J.-C., Butor C.;
RT "Chimpanzee CXCR4 and CCR5 act as coreceptors for HIV type 1.";
RL AIDS Res. Hum. Retroviruses 13:1583-1587(1997).
RN [11]
RP FUNCTION.
RA Bleul C.C., Farzan M., Choe H., Parolin C., Clark-Lewis I.,
RT "The lymphocyte chemoattractant SDF-1 is a ligand for LESTR/fusin and
blocks HIV-1 entry.";
RL Nature 382:829-833(1996).
RN [12]
RP FUNCTION.
RA Oberlin E., Amara A., Bachevalier F., Bessia C., Virelizier J.-L.,
RT Arenzana-Seisdedos F., Schwartz O., Heard J.-M., Clark-Lewis I.,
RA Legler D.F., Loetscher M., Baggiolini M., Moser B.;
RT "The CXCR chemokine SDF-1 is the ligand for LESTR/fusin and prevents
infection by T-cell-line-adapted HIV-1.";
RL Nature 382:833-835(1996).
RN [13]
RP ERRATUM.
RA Oberlin E., Amara A., Bachevalier F., Bessia C., Virelizier J.-L.,
RT Arenzana-Seisdedos F., Schwartz O., Heard J.-M., Clark-Lewis I.,
RA Legler D.F., Loetscher M., Baggiolini M., Moser B.;
RL Nature 384:288-288(1996).
RN [14]
RP CHARACTERIZATION OF ITS HIV-1 RECEPTOR FUNCTION.
RA MEDLINE=96217947; PubMed=8629022;
RX Feng Y., Broder C.C., Kennedy P.E., Berger E.A.;
RT "HIV-1 entry cofactor: functional cDNA cloning of a
seven-transmembrane, G protein-coupled receptor.";
RL Science 272:872-877(1996).
CC -!- FUNCTION: RECEPTOR FOR THE C-X-C CHEMOKINE SDF-1. TRANSDUCES A
A CO-RECEPTOR WITH CD4 FOR SYNCYTIIUM-INDUCING STRAINS (SI) (1-
CELL-LINE-ADAPTED) OF HIV-1 VIRUS. IT PROMOTES ENV-MEDIATED FUSION
OF THE VIRUS.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -!- CAUTION: WAS ORIGINALLY THOUGHT TO BE A RECEPTOR FOR NEUROPEPTIDE
Y, TYPE 3 (NPY3-R).
CC
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CC
CC EMBL; L01639; AAA16594.1; -
DR EMBL; M99293; AAA16617.1; -
DR EMBL; X71635; CAA50641.1; -
DR EMBL; L06797; AAA03209.1; -
DR EMBL; D10924; BAA01722.1; -
DR EMBL; AF005058; AAB93982.1; -

DR EMBL; AF052572; AAC34581.1; -
DR EMBL; AF025375; AAB81970.1; -
DR EMBL; Y14739; CAA75034.1; -
DR EMBL; U89798; AAC03718.1; -
DR PIR; S32761; S32761.
DR PIR; A45747; A45747.
DR GCRDB; GCR_0438; -
DR GCRDB; GCR_0448; -
DR GCRDB; GCR_0475; -
DR GCRDB; GCR_0529; -
DR GCRDB; GCR_0903; -
DR GCRDB; GCR_2433; -
DR GCRDB; GCR_2568; -
DR MIM; 162643; -
DR InterPro; IPR000276; -
DR InterPro; IPR001277; -
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPS.
DR PRINTS; PR00645; LCR1ORPHAN.
DR PROSITE; PS00237; G_PROTEIN_RECPT_FL_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECPT_FL_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 39
FT TRANSMEM 40 63
FT DOMAIN 64 79
FT TRANSMEM 80 99
FT DOMAIN 100 110
FT TRANSMEM 111 132
FT DOMAIN 133 154
FT TRANSMEM 155 175
FT DOMAIN 176 200
FT TRANSMEM 201 220
FT DOMAIN 221 240
FT TRANSMEM 241 261
FT DOMAIN 262 285
FT TRANSMEM 286 305
FT DOMAIN 306 352
FT CARBOHYD 11 11
FT DISULFID 109 186
FT SEQUENCE 352 AA; 39745 MW; 8C8476A186786B83 CRC64;
Query Match 68.4%; Score 39; DB 1; Length 352;
Best Local Similarity 80.0%; Pred. No. 1.7;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 KKARSMTDYY 11
DB 67 KKLRSMTDKY 76
RESULT 15
ID CCR4_MACFA STANDARD; PRT; 352 AA.
AC Q28474;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE C-X-C CHEMOKINE RECEPTOR TYPE 4 (CXCR-4) (CXCR-4) (SDF-1 RECEPTOR)
GN (STROMAL CELL-DERIVED FACTOR 1 RECEPTOR) (FUSIN) (LESTR).
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RA Tatsumi M., Takahashi H.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: RECEPTOR FOR THE C-X-C CHEMOKINE SDF-1. TRANSDUCES A
SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.


```
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; D86579; BAA13126.1; -.
DR GCRDB; GCR_1143; -.
DR InterPro; IPR000276; -.
DR InterPro; IPR001277; -.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOPOPSN.
DR PRINTS; PR00645; LCKRIORPHANR.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 39 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 40 63 1 (POTENTIAL).
FT DOMAIN 64 79 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 80 99 2 (POTENTIAL).
FT DOMAIN 100 110 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 111 132 3 (POTENTIAL).
FT DOMAIN 133 154 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 155 175 4 (POTENTIAL).
FT DOMAIN 176 200 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 201 220 5 (POTENTIAL).
FT DOMAIN 221 240 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 241 261 6 (POTENTIAL).
FT DOMAIN 262 285 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 286 305 7 (POTENTIAL).
FT DOMAIN 306 352 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 11 11 N-LINKED (GLCNAC...) (POTENTIAL).
FT DISULFID 109 186 BY SIMILARITY.
SQ SEQUENCE 352 AA; 39753 MW; 432DA6C11859EF8A CRC64;
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Query Match 68.4%; Score 39; DB 1; Length 352;
Best Local Similarity 80.0%; Pred. No. 1.7;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 KKARSMTDYY 11
Db 111111111
67 KKLRSMTDKY 76
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Search completed: May 23, 2001, 15:36:17
Job time: 648 sec

Result No.	Score	Query		Length	DB	ID	Description
		Match					
1	57	100.0	367	11	Q9R1V0	Q9r1v0 mus musculu	
2	49	86.0	360	4	Q9ULX7	Q9ulx7 homo sapien	
3	49	86.0	360	4	Q9ULY6	Q9uly6 homo sapien	
4	43	75.4	350	4	Q9NPB9	Q9npb9 homo sapien	
5	42	73.7	351	6	Q9MYU9	Q9myj9 oryctolagus	
6	41	71.9	334	6	Q9WTZ4	Q9wtz4 felis silve	
7	41	71.9	339	6	Q9TUS4	Q9tus4 lemur varie	
8	41	71.9	339	6	Q9TUS3	Q9tus3 lemur catta	
9	41	71.9	339	6	Q9TUS2	Q9tus2 lemur catta	
10	41	71.9	339	6	Q9TUS1	Q9tus1 lemur varie	
11	41	71.9	339	6	Q9TUS0	Q9tus0 lemur varie	
12	41	71.9	339	6	Q9TQU3	Q9tqu3 lemur catta	
13	41	71.9	351	6	Q9W774	Q9w774 felis silve	
14	41	71.9	373	11	O55193	O55193 rattus norv	
15	39	68.4	332	11	O62973	O62973 rattus norv	
16	39	68.4	334	6	Q9N1P4	Q9n1p4 cercopithec	
17	39	68.4	334	6	Q9N1P2	Q9n1p2 saguinus oe	
18	39	68.4	334	6	Q9N1M3	Q9n1m3 saimiri bol	
19	39	68.4	346	6	O9M2M4	O9m2m4 nvticebus	

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Q9ULY7
ID Q9ULY7 PRELIMINARY; PRT; 360 AA.
AC Q9ULY7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE B-CHEMOKINE RECEPTOR CCR4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kato H., Tsuchiya N., Izumi S., Miyamasu M., Nakajima T., Kawasaki H.,
RA Hirai K., Tokunaga K.;
RT "New variations of human CC-chemokine receptors CCR3 and CCR4.";
RL Genes Immun. 1:97-104(1999).
DR EMBL; AB023889; BAA86966.1; -.
DR INTERPRO; IPR000190; -.
DR INTERPRO; IPR000248; -.
DR INTERPRO; IPR000276; -.
DR INTERPRO; IPR000355; -.
DR INTERPRO; IPR001277; -.
DR INTERPRO; IPR002236; -.
DR INTERPRO; IPR002239; -.
DR PFAM; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PRINTS; PR00241; ANGIOTENSINR.
DR PRINTS; PR00635; ANGIOTENSINR.
DR PRINTS; PR00645; LCRIORPHANR.
DR PRINTS; PR00657; CCHEMOKINER.
DR PRINTS; PR01106; CHEMOKINER1.
DR PRINTS; PR01109; CHEMOKINER4.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
KW Receptor.
FT VARIANT 130 130 V -> L.
SQ SEQUENCE 360 AA; 41388 MW; F52DA1A8D9DA7DDB CRC64;

Query Match 86.0%; Score 49; DB 4; Length 360;
Best Local Similarity 81.8%; Pred. No. 0.078; 1; Indels 0; Gaps 0;
Matches 9; Conservative 1; Mismatches 1;

QY 1 YKKARSMTDVY 11
Db 67 YKRLRSMTDVY 77
II: |||||

RESULT 3
ID Q9ULY6 PRELIMINARY; PRT; 360 AA.
AC Q9ULY6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE B-CHEMOKINE RECEPTOR CCR4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kato H., Tsuchiya N., Izumi S., Miyamasu M., Nakajima T., Kawasaki H.,
RA Hirai K., Tokunaga K.;
RT "New variations of human CC-chemokine receptors CCR3 and CCR4.";
RL Genes Immun. 1:97-104(1999).
DR EMBL; AB023891; BAA86968.1; -.
DR INTERPRO; IPR000190; -.
DR INTERPRO; IPR000248; -.
DR INTERPRO; IPR000276; -.
DR INTERPRO; IPR000355; -.
DR INTERPRO; IPR001277; -.
DR INTERPRO; IPR002236; -.
DR PFAM; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PRINTS; PR00241; ANGIOTENSINR.
DR PRINTS; PR00635; ANGIOTENSINR.
DR PRINTS; PR00645; LCRIORPHANR.
DR PRINTS; PR00657; CCHEMOKINER.
DR PRINTS; PR01106; CHEMOKINER1.
DR PRINTS; PR01109; CHEMOKINER4.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
KW Receptor.
FT VARIANT 130 130 V -> L.
SQ SEQUENCE 360 AA; 41388 MW; F52DA1A8D9DA7DDB CRC64;

Query Match 86.0%; Score 49; DB 4; Length 360;
Best Local Similarity 81.8%; Pred. No. 0.078; 1; Indels 0; Gaps 0;
Matches 9; Conservative 1; Mismatches 1;

QY 1 YKKARSMTDVY 11
Db 67 YKRLRSMTDVY 77
II: |||||

RESULT 3
ID Q9ULY6 PRELIMINARY; PRT; 360 AA.
AC Q9ULY6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE B-CHEMOKINE RECEPTOR CCR4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kato H., Tsuchiya N., Izumi S., Miyamasu M., Nakajima T., Kawasaki H.,
RA Hirai K., Tokunaga K.;
RT "New variations of human CC-chemokine receptors CCR3 and CCR4.";
RL Genes Immun. 1:97-104(1999).
DR EMBL; AB023891; BAA86968.1; -.
DR INTERPRO; IPR000190; -.
DR INTERPRO; IPR000248; -.
DR INTERPRO; IPR000276; -.
DR INTERPRO; IPR000355; -.
DR INTERPRO; IPR001277; -.
DR INTERPRO; IPR002236; -.
DR PFAM; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PRINTS; PR00241; ANGIOTENSINR.
DR PRINTS; PR00635; ANGIOTENSINR.
DR PRINTS; PR00645; LCRIORPHANR.
DR PRINTS; PR00657; CCHEMOKINER.
DR PRINTS; PR01106; CHEMOKINER1.
DR PRINTS; PR01109; CHEMOKINER4.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
KW Receptor.
FT VARIANT 130 130 V -> L.
SQ SEQUENCE 360 AA; 41388 MW; F52DA1A8D9DA7DDB CRC64;

Query Match 86.0%; Score 49; DB 4; Length 360;
Best Local Similarity 81.8%; Pred. No. 0.078; 1; Indels 0; Gaps 0;
Matches 9; Conservative 1; Mismatches 1;

QY 1 YKKARSMTDVY 11
Db 67 YKRLRSMTDVY 77
II: |||||

RESULT 3
ID Q9NPB9 PRELIMINARY; PRT; 350 AA.
AC Q9NPB9;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE CHEMOKINE RECEPTOR (CC CHEMOKINE RECEPTOR) (ORPHAN SEVEN-TRANSMEMBRANE RECEPTOR).
DE RECEPTOR.
GN CCR11 OR CCBP2 OR VSHK1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Schweickart V.L., Epp A., Raport C.J., Gray P.W.;
RT "CCR11 is a Functional Receptor for the Monocyte Chemoattractant Protein Family of Chemokines.";
RT J. Biol. Chem. 275:9550-9556(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20171478; PubMed=10706668;
RA Gosling J., Dairaghi D.J., Wang Y., Hanley M., Talbot D., Miao Z., Schall T.J.;
RT "Cutting edge: identification of a novel chemokine receptor that binds dendritic cell- and T cell-active chemokines including ELC, SLC, and TECK.";
RT J. Immunol. 164:2851-2856(2000).
RN [3]
RP SEQUENCE FROM N.A.
RA Khoja H., Wang G., Lee Ng C.-T., Tucker J., Brown T., Shymala V.;
RT "Cloning of CCR11, an orphan seven transmembrane receptor related to chemokine receptors, expressed abundantly in heart.";
RL Gene 246:229-238(2000).
RN [4]
RP SEQUENCE FROM N.A.
RA Shyamala V., Khoja H.;
RL Submitted (DEC-1998) to the EMBL/GenBank/DBDJ databases.
DR EMBL; AF193507; AAF61299.1; -.
DR EMBL; AF233281; AAF44751.1; -.
DR EMBL; AF110640; AAF59827.1; -.
KW Receptor; Transmembrane.
SQ SEQUENCE 350 AA; 39913 MW; 8E26049D2D5757C8 CRC64;

Query Match 75.4%; Score 43; DB 4; Length 350;
Best Local Similarity 72.7%; Pred. No. 1.2;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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QY 1 YKKARSMTDVY 11
| | | | |
Db 69 YKKQRTKTDVY 79

RESULT 5
Q9MYJ9 PRELIMINARY; PRT; 351 AA.
AC Q9MYJ9
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DE CHEMOKINE RECEPTOR.
GN CCR1.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20153429; PubMed=10686294;
RA Liang M., Rosser M.P., Ng H.P., May K., Bauman J.G., Islam I.,
RA Ghannam A., Kretschmer P.J., Pu H., Dunning L., Snider R.M.,
RA Morrissey M.M., Hesselgeser J., Perez H.D., Horuk R.;
RT "Species selectivity of a small molecule antagonist for the CCR1
chemokine receptor";
RL Eur. J. Pharmacol. 389:41-49(2000).
DR EMBL; AF127527; AAF36452.1; -.
KW Receptor.
SQ SEQUENCE 351 AA; 40534 MW; B3FED6117A141552 CRC64;

Query Match 73.7%; Score 42; DB 6; Length 351;
Best Local Similarity 63.6%; Pred. No. 2;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 YKKARSMTDVY 11
| | | | |
Db 62 YKLRSMTSIY 72

RESULT 6
O97724 PRELIMINARY; PRT; 334 AA.
AC O97724
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE CCR5 CHEMOKINE RECEPTOR (CHEMOKINE RECEPTOR 5).
GN CCR5.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RA Kovacs E.M., Baxter G.D., Robinson W.F.;
RT "Feline peripheral blood mononuclear cells express message for both
CXC and CC type chemokine receptors";
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 1-73 FROM N.A.
RA Leutenegger C.M., Mislin C., Lutz H.;
RT "Molecular cloning and expression of the 5' region of the feline
chemokine receptor (CCR) 5";
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ009815; CAA08838.1; -.
DR EMBL; AF059714; AAC69545.1; -.
DR INTERPRO; IPR000248; -.
DR INTERPRO; IPR000276; -.
DR INTERPRO; IPR000355; -.
DR INTERPRO; IPR001277; -.

DR INTERPRO; IPR002236; -.
DR INTERPRO; IPR002237; -.
DR INTERPRO; IPR002240; -.
DR PFAM; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PRINTS; PR00241; ANGIOTENSINR.
DR PRINTS; PR00645; LCR1ORPHANR.
DR PRINTS; PR00657; CCHEMOKINER.
DR PRINTS; PR01106; CHEMOKINER1.
DR PRINTS; PR01107; CHEMOKINER2.
DR PRINTS; PR01110; CHEMOKINER5.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
KW Receptor.
SQ SEQUENCE 334 AA; 37594 MW; 695B0FE18DB5532E CRC64;

Query Match 71.9%; Score 41; DB 6; Length 334;
Best Local Similarity 80.0%; Pred. No. 2.9;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 KKRSMTDVY 11
| | | | |
Db 59 KKLGRMTDVY 68

RESULT 7
Q9TUS4 PRELIMINARY; PRT; 339 AA.
AC Q9TUS4
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE C-C CHEMOKINE RECEPTOR 5 (FRAGMENT).
GN CCR5.
OS Lemur variegatus (Ruffed lemur) (Varecia variegata).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Strepsirhini; Lemuridae; Varecia.
OX NCBI_TaxID=9455;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
species";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162009; AAD47764.1; -.
DR INTERPRO; IPR000248; -.
DR INTERPRO; IPR000276; -.
DR INTERPRO; IPR000355; -.
DR INTERPRO; IPR001277; -.
DR INTERPRO; IPR002236; -.
DR INTERPRO; IPR002237; -.
DR INTERPRO; IPR002238; -.
DR INTERPRO; IPR002240; -.
DR PFAM; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PRINTS; PR00241; ANGIOTENSINR.
DR PRINTS; PR00645; LCR1ORPHANR.
DR PRINTS; PR00657; CCHEMOKINER.
DR PRINTS; PR01106; CHEMOKINER1.
DR PRINTS; PR01107; CHEMOKINER2.
DR PRINTS; PR01108; CHEMOKINER3.
DR PRINTS; PR01110; CHEMOKINER5.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 38664 MW; B53CFE4F66B09E1A CRC64;

Query Match 71.9%; Score 41; DB 6; Length 339;
Best Local Similarity 70.0%; Pred. No. 3;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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QY      2 KKARSMTDVIY 11
Db      52 KKLKSMTDIY 61

RESULT 8
Q9TUS3
ID      Q9TUS3          PRELIMINARY;      PRT;      339 AA.
AC      Q9TUS2;
DT      01-MAY-2000 (TReMBLrel. 13, Created)
DT      01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT      01-OCT-2000 (TReMBLrel. 15, Last annotation update)
DE      C-C CHEMOKINE RECEPTOR 5 (FRAGMENT).
GN      CCR5.
OS      Lemur catta (Ring-tailed lemur).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Strepsirrhini; Lemnidae; Lemur.
OX      NCBI_TaxID=9447;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA      Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT      "Sequences of the CCR5 genes from diverse simian and prosimian
RT      species.";
RL      Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AF162010; AAD47765.1; -
DR      INTERPRO; IPR000248; -
DR      INTERPRO; IPR000276; -
DR      INTERPRO; IPR000355; -
DR      INTERPRO; IPR001277; -
DR      INTERPRO; IPR002236; -
DR      INTERPRO; IPR002237; -
DR      INTERPRO; IPR002238; -
DR      INTERPRO; IPR002240; -
DR      PFAM; PF00001; 7tm_1; 1.
DR      PRINTS; PR00237; GPCRHHODOPSN.
DR      PRINTS; PR00241; ANGIOTENSINR.
DR      PRINTS; PR00645; LCR1ORPHANR.
DR      PRINTS; PR00657; CCHEMOKINER.
DR      PRINTS; PR01106; CHEMOKINER1.
DR      PRINTS; PR01107; CHEMOKINER2.
DR      PRINTS; PR01108; CHEMOKINER3.
DR      PRINTS; PR01110; CHEMOKINER5.
DR      PROSITE; PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
KW      Receptor.
FT      NON_TER      1      1
FT      NON_TER      339      339
SQ      SEQUENCE      339 AA; 38678 MW; 4CF60C5648C8DC1 CRC64;

Query Match      71.9%; Score 41; DB 6; Length 339;
Best Local Similarity 70.0%; Pred. No. 3;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      2 KKARSMTDVIY 11
Db      52 KKLKSMTDIY 61

RESULT 9
Q9TUS2
ID      Q9TUS2          PRELIMINARY;      PRT;      339 AA.
AC      Q9TUS2;
DT      01-MAY-2000 (TReMBLrel. 13, Created)
DT      01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT      01-OCT-2000 (TReMBLrel. 15, Last annotation update)
DE      C-C CHEMOKINE RECEPTOR 5 (FRAGMENT).
GN      CCR5.
OS      Lemur catta (Ring-tailed lemur).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Strepsirrhini; Lemnidae; Lemur.
OX      NCBI_TaxID=9447;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA      Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT      "Sequences of the CCR5 genes from diverse simian and prosimian
RT      species.";
RL      Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AF162013; AAD47768.1; -
DR      INTERPRO; IPR000248; -
DR      INTERPRO; IPR000276; -
DR      INTERPRO; IPR000355; -
DR      INTERPRO; IPR001277; -
DR      INTERPRO; IPR002236; -
DR      INTERPRO; IPR002237; -
DR      INTERPRO; IPR002238; -
DR      INTERPRO; IPR002240; -
DR      PFAM; PF00001; 7tm_1; 1.
DR      PRINTS; PR00237; GPCRHHODOPSN.
DR      PRINTS; PR00241; ANGIOTENSINR.
DR      PRINTS; PR00645; LCR1ORPHANR.
DR      PRINTS; PR00657; CCHEMOKINER.
DR      PRINTS; PR01106; CHEMOKINER1.
DR      PRINTS; PR01107; CHEMOKINER2.
DR      PRINTS; PR01108; CHEMOKINER3.
DR      PRINTS; PR01110; CHEMOKINER5.
DR      PROSITE; PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
KW      Receptor.
FT      NON_TER      1      1
FT      NON_TER      339      339
SQ      SEQUENCE      339 AA; 38678 MW; 4CF60C5648C8DC1 CRC64;

Query Match      71.9%; Score 41; DB 6; Length 339;
Best Local Similarity 70.0%; Pred. No. 3;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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RN      [1]
RP      SEQUENCE FROM N.A.
RA      Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA      Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT      "Sequences of the CCR5 genes from diverse simian and prosimian
RT      species.";
RL      Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AF162012; AAD47767.1; -
DR      INTERPRO; IPR000248; -
DR      INTERPRO; IPR000276; -
DR      INTERPRO; IPR000355; -
DR      INTERPRO; IPR001277; -
DR      INTERPRO; IPR002236; -
DR      INTERPRO; IPR002237; -
DR      INTERPRO; IPR002238; -
DR      INTERPRO; IPR002240; -
DR      PFAM; PF00001; 7tm_1; 1.
DR      PRINTS; PR00237; GPCRHHODOPSN.
DR      PRINTS; PR00241; ANGIOTENSINR.
DR      PRINTS; PR00645; LCR1ORPHANR.
DR      PRINTS; PR00657; CCHEMOKINER.
DR      PRINTS; PR01106; CHEMOKINER1.
DR      PRINTS; PR01107; CHEMOKINER2.
DR      PRINTS; PR01108; CHEMOKINER3.
DR      PRINTS; PR01110; CHEMOKINER5.
DR      PROSITE; PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
KW      Receptor.
FT      NON_TER      1      1
FT      NON_TER      339      339
SQ      SEQUENCE      339 AA; 38646 MW; BA7E73C6F05E2CA4 CRC64;

Query Match      71.9%; Score 41; DB 6; Length 339;
Best Local Similarity 70.0%; Pred. No. 3;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      2 KKARSMTDVIY 11
Db      52 KKLKSMTDIY 61

RESULT 10
Q9TUS1
ID      Q9TUS1          PRELIMINARY;      PRT;      339 AA.
AC      Q9TUS1;
DT      01-MAY-2000 (TReMBLrel. 13, Created)
DT      01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT      01-OCT-2000 (TReMBLrel. 15, Last annotation update)
DE      C-C CHEMOKINE RECEPTOR 5 (FRAGMENT).
GN      CCR5.
OS      Lemur variegatus (Ruffed lemur) (Varecia variegata).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Strepsirrhini; Lemnidae; Varecia.
OX      NCBI_TaxID=9455;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA      Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT      "Sequences of the CCR5 genes from diverse simian and prosimian
RT      species.";
RL      Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AF162013; AAD47768.1; -
DR      INTERPRO; IPR000248; -
DR      INTERPRO; IPR000276; -
DR      INTERPRO; IPR000355; -
DR      INTERPRO; IPR001277; -
DR      INTERPRO; IPR002236; -
DR      INTERPRO; IPR002237; -
DR      INTERPRO; IPR002238; -
DR      INTERPRO; IPR002240; -
DR      PFAM; PF00001; 7tm_1; 1.
DR      PRINTS; PR00237; GPCRHHODOPSN.
DR      PRINTS; PR00241; ANGIOTENSINR.

```

DR PRINTS; PR00645; LCR1ORPHANR.
DR PRINTS; PR00657; CCHEMOKINER1.
DR PRINTS; PR01106; CHEMOKINER1.
DR PRINTS; PR01107; CHEMOKINER2.
DR PRINTS; PR01108; CHEMOKINER3.
DR PRINTS; PR01110; CHEMOKINER5.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 38682 MW; 6A770AFCA7E02F6 CRC64;

Query Match 71.9%; Score 41; DB 6; Length 339;
Best Local Similarity 70.0%; Pred. No. 3;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 KKARSMTDVIY 11
|| :||||:|
Db 52 KKLKSMTDIY 61

RESULT 11
Q9TUS0 PRELIMINARY; PRT; 339 AA.
AC Q9TUS0;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE C-C CHEMOKINE RECEPTOR 5 (FRAGMENT).
GN CCR5.
OS Lemur variegatus (Ruffed lemur) (Varecia variegata).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Strepsirhini; Lemnridae; Varecia.
OX NCBI_TaxID=9455;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162014; AAD47769.1; -
DR INTERPRO; IPR000248; -
DR INTERPRO; IPR000276; -
DR INTERPRO; IPR000355; -
DR INTERPRO; IPR001277; -
DR INTERPRO; IPR002236; -
DR INTERPRO; IPR002237; -
DR INTERPRO; IPR002238; -
DR INTERPRO; IPR002240; -
DR PFAM; PF00001; 7tm1; 1.
DR PRINTS; PR00237; GPCRHOPOPSN.
DR PRINTS; PR00241; ANGIOTENSINR.
DR PRINTS; PR00645; LCR1ORPHANR.
DR PRINTS; PR00657; CCHEMOKINER.
DR PRINTS; PR01106; CHEMOKINER1.
DR PRINTS; PR01107; CHEMOKINER2.
DR PRINTS; PR01108; CHEMOKINER3.
DR PRINTS; PR01110; CHEMOKINER5.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 38713 MW; 77DCE451AA3A4CB6 CRC64;

Query Match 71.9%; Score 41; DB 6; Length 339;
Best Local Similarity 70.0%; Pred. No. 3;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 KKARSMTDVIY 11
|| :||||:|

Db 52 KKLKSMTDIY 61
RESULT 12
Q9TQU3 PRELIMINARY; PRT; 339 AA.
AC Q9TQU3;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE C-C CHEMOKINE RECEPTOR 5 (FRAGMENT).
GN CCR5.
OS Lemur catta (Ring-tailed lemur).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Strepsirhini; Lemnridae; Lemur.
OX NCBI_TaxID=9447;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162011; AAD47766.1; -
DR EMBL; AF162008; AAD47763.1; -
DR INTERPRO; IPR000248; -
DR INTERPRO; IPR000276; -
DR INTERPRO; IPR000355; -
DR INTERPRO; IPR001277; -
DR INTERPRO; IPR002236; -
DR INTERPRO; IPR002237; -
DR INTERPRO; IPR002238; -
DR INTERPRO; IPR002240; -
DR PFAM; PF00001; 7tm1; 1.
DR PRINTS; PR00237; GPCRHOPOPSN.
DR PRINTS; PR00241; ANGIOTENSINR.
DR PRINTS; PR00645; LCR1ORPHANR.
DR PRINTS; PR00657; CCHEMOKINER.
DR PRINTS; PR01106; CHEMOKINER1.
DR PRINTS; PR01107; CHEMOKINER2.
DR PRINTS; PR01108; CHEMOKINER3.
DR PRINTS; PR01110; CHEMOKINER5.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 38712 MW; 8A2D0D74093A56AE CRC64;

Query Match 71.9%; Score 41; DB 6; Length 339;
Best Local Similarity 70.0%; Pred. No. 3;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 KKARSMTDVIY 11
|| :||||:|
Db 52 KKLKSMTDIY 61

RESULT 13
O97774 PRELIMINARY; PRT; 351 AA.
AC O97774;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE CCR5.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RA Lerner D.L., Elder J.H.;

"Feline CCR5";
 RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U92796; AAC00729.1; -
 DR INTERPRO; IPR000248; -
 DR INTERPRO; IPR000276; -
 DR INTERPRO; IPR000355; -
 DR INTERPRO; IPR000923; -
 DR INTERPRO; IPR002236; -
 DR INTERPRO; IPR002237; -
 DR INTERPRO; IPR002240; -
 DR PFAM; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PRINTS; PR00241; ANGIOTENSINR.
 DR PRINTS; PR00657; CCHEMOKINER.
 DR PRINTS; PR01106; CHEMOKINER1.
 DR PRINTS; PR01107; CHEMOKINER2.
 DR PRINTS; PR01110; CHEMOKINER5.
 DR PROSITE; PS00196; COPPER_BLUE; UNKNOWN_1.
 DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
 SQ SEQUENCE 351 AA; 39601 MW; 14EAE1C32D42B7FB CRC64;

Query Match 71.9%; Score 41; DB 6; Length 351;
 Best Local Similarity 80.0%; Pred. No. 3.1; Mismatches 2; Indels 0; Gaps 0;
 Matches 8; Conservative 0;

QY 2 KKARSMTDVIY 11
 || | |||||
 DB 59 KKLKGMTDVIY 68

RESULT 14
 ID 055193 PRELIMINARY; PRT; 373 AA.
 AC 055193;
 DT 01-JUN-1998 (TREMBLrel. 06, Created)
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
 DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
 DE C-C CHEMOKINE RECEPTOR TYPE 2 (C-C CCR-2) (CCR-2) (CCR2).
 GN CMKR2.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SPRAGUE DAWLEY;
 RX MEDLINE=98318173; PubMed=9655467;
 RA Jiang Y., Salafranca M.N., Adhikari S., Xia Y., Feng L., Sonntag M.K.,
 RA deFebre C.M., Pennell N.A., Streit W.J., Harrison J.K.;
 RT "Chemokine receptor expression in cultured glia and rat experimental
 RT allergic encephalomyelitis";
 RL J. Neuroimmunol. 86:1-12(1998).
 CC -!- FUNCTION: RECEPTOR FOR THE MCP-1 (JE), MCP-3 (FIC) AND MCP-5
 CC CHEMOKINES. TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR
 CC CALCIUM IONS LEVEL (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN LUNG, SPLEEN, KIDNEY, THYMUS AND
 CC MACROPHAGES.
 CC -!- INDUCTION: IN ANIMALS IN WHICH EXPERIMENTAL ALLERGIC
 CC ENCEPHALOMYELITIS (EAE) HAS BEEN INDUCED.
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 DR EMBL; U77349; AAC03242.1; -
 DR INTERPRO; IPR000276; -
 DR INTERPRO; IPR000355; -
 DR INTERPRO; IPR002237; -
 DR PFAM; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PRINTS; PR00657; CCHEMOKINER.
 DR PRINTS; PR01107; CHEMOKINER2.
 DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
 KW G-protein coupled receptor; Transmembrane.
 FT DOMAIN 1 60 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 61 81 POTENTIAL.
 FT DOMAIN 82 91 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 92 112 POTENTIAL.
 FT DOMAIN 113 128 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 129 149 POTENTIAL.
 FT DOMAIN 150 170 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 171 191 POTENTIAL.
 FT DOMAIN 192 220 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 221 241 POTENTIAL.
 FT DOMAIN 242 256 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 257 277 POTENTIAL.
 FT DOMAIN 278 301 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 302 322 POTENTIAL.
 FT DOMAIN 323 373 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 126 203 BY SIMILARITY.
 SQ SEQUENCE 373 AA; 42763 MW; 2E7BB012F5D6FD09 CRC64;

Query Match 71.9%; Score 41; DB 11; Length 373;
 Best Local Similarity 70.0%; Pred. No. 3.3;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 KKARSMTDVIY 11
 || | |||||
 DB 84 KKLKGMTDIY 93

RESULT 15
 ID 062973 PRELIMINARY; PRT; 332 AA.
 AC 062973;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE CHEMOKINE RECEPTOR LCRI.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SPRAGUE-DAWLEY;
 RA Wong M., Xin W.W., Duman R.S.;
 RL Mol. Psych. 0:0-0(0).
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 DR EMBL; U54791; AAB01981.1; -
 DR INTERPRO; IPR000276; -
 DR INTERPRO; IPR001277; -
 DR INTERPRO; IPR003006; -
 DR PFAM; PF00001; 7tm_1; 2.
 DR PRINTS; PR00845; LCRIORPHANR.
 DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; 1.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 SQ SEQUENCE 332 AA; 37442 MW; 0FFED9BF8C7150BE CRC64;

Query Match 68.4%; Score 39; DB 11; Length 332;
 Best Local Similarity 80.0%; Pred. No. 7.4;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 KKARSMTDVIY 11
 || | |||||
 DB 64 KKLKGMTDKY 73

Search completed: May 23, 2001, 15:35:12
 Job time: 618 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 23, 2001, 15:28:27 ; Search time 184.73 Seconds
(without alignments)
5.570 Million cell updates/sec

Title: US-08-887-977-10_COPY_79_96

Perfect score: 90

Sequence: 1 MATADILFVLTLPFAVS 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 390729 seqs, 57163235 residues

Total number of hits satisfying chosen parameters: 390729

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	90	100.0	365	19 W48086	Human dendritic ce
2	90	100.0	365	21 Y97077	Primate (human) ch
3	78	86.7	40	19 W56165	Partial amino acid
4	78	86.7	358	15 R53745	Partial sequence o
5	78	86.7	358	21 B21689	Human 7TM receptor
6	78	86.7	361	20 W97348	An Epstein-Barr vi
7	78	86.7	378	15 R54079	Epstein Barr virus
8	78	86.7	378	15 R53744	Putative seven tra
9	78	86.7	378	19 W48724	Human V31 seven tr
10	78	86.7	378	19 W56164	G-protein coupled
11	78	86.7	378	19 W53622	Epstein Barr virus

12	78	86.7	378	21 B21688	Human 7TM receptor
13	78	86.7	378	21 Y90629	Human G protein-co
14	78	86.7	378	21 Y90663	Human mutant G pro
15	78	86.7	378	22 B50859	Human CCR7. Homo
16	78	86.7	410	15 R53743	Putative seven tra
17	78	86.7	410	19 W48723	Polypeptide sequen
18	78	86.7	410	21 B21687	Genomic clone of 7
19	75	83.3	24	20 Y39273	G-protein coupled
20	75	83.3	32	20 Y39262	G-protein coupled
21	75	83.3	116	21 G01911	Human secreted pro
22	75	83.3	337	15 R53753	Seven transmembran
23	75	83.3	337	19 W48734	Human RM3 seven tr
24	75	83.3	337	21 B21698	Human 7TM receptor
25	75	83.3	352	13 R27792	New platelet facto
26	75	83.3	352	16 R68812	Human monocyte PF4
27	75	83.3	352	16 R80757	Chemokine superfam
28	75	83.3	352	20 Y39993	Human CXCR4 protei
29	75	83.3	352	21 Y52507	G-protein coupled
30	75	83.3	356	20 W97362	Human CXCR4 protei
31	75	83.3	357	21 B19605	G-protein coupled
32	75	83.3	357	21 Y90615	Human CC chemokine
33	75	83.3	357	21 Y90649	Human G protein-co
34	75	83.3	359	19 W64778	Human mutant G pro
35	75	83.3	359	20 Y39994	A murine CXCR4 chemo
36	72	80.0	359	15 R53747	Mouse CXCR4 protei
37	72	80.0	359	19 W48728	Seven transmembran
38	72	80.0	359	21 B21691	Murine V31 seven t
39	72	80.0	378	21 B21699	7TM receptor prote
40	71	78.9	354	19 W54037	Mouse CC-CKR5 prot
41	70	77.8	312	15 W48717	G-protein coupled
42	70	77.8	312	17 W02689	G-protein coupled
43	70	77.8	350	20 Y57291	Mouse BGCR protei
44	70	77.8	355	13 R28272	Sequence in a high
45	70	77.8	355	16 R80950	Recombinant high a

ALIGNMENTS

RESULT 1

W48086	ID	W48086 standard; Protein; 365 AA.
XX	AC	W48086;
XX	DT	11-JUN-1998 (first entry)
XX	DE	Human dendritic cell chemokine receptor.
XX	DE	Human; thymus expressed chemokine; TECK; MIP-3alpha; MIP-3beta;
KW	KW	receptor; dendritic cell; macrophage; inflammation; asthma.
XX	OS	Homo sapiens.
XX	XX	Key Location/Qualifiers
PH	PH	Misc-difference 193
FT	FT	/note= "encoded by CAN"
XX	XX	WO9801557-A2.
PN	PN	15-JAN-1998.
PD	PD	02-JUL-1997; 97WO-US10819.
XX	XX	04-JUN-1997; 97US-0048593.
PR	PR	05-JUL-1996; 96US-0675814.
PR	PR	11-OCT-1996; 96US-0028329.
XX	XX	(SCHE) SCHERING CORP.
PA	PA	Gish KC, Schall TJ, Vicari A, Wang W, Zlotnik A;
PI	PI	WPI; 1998-101054/09.
XX	XX	
DR	DR	

DR N-PSDB; V15418.
 XX Novel chemokines, e.g. thymus expressed chemokine - used for
 PT treating inflammatory conditions including asthma.
 XX
 XX Claim 3: Page 94-95; 202pp; English.
 XX
 CC The present sequence represents human dendritic cell chemokine receptor.
 CC Antibodies which bind to the protein can be used in detecting or
 CC diagnosing various immunological conditions related to expression
 CC of the protein. The nucleic acid can be used for screening and
 CC isolating DNA clones for the chemokines, especially from other
 CC species. The chemokine can be used in the treatment of conditions
 CC associated with abnormal physiology or development, including
 CC inflammatory conditions such as asthma.
 XX
 XX Sequence 365 AA;

Query Match 100.0%; Score 90; DB 19; Length 365;
 Best Local Similarity 100.0%; Pred. No. 1.6e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAIADILFVLTLPFWAVS 18
 DB 79 maiadilfvltlpfwavs 96
 |||||

RESULT 2
 Y97077
 ID Y97077 standard; Protein: 365 AA.
 XX
 AC Y97077;
 XX
 DT 04-DEC-2000 (first entry)
 DE
 DE Primate (human) chemokine receptor CCR6.
 XX
 KW MIP-3-alpha; chemokine; CCR6 receptor; ligand; cytostatic; agonist;
 KW antagonist; anti-psoriatic; dermatological; immunosuppressive;
 KW anti-inflammatory.
 XX

OS Homo sapiens.
 PH Key Location/Qualifiers
 FT Misc-difference 193
 FT /note= "Encoded by CAN#"

XX WO200046248-A1.
 XX
 XX 10-AUG-2000.
 XX
 XX 02-FEB-2000; 2000WO-US00511.
 XX
 XX 03-FEB-1999; 99US-0244281.
 XX (SCHE) SCHERING CORP.
 XX
 XX Oldham ER, Honey B, Dieu-Nosjean M, Caux C, Zlotnik A;
 XX WPI; 2000-543477/49.
 XX N-PSDB; A51971.
 XX
 PT Novel methods for modulating the migration of cells within or to the
 PT skin using MIP-3-alpha or CCR6 agonists or antagonists, useful for
 PT treating skin disorders, e.g. cancer
 XX
 PS Disclosure; Page 53-54; 61pp; English.

XX The MIP-3-alpha chemokine is expressed in inflamed skin cells. This
 CC chemokine is the ligand for the CCR6 receptor. MIP-3-alpha or CCR6
 CC agonists or antagonists can be used to modulate the migration of a cell
 CC within or to the skin of a mammal. MIP-3-alpha can be used to purify a

CC population of cells expressing a MIP-3-alpha receptor. The methods are
 CC useful for treating a mammalian subject with a skin disease or condition,
 CC e.g. cancer, metastasis, psoriasis, atopic or contact dermatitis,
 CC systemic lupus erythematosus and lichen ruber planus, or for treating
 CC skin transplants or grafts.
 XX

SQ Sequence 365 AA;

Query Match 100.0%; Score 90; DB 21; Length 365;
 Best Local Similarity 100.0%; Pred. No. 1.6e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAIADILFVLTLPFWAVS 18
 DB 79 maiadilfvltlpfwavs 96
 |||||

RESULT 3
 W56165
 ID W56165 standard; Peptide: 40 AA.
 XX
 AC W56165;
 XX
 DT 20-JUL-1998 (first entry)
 XX
 DE Partial amino acid sequence of an opiate/opioid receptor protein.
 XX
 KW Lymphocyte R7G; EB11; G-protein coupled receptor;
 KW opiate/opioid recognition site; opiate; opioid; opioid binding protein;
 KW screening; lymphocyte receptor; compound; agonist; antagonist;
 KW lymphocyte receptor protein; immune-cell specific lymphocyte receptor;
 KW neuronal type opioid receptor.
 XX

OS Homo sapiens.

XX US5753516-A.
 XX
 XX 19-MAY-1998.
 XX
 XX 03-FEB-1995; 95US-0383751.
 XX
 XX 03-FEB-1995; 95US-0383751.
 XX

PA (FINB/) FINBERG R W.
 PA (HEAG/) HEAGY W E.

XX Finberg RW, Heagy WE;
 XX WPI; 1998-311410/27.
 XX

XX Screening assay for lymphocyte opioid receptor ligands - using
 PT recombinant receptor protein

XX Disclosure; Fig 17; 70pp; English.

XX The present sequence represents the partial amino acid sequence in
 CC the second transmembrane region of an opiate/opioid receptor protein.
 CC The specification describes a novel lymphocyte R7G, termed EB11. R7G
 CC proteins are part of the G-protein coupled receptor superfamily. EB11 is
 CC a functional opiate/opioid recognition site that probably plays a major
 CC role in mediating the effects that opiate/opioids have on lymphocytes.
 CC The EB11 protein is an opioid binding protein that is displayed on the
 CC surface of lymphocytes. A process for screening a candidate substance for
 CC ability to interact with a lymphocyte receptor comprises selecting a
 CC candidate substance having a chemical structure or biological activity
 CC suggestive of an ability to mimic the biological activity of an
 CC opiate, opioid drug or opioid peptide having known binding affinity for
 CC EB11. The ability of the candidate substance is tested to interact with
 CC the lymphocyte receptor protein. This method can be used to screen for
 CC agonists or antagonists to the lymphocyte receptor protein. The method
 CC can be modified and used to screen for agonists or antagonists to the
 CC immune-cell specific lymphocyte receptor polypeptide or the neuronal type

CC opioid receptor polypeptide.
XX
SQ Sequence 40 AA;

Query Match 86.7%; Score 78; DB 19; Length 40;
Best Local Similarity 77.8%; Pred. No. 1.7e-06;
Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAIADILFVLTPFWAVS 18
:|:||||:|||||
Db 20 lavadilfltltpfwavs 37

RESULT 4
ID R53745
XX R53745 standard; Protein; 358 AA.
AC R53745;
XX
DT 02-FEB-1995 (first entry)
XX
DE Partial sequence of seven transmembrane receptor (V31).
XX
KW Primer; seven transmembrane receptor; receptor; amplification; PCR;
KW polymerase chain reaction.
XX
OS Homo sapiens.
XX
PN W09412635-A.
XX
PD 09-JUN-1994.
XX
PF 17-NOV-1993; 93WO-US11153.
XX
PR 17-NOV-1992; 92US-0977452.
XX
PA (ICOS-) ICOS CORP.
XX
PI Godiska R, Gray PW, Schweickart VL;
XX
DR WPI; 1994-200264/24.
DR N-PSDB; Q66162.
XX
PT DNA encoding seven transmembrane receptors - used to develop
PT prods. for use as therapeutic or diagnostic agents for conditions
PT involving the receptors.
XX
PS Example 3; Page 56-57; 100pp; English.
XX

CC Two primers (Q66148, Q66149) were used to amplify human genomic DNA
CC purified from leukocytes. Approximately 1000 clones were isolated
CC after the initial amplification reaction and probed with sequences
CC specific for seven transmembrane receptors IL8R1, AT2R and R20.
CC Clones which did not hybridise were then chosen for sequence
CC analysis. Three new clones were identified that appeared to encode
CC seven transmembrane receptor segments. Two more primers (Q66151,
CC Q66152) were used to isolate a full length version of one of these
CC clones designated V31 (See Q66153). This is the sequence encoded
CC by exon 3 of the V31 genomic clone.
XX
SQ Sequence 358 AA;

Query Match 86.7%; Score 78; DB 15; Length 358;
Best Local Similarity 77.8%; Pred. No. 1.7e-05;
Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAIADILFVLTPFWAVS 18
:|:||||:|||||
Db 80 lavadilfltltpfwavs 97

RESULT 5

B21689
ID B21689 standard; Protein; 358 AA.
XX
AC B21689;
XX
DT 26-JAN-2001 (first entry)
XX
DE Human 7TM receptor V31-B cDNA clone exon 1 protein.
XX
KW Seven transmembrane receptor; 7TM; heptahelical; serpentine;
KW G-protein-coupled; V28; V31; V112; R20; R2; R12; Rm3; gene therapy;
KW cancer.
XX
OS Homo sapiens.
XX
PN US6107475-A.
XX
PD 22-AUG-2000.
XX
PF 26-APR-1999; 99US-0299843.
XX
PR 17-MAY-1994; 94US-0245242.
PR 01-JUN-1998; 98US-0088337.
PR 17-NOV-1992; 92US-0977452.
PR 17-NOV-1993; 93US-0153848.
XX
PA (ICOS-) ICOS CORP.

XX
PI Schweickart VL, Gray PW, Godiska R;
XX
DR WPI; 2000-571335/53.
DR N-PSDB; A91709.
XX
PT Polynucleotide encoding seven transmembrane receptors, antibody
PT specific to the receptor, agonist and antagonist of the receptor useful
PT for treating inflammation in a mammal
XX
PS Example 3; Columns 49-52; 61pp; English.
XX
CC The present sequence is a novel seven transmembrane (7TM) receptors
CC (also known as heptahelical, serpentine or G-protein-coupled receptors).
CC The coding sequence for the present sequence may be used for gene
CC therapy for diseases such as cancer.
XX
SQ Sequence 358 AA;

Query Match 86.7%; Score 78; DB 21; Length 358;
Best Local Similarity 77.8%; Pred. No. 1.7e-05;
Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAIADILFVLTPFWAVS 18
:|:||||:|||||
Db 80 lavadilfltltpfwavs 97

RESULT 6
W97348
ID W97348 standard; Protein; 361 AA.
XX
AC W97348;
XX
DT 12-MAY-1999 (first entry)
XX
DE An Epstein-barr virus-induced G-protein coupled receptor.
XX

KW Epstein-barr virus-induced G-protein coupled receptor; EB1 3;
KW splicing variant; EB1 1; vaccine; infection; HIV-1; HIV-2; pain;
KW cancer; anorexia; bulimia; asthma; parkinson's disease;
KW acute heart failure; hypotension; hypertension; urinary retention;
KW osteoporosis; angina pectoris; myocardial infarction; ulcer; allergy;
KW benign prostatic hypertrophy; psychotic disorder; neurological disorder;

KW anxiety; schizophrenia; manic depression; delirium; dementia;
 KW severe mental retardation; dyskinesias; Huntington's disease;
 KW Gilles de la Tourette's syndrome.

XX Homo sapiens.

XX EP894854-A2.

XX 03-FEB-1999.

PD 04-DEC-1997; 97EP-0309791.

PF 29-JUL-1997; 97US-0902294.

PR (SMIK) SMITHKLINE BEECHAM CORP.

XX Zhu Y;

XX WPI; 1999-108346/10.

DR N-PSDB; X15857.

XX New Epstein-barr virus-induced G-protein coupled receptor (EBI 3)
 PT gene and protein - useful as diagnostic reagents and for prevention
 PT and treatment of HIV infections and cancer

XX Claim 2; Page 7; 20pp; English.

XX The present sequence represents a Epstein-barr virus-induced G-protein
 CC coupled receptor (EBI 3), which is a splicing variant of EBI 1. EBI 3
 CC antibodies are useful for inducing an immune response to immunize and
 CC prevent disease, and for isolating EBI 3 clones or purifying the
 CC polypeptides by affinity chromatography. EBI 3 polypeptides can be
 CC administered directly or as a vaccine to inoculate against disease.
 CC Diseases diagnosed, prevented and treated include: bacterial, fungal,
 CC viral and protozoan infections, particularly infections caused by HIV-1
 CC or HIV-2; pain; cancers; anorexia; bulimia; asthma; Parkinson's disease;
 CC acute heart failure; hypotension; hypertension; urinary retention;
 CC osteoporosis; angina pectoris; myocardial infarction; ulcers; allergies;
 CC benign prostatic hypertrophy; and psychotic and neurological disorders,
 CC including anxiety, schizophrenia, manic depression, delirium, dementia,
 CC severe mental retardation and dyskinesias, such as Huntington's disease
 CC or Gilles de la Tourette's syndrome.

XX Sequence 361 AA;

Query Match 86.7%; Score 78; DB 20; Length 361;
 Best Local Similarity 77.8%; Pred. No. 1.7e-05;
 Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 MAIADILFVLTLFPWAVS 18

Db 100 lavadilfvltpfwavs 117

RESULT 7

R54079
 ID R54079 standard; Protein; 378 AA.

XX R54079;

XX 03-FEB-1995 (first entry)

DE Epstein Barr virus induced (EBI-1) polypeptide.

XX Epstein Barr virus; EBV; induction; detection; diagnosis;
 KW lymphocytes; antigen; growth; differentiation; mediator;
 KW infectious mononucleosis.

XX Homo sapiens.

XX Key Location/Qualifiers
 FT Region 1..24

FT /label= Hydrophobic region.
 FT /note= "Predicted to be a signal peptide for
 FT membrane translocation."
 FT 36
 FT Modified-site
 FT /note= "Potential N-linked glycosylation site."
 FT 60..86
 FT Region
 FT /label= Hydrophobic region.
 FT 96..116
 FT Region
 FT /label= Hydrophobic region.
 FT 131..152
 FT Region
 FT /label= Hydrophobic region.
 FT 151..159
 FT Region
 FT /note= "This sequences motif
 FT (S-[I/V]-D-R-[Y/F]-X-X-X) is highly
 FT conserved among a large number of G-protein
 FT coupled receptors."
 FT 171..191
 FT Region
 FT /label= Hydrophobic region.
 FT 220..247
 FT Region
 FT /label= Hydrophobic region.
 FT 264..289
 FT Region
 FT /label= Hydrophobic region.
 FT 292
 FT Modified-site
 FT /note= "Potential N-linked glycosylation site."
 FT 314..331
 FT Region
 FT /label= Hydrophobic region.

XX WO9412519-A.

PN 09-JUN-1994.

XX 08-OCT-1993; 93WO-US09636.

XX 25-NOV-1992; 92US-0980518.

XX (BGHM) BRIGHAM & WOMENS HOSPITAL.

PA Birkenbach M, Kieff E;

XX WPI; 1994-200183/24.

DR N-PSDB; Q64125.

XX DNA coding for Epstein Barr Virus induced (EBI) polypeptide(s)
 PT and antibodies to EBI1, 2 and 3 - useful for detecting EBV by
 PT hybridisation or by immunoassay

XX Claim 8; Page 54-56; 84pp; English.

XX EBV infected B lymphocytes recapitulate features of antigen
 CC stimulation in enlarging, increasing RNA synthesis, expressing
 CC activation antigens and adhesion molecules, secreting Ig and
 CC proliferating. Unlike antigen stimulated B lymphocytes, EBV
 CC infected B lymphocytes continue to proliferate (in vitro) as
 CC immortalised lymphoblastoid cell lines. Because of the similar
 CC effects of EBV and antigen, EBV induced genes are likely to include
 CC mediators of antigen induced B lymphocyte growth or differentiation.

XX Sequence 378 AA;

Query Match 86.7%; Score 78; DB 15; Length 378;
 Best Local Similarity 77.8%; Pred. No. 1.8e-05;
 Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 MAIADILFVLTLFPWAVS 18

Db 100 lavadilfvltpfwavs 117

RESULT 8

R53744

ID R53744 standard; Protein; 378 AA.

XX

```

AC R53744;
XX
XX 02-FEB-1995 (first entry)
XX
XX Putative seven transmembrane receptor (V31).
XX
XX Primer; seven transmembrane receptor; receptor; amplification; PCR;
KW polymerase chain reaction.
XX
XX Homo sapiens.
XX
XX W09412635-A.
XX
XX 09-JUN-1994.
XX
XX 17-NOV-1993; 93WO-US11153.
XX
XX 17-NOV-1992; 92US-0977452.
XX
XX (ICOS-) ICOS CORP.
XX
XX Godiska R, Gray PW, Schweickart VL;
XX
XX WPI; 1994-200264/24.
XX
XX N-PSDB; Q66160.
XX
XX DNA encoding seven transmembrane receptors - used to develop
XX prods. for use as therapeutic or diagnostic agents for conditions
XX involving the receptors.
XX
XX Claim 1; Page 52-53; 100pp; English.
XX
XX A human cDNA encoding the seven transmembrane receptor V31 was
XX isolated by first amplifying a partial cDNA clone from a human
XX tonsil cDNA library using two primers (Q66154, Q66155). The resulting
XX amplified products were probed using two radioactively labelled
XX sequences (Q66156, Q66157). A hybridising band was isolated from the
XX gel and cloned. The resulting clone was named pV31-5'end (Q66158). A
XX full length cDNA clone was isolated from a peripheral blood
XX mononuclear cell library using V31 specific primers (Q66159, Q66152).
XX Clone PMWC75 was isolated and the V31 cDNA insert in the clone was
XX designated cDNA V31-B (Q66160).
XX
XX Sequence 378 AA;

Query Match 86.7%; Score 78; DB 15; Length 378;
Best Local Similarity 77.8%; Pred. No. 1.8e-05;
Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAIADILFVLTLPLFWAVS 18
Db 100 lavadilfvltpfwavs 117
:|:|||||:||||| |

RESULT 9
W48724
ID W48724 standard; Protein; 378 AA.
XX
XX W48724;
XX
XX 25-SEP-1998 (first entry)
XX
XX Human V31 seven transmembrane receptor.
XX
XX V28; placenta; seven transmembrane receptor; 7TM; signal transduction;
XX immunology; inflammation; V31.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Domain 58..86
XX
XX /note= "Transmembrane domain 1"

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FT Domain 96..119
FT /note= "Transmembrane domain 2"
FT Domain 131..152
FT /note= "Transmembrane domain 3"
FT Domain 171..196
FT /note= "Transmembrane domain 4"
FT Domain 219..247
FT /note= "Transmembrane domain 5"
FT Domain 264..285
FT /note= "Transmembrane domain 6"
FT Domain 306..331
FT /note= "Transmembrane domain 7"
XX
XX US5759804-A.
XX
XX 02-JUN-1998.
XX
XX 17-NOV-1993; 93US-0153848.
XX
XX 17-NOV-1992; 92US-0977452.
XX
XX (ICOS-) ICOS CORP.
XX
XX Godiska R, Gray PW, Schweickart VL;
XX
XX WPI; 1998-332132/29.
XX
XX N-PSDB; V18347.
XX
XX DNA encoding V28 seven transmembrane receptor polypeptide - useful
XX PT for producing recombinant polypeptide and anti-V28 antibodies, and
XX PT in screening assays for V28 agonists and antagonists
XX
XX Example 3; Columns 39-42; 56pp; English.
XX
XX The present sequence represents the V31 seven transmembrane (7TM)
XX receptor encoded by the V31 cDNA (V18347). The invention claims for
XX a full length V28 genomic DNA (V18343) and the V28 protein it
XX encodes (W48722). V28 and V31 proteins are 7TM receptors which
XX are probably involved in signal transduction. The invention also
XX claims that cells transformed with V28 DNA can be used to produce the
XX recombinant polypeptide, to produce anti-V28 antibodies or in screening
XX assays for V28 agonists or antagonists. The antibodies, agonists and
XX antagonists could then be used to modulate V28 receptor-ligand binding,
XX for e.g. in immunological and/or inflammatory events in vivo.
XX
XX Sequence 378 AA;

Query Match 86.7%; Score 78; DB 19; Length 378;
Best Local Similarity 77.8%; Pred. No. 1.8e-05;
Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAIADILFVLTLPLFWAVS 18
Db 100 lavadilfvltpfwavs 117
:|:|||||:||||| |

RESULT 10
W56164
ID W56164 standard; Protein; 378 AA.
XX
XX W56164;
XX
XX 20-JUL-1998 (first entry)
XX
XX G-protein coupled receptor (R7G) designated EB11.
XX
XX Lymphocyte R7G; EB11; G-protein coupled receptor;
XX opiate/opioid recognition site; opiate; opioid; opioid binding protein;
XX screening; lymphocyte receptor; compound; agonist; antagonist;
XX lymphocyte receptor protein; immune-cell specific lymphocyte receptor;
XX neuronal type opioid receptor.

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OS Homo sapiens.
XX US5753516-A.
XX
XX PD 19-MAY-1998.
XX
XX PF 03-FEB-1995; 95US-0383751.
XX
XX PR 03-FEB-1995; 95US-0383751.
XX
XX PA (FINB/) FINBERG R W.
XX (HEAG/) HEAGY W E.
XX
XX PI Finberg RW, Heagy WE;
XX
XX WPI; 1998-311410/27.
XX
XX DR N-PSDB; V22684.
XX
XX PT Screening assay for lymphocyte opioid receptor ligands - using
XX recombinant receptor protein
XX
XX PS Claim 1; Columns 87-88; 70pp; English.
XX
XX CC The present sequence represents a novel lymphocyte R7G, termed EBI1. R7G
XX proteins are part of the G-protein coupled receptor superfamily. EBI1 is
XX a functional opiate/opioid recognition site that probably plays a major
XX role in mediating the effects that opiate/opioids have on lymphocytes.
XX The EBI1 protein is an opioid-binding protein that is displayed on the
XX surface of lymphocytes. A process for screening a candidate substance for
XX ability to interact with a lymphocyte receptor comprises selecting a
XX candidate substance having a chemical structure or biological activity
XX suggestive of an ability to mimic the biological activity of an
XX opiate, opioid drug or opioid peptide having known binding affinity for
XX EBI1. The ability of the candidate substance is tested to interact with
XX the lymphocyte receptor protein. This method can be used to screen for
XX agonists or antagonists to the lymphocyte receptor protein. The method
XX can be modified and used to screen for agonists or antagonists to the
XX immune-cell specific lymphocyte receptor polypeptide or the neuronal type
XX opioid receptor polypeptide.
XX
XX SQ Sequence 378 AA;

Query Match 86.7%; Score 78; DB 19; Length 378;
Best Local Similarity 77.8%; Pred. No. 1.8e-05;
Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAIADILFVLTPFWAVS 18
Db :|:||||:|||||
100 lavadilflitpways 117

RESULT 11
W53622
ID W53622 standard; Protein; 378 AA.
XX
XX AC W53622;
XX
XX DT 09-JUL-1998 (first entry)
XX
XX DE Epstein Barr virus induced protein 1 (EBI-1).
XX
XX KW Assessing; monitoring; foetal development; placental development;
XX Epstein Barr virus; EBV; induced gene 1; EBI-1.
XX
XX OS Homo sapiens.
XX
XX PN US5744301-A.
XX
XX PD 28-APR-1998.
XX
XX PF 02-FEB-1995; 95US-0383750.
XX
XX PT Polynucleotide encoding seven transmembrane receptors, antibody
XX specific to the receptor, agonist and antagonist of the receptor useful
XX for treating inflammation in a mammal

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PR 02-FEB-1995; 95US-0383750.
PR 25-NOV-1992; 92US-0980518.
PR 30-NOV-1994; 94US-0352678.
XX
XX PA (BGHM ) BRIGHAM & WOMENS HOSPITAL.
XX
XX PI Birkenbach M, Kieff E;
XX
XX WPI; 1998-271060/24.
XX
XX DR N-PSDB; V25490.
XX
XX PT Assessing or monitoring foetal or placental development - comprises
XX detecting the level or size of Epstein Barr virus induced nucleic
XX acid or protein in maternal serum samples
XX
XX PS Example 2; Columns 37-40; 45pp; English.
XX
XX CC The present sequence was used in the development of a novel method
XX for assessing or monitoring foetal or placental development. The
XX method comprises taking a maternal serum sample, and detecting the
XX level or size of Epstein Barr virus (EBV) induced gene or protein 3
XX (EBI-3) to obtain a result, which can be compared to a control to
XX assess or monitor foetal or placental development.
XX
XX SQ Sequence 378 AA;

Query Match 86.7%; Score 78; DB 19; Length 378;
Best Local Similarity 77.8%; Pred. No. 1.8e-05;
Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAIADILFVLTPFWAVS 18
Db :|:||||:|||||
100 lavadilflitpways 117

RESULT 12
B21688
ID B21688 standard; Protein; 378 AA.
XX
XX AC B21688;
XX
XX DT 26-JAN-2001 (first entry)
XX
XX DE Human 7TM receptor V31-B cDNA clone protein.
XX
XX KW Seven transmembrane receptor; 7TM; heptahelical; serpentine;
XX G-protein-coupled; V28; V31; V112; R20; R2; RM3; gene therapy;
XX cancer.
XX
XX OS Homo sapiens.
XX
XX PN US6107475-A.
XX
XX PD 22-AUG-2000.
XX
XX PF 26-APR-1999; 99US-0299843.
XX
XX PR 17-MAY-1994; 94US-0245242.
XX 01-JUN-1998; 98US-0088337.
XX 17-NOV-1992; 92US-0977452.
XX 17-NOV-1993; 93US-0153848.
XX
XX PA (ICOS-) ICOS CORP.
XX
XX PI Schweickart VL, Gray PW, Godiska R;
XX
XX DR WPI; 2000-571335/53.
XX
XX DR N-PSDB; A91707.
XX
XX PT Polynucleotide encoding seven transmembrane receptors, antibody
XX specific to the receptor, agonist and antagonist of the receptor useful
XX for treating inflammation in a mammal

```


CC agents. The mutant proteins are also useful in research settings for
 CC elucidating the roles of the receptors in normal and diseased conditions.
 CC Antagonists for a particular GPCR are useful for treating diseases and
 CC disorders associated with that receptor. Because the novel mutant GPCRs
 CC are constitutively active, they can be used directly for screening of
 CC compounds without the need for endogenous ligands. Sequences Y90643-
 CC Y90677 and Y90683-Y90687 the mutant human GPCRs of the invention.
 XX

SQ Sequence 378 AA;

Query Match 86.7%; Score 78; DB 21; Length 378;
 Best Local Similarity 77.8%; Pred. No. 1.8e-05;
 Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAIADILFVLTLPEFWAVS 18
 :|:|||||:||||||| |
 Db 100 lavadi|fltlp|fways 117

RESULT 15

B50859
 ID B50859 standard; protein; 378 AA.

XX AC B50859;

DT 16-MAR-2001 (first entry)

DE Human CCR7.

XX Human; chemokine receptor 7; CCR7; chemokine beta-9; Ckbeta-9;
 KW allergy; autoimmune disease; ischaemia; atherosclerosis; cancer;
 KW chronic inflammatory disorder; organ transplant; tissue graft;
 KW chronic myelogenous leukaemia; infection.

XX OS Homo sapiens.

XX US6153441-A.

XX 28-NOV-2000.

PF 17-FEB-1999; 99US-0251545.

XX 17-FEB-1998; 98US-0074883.

XX (SMIK) SMITHKLINE BEECHAM CORP.

XX Appelbaum ER, White JR, Sarau HM;

XX WPI; 2001-049151/06.

XX Identifying agonists or antagonists of interaction between human
 PT protein, chemokine beta-9 and human CC chemokine receptor 7, by
 PT contacting cell expressing receptor with test compound -

XX Claim 1; Fig 1; 20pp; English.

XX The present sequence is human chemokine receptor 7 (CCR7), a cellular
 CC receptor for chemokine beta-9 (Ckbeta-9). The sequence may be
 CC used in a method for discovering agonists and antagonists of the
 CC interaction between Ckbeta-9 and CCR7. A cell expressing CCR7
 CC polypeptide on its surface, associated with a component capable of
 CC providing a detectable signal in response to binding of Ckbeta-9, is
 CC contacted with a compound in the presence of labelled or unlabelled
 CC Ckbeta-9. The compound is identified as an agonist/antagonist by
 CC determining whether it activates or inhibits the detectable signal.
 CC The method is useful for identifying agonists and antagonists of the
 CC interaction between Ckbeta-9 and CCR7 which are useful for treating
 CC diseases including allergic disorders, autoimmune diseases,
 CC ischaemia/reperfusion injury, development of atherosclerotic plaques,
 CC cancer, chronic inflammatory disorders, chronic rejection of
 CC transplanted organs or tissue grafts, chronic myelogenous leukaemia, and
 CC infection by HIV and other pathogens.

XX SQ Sequence 378 AA;

Query Match 86.7%; Score 78; DB 22; Length 378;
 Best Local Similarity 77.8%; Pred. No. 1.8e-05;
 Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAIADILFVLTLPEFWAVS 18
 :|:|||||:||||||| |
 Db 100 lavadi|fltlp|fways 117

Search completed: May 23, 2001, 15:28:27
 Job time: 404 sec

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OM protein - protein search, using sw model

Run on: May 23, 2001, 15:30:05 ; Search time 95.91 Seconds
(without alignments)
3.605 Million cell updates/sec

Title: US-08-887-977-10_COPY_79_96
Perfect score: 90
Sequence: 1 MAIADILFVLTLFPNFAVS 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 185757 seqs, 19210857 residues

Total number of hits satisfying chosen parameters: 185757

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_AA*
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5: /cgn2_6/ptodata/2/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	78	86.7	40	1 US-08-383-751A-3	Sequence 3, Appli
2	78	86.7	358	1 US-08-153-848-19	Sequence 19, Appl
3	78	86.7	358	3 US-09-299-843A-19	Sequence 19, Appl
4	78	86.7	358	5 PCT-US93-11153-19	Sequence 19, Appl
5	78	86.7	361	2 US-08-902-234-2	Sequence 2, Appli
6	78	86.7	361	3 US-09-178-637-2	Sequence 2, Appli
7	78	86.7	378	1 US-08-383-750-2	Sequence 2, Appli
8	78	86.7	378	1 US-08-153-848-15	Sequence 15, Appl
9	78	86.7	378	3 US-08-352-678-2	Sequence 2, Appli
10	78	86.7	378	3 US-09-299-843A-15	Sequence 15, Appl
11	78	86.7	378	4 US-09-251-545-1	Sequence 1, Appli
12	78	86.7	378	5 PCT-US93-09636-2	Sequence 2, Appli
13	78	86.7	378	5 PCT-US93-11153-15	Sequence 15, Appl
14	78	86.7	410	1 US-08-153-848-7	Sequence 7, Appli
15	78	86.7	410	5 US-09-299-843A-7	Sequence 7, Appli
16	78	86.7	410	5 PCT-US93-11153-7	Sequence 7, Appli
17	78	86.7	410	5 US-08-153-848-46	Sequence 46, Appl
18	75	83.3	337	3 US-09-299-843A-46	Sequence 46, Appl
19	75	83.3	337	5 PCT-US93-11153-46	Sequence 46, Appl
20	75	83.3	352	1 US-08-202-056-3	Sequence 3, Appli
21	75	83.3	352	1 US-08-076-093A-4	Sequence 4, Appli
22	75	83.3	352	1 US-08-450-393A-6	Sequence 6, Appli
23	75	83.3	352	1 US-08-701-265-4	Sequence 4, Appli
24	75	83.3	352	2 US-08-284-586-4	Sequence 4, Appli
25	75	83.3	352	2 US-08-805-478-4	Sequence 4, Appli
26	75	83.3	352	2 US-08-802-627A-4	Sequence 4, Appli
27	75	83.3	352	2	

28	75	83.3	352	2	US-08-801-238-4	Sequence 4, Appli
29	75	83.3	352	2	US-08-801-228-4	Sequence 4, Appli
30	75	83.3	352	3	US-09-104-296-4	Sequence 4, Appli
31	75	83.3	352	4	US-08-446-669-6	Sequence 6, Appli
32	75	83.3	352	5	PCT-US95-00476-6	Sequence 6, Appli
33	72	80.0	359	1	US-08-153-848-24	Sequence 24, Appl
34	72	80.0	359	3	US-09-299-843A-24	Sequence 24, Appl
35	72	80.0	359	5	PCT-US93-11153-24	Sequence 24, Appl
36	72	80.0	378	3	US-09-299-843A-66	Sequence 66, Appl
37	70	77.8	312	1	US-08-118-270-38	Sequence 38, Appl
38	70	77.8	312	5	PCT-US93-08528-38	Sequence 38, Appl
39	69	76.7	350	1	US-08-202-056-1	Sequence 1, Appli
40	69	76.7	350	1	US-08-076-093A-2	Sequence 2, Appli
41	69	76.7	350	1	US-08-450-393A-7	Sequence 7, Appli
42	69	76.7	350	1	US-08-410-453A-1	Sequence 1, Appli
43	69	76.7	350	1	US-08-701-265-2	Sequence 2, Appli
44	69	76.7	350	1	US-08-410-454A-1	Sequence 1, Appli
45	69	76.7	350	2	US-08-284-586-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-08-383-751A-3
; Sequence 3, Application US/08383751A
; Patent No. 5753516
; GENERAL INFORMATION:
; APPLICANT: Heagy, Wyrta E.
; APPLICANT: Finberg, Robert W.
; TITLE OF INVENTION: Identification and Uses of Opioid
; TITLE OF INVENTION: Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: US
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/383,751A
; FILING DATE: 03-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilson, Mark B.
; REGISTRATION NUMBER: 37,259
; REFERENCE/DOCKET NUMBER: DFCI:001/WIM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; TELEX: 79-0924
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-383-751A-3

Query Match 86.7%; Score 78; DB 1; Length 40;
Best Local Similarity 77.8%; Pred. No. 5.3e-06;
Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 1 MAIADILFVLTLFPNFAVS 18
DB 20 LAVADILFLTLFPNFAVS 37

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RESULT 2
US-08-153-848-19
; Sequence 19, Application US/08153848
; Patent No. 5759804
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schweikart, Vicki L.
; TITLE OF INVENTION: No. 5759804el Seven Transmembrane Receptors
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/153,848
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/977,452
; FILING DATE: 17-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5759804and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31794
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 358 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-153-848-19

Query Match 86.7%; Score 78; DB 1; Length 358;
Best Local Similarity 77.8%; Pred. No. 4.9e-05;
Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAIADILFVLTLFPWAVS 18
; :|||||:|||||
Db 80 LAVADILFLLTLFPWAVS 97

RESULT 3
US-09-299-843A-19
; Sequence 19, Application US/09299843A
; Patent No. 6107475
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schweikart, Vicki L.
; TITLE OF INVENTION: No. 6107475el Seven Transmembrane Receptors
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago

```

```

; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/299,843A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/088,337
; FILING DATE: 01-JUN-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/153,848
; FILING DATE: 17-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/977,452
; FILING DATE: 17-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Jill E. Uhl
; REGISTRATION NUMBER: 43,213
; REFERENCE/DOCKET NUMBER: 27866/32059B
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX:
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 358 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-299-843A-19

Query Match 86.7%; Score 78; DB 3; Length 358;
Best Local Similarity 77.8%; Pred. No. 4.9e-05;
Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAIADILFVLTLFPWAVS 18
; :|||||:|||||
Db 80 LAVADILFLLTLFPWAVS 97

RESULT 4
PCT-US93-11153-19
; Sequence 19, Application PC/TUS93111153
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schweikart, Vicki L.
; TITLE OF INVENTION: Novel Seven Transmembrane Receptors
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/11153
; FILING DATE:
; CLASSIFICATION:

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;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/977,452
;; FILING DATE: 17-NOV-1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Noland, Greta E.
;; REGISTRATION NUMBER: 35,302
;; REFERENCE/DOCKET NUMBER: 31794
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (312) 474-6300
;; TELEFAX: (312) 474-0448
;; TELEX: 25-3856
;; INFORMATION FOR SEQ ID NO: 19:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 358 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
PCT-US93-11153-19

Query Match 86.7%; Score 78; DB 5; Length 358;
Best Local Similarity 77.8%; Pred. No. 4.9e-05;
Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAIADILFVLTLFPWAVS 18
:|:||||:||||| I
Db 80 LAVADILFLLTLFPWAVS 97

RESULT 5
US-08-902-294-2
; Sequence 2, Application US/08902294
; Patent No. 5874252
; GENERAL INFORMATION:
; APPLICANT: ZHU, YUAN
; TITLE OF INVENTION: A NOVEL SPLICING VARIANT OF
; THE EPSTEIN-BARR VIRUS-INDUCED G-PROTEIN COUPLED
; RECEPTOR
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RATNER & PRESTIA
; STREET: P.O. BOX 980
; CITY: VALLEY FORGE
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/902,294
; FILING DATE: 29-JUL-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GP-70177
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 361 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-902-294-2

Query Match 86.7%; Score 78; DB 2; Length 361;
Best Local Similarity 77.8%; Pred. No. 5e-05;
Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAIADILFVLTLFPWAVS 18
:|:||||:||||| I
Db 100 LAVADILFLLTLFPWAVS 117

RESULT 6
US-09-178-637-2
; Sequence 2, Application US/09178637
; Patent No. 6001972
; GENERAL INFORMATION:
; APPLICANT: ZHU, YUAN
; TITLE OF INVENTION: A No. 6001972el Splicing Variant of
; THE EPSTEIN-BARR VIRUS-INDUCED G-PROTEIN COUPLED RECEPTOR
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RATNER & PRESTIA
; STREET: P.O. BOX 980
; CITY: VALLEY FORGE
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/178,637
; FILING DATE: 26-OCT-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/902,294
; FILING DATE: 29-JUL-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GP-70177-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 361 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-09-178-637-2

Query Match 86.7%; Score 78; DB 3; Length 361;
Best Local Similarity 77.8%; Pred. No. 5e-05;
Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAIADILFVLTLFPWAVS 18
:|:||||:||||| I
Db 100 LAVADILFLLTLFPWAVS 117

RESULT 7
US-08-383-750-2
; Sequence 2, Application US/08383750
; Patent No. 5744301
; GENERAL INFORMATION:
; APPLICANT: Birkenbach, Mark

```
;
; APPLICANT: Kieff, Elliot
; TITLE OF INVENTION: Epstein Barr Virus Induced Genes
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, N.W.,
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/383,750
; FILING DATE: Herewith
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Fox, Samuel, L.
; REGISTRATION NUMBER: 30,353
; REFERENCE/DOCKET NUMBER: 0627.3300001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 378 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-383-750-2

Query Match 86.7%; Score 78; DB 1; Length 378;
Best Local Similarity 77.8%; Pred. No. 5.2e-05;
Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAIADILFVLTLPFWAYS 18
Db 100 LAVADILFLLTLPFWAYS 117

RESULT 8
US-08-383-751A-2
; Sequence 2, Application US/08383751A
; Patent No. 5753516
; GENERAL INFORMATION:
; APPLICANT: Heagy, Wyrtia E.
; APPLICANT: Finberg, Robert W.
; TITLE OF INVENTION: Identification and Uses of Opioid
; TITLE OF INVENTION: Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P. O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: US
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/383,751A
; FILING DATE: 03-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Willson, Mark B.
; REGISTRATION NUMBER: 37,259
; REFERENCE/DOCKET NUMBER: DFCI:001/WIM
```

```
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; TELEX: 79-0924
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 378 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-383-751A-2

Query Match 86.7%; Score 78; DB 1; Length 378;
Best Local Similarity 77.8%; Pred. No. 5.2e-05;
Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAIADILFVLTLPFWAYS 18
Db 100 LAVADILFLLTLPFWAYS 117

RESULT 9
US-08-153-848-15
; Sequence 15, Application US/08153848
; Patent No. 5759804
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schweikart, Vicki L.
; TITLE OF INVENTION: NO. 5759804el Seven Transmembrane Receptors
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/153,848
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/977,452
; FILING DATE: 17-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5759804and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31794
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 378 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-153-848-15

Query Match 86.7%; Score 78; DB 1; Length 378;
Best Local Similarity 77.8%; Pred. No. 5.2e-05;
Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
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QY 1 MAIADILFVLTLFPWAVS 18
:|:||||:|||||
Db 100 LAVADILFLTLFPWAVS 117

RESULT 10
US-08-352-678-2
; Sequence 2, Application US/08352678
; Patent No. 6043351
; GENERAL INFORMATION:
; APPLICANT: Birkenbach, Mark
; APPLICANT: Kieff, Elliott
; TITLE OF INVENTION: EPSTEIN BARR VIRUS INDUCED GENES
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/352,678
; FILING DATE: 30-NOV-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/980,518
; FILING DATE: 25-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Gates, Edward R.
; REGISTRATION NUMBER: 31,616
; REFERENCE/DOCKET NUMBER: B0801/7044
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 378 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-352-678-2

Query Match 86.7%; Score 78; DB 3; Length 378;
Best Local Similarity 77.8%; Pred. No. 5.2e-05;
Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAIADILFVLTLFPWAVS 18
:|:||||:|||||
Db 100 LAVADILFLTLFPWAVS 117

RESULT 11
US-09-299-843A-15
; Sequence 15, Application US/09299843A
; Patent No. 6107475
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schweikart, Vicki L.
; TITLE OF INVENTION: No. 6107475e1 Seven Transmembrane Receptors
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESS: Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago

; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/299,843A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/088,337
; FILING DATE: 01-JUN-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/153,848
; FILING DATE: 17-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/977,452
; FILING DATE: 17-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Jill E. Uhl
; REGISTRATION NUMBER: 43,213
; REFERENCE/DOCKET NUMBER: 27866/32059B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX:
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 378 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-299-843A-15

Query Match 86.7%; Score 78; DB 3; Length 378;
Best Local Similarity 77.8%; Pred. No. 5.2e-05;
Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAIADILFVLTLFPWAVS 18
:|:||||:|||||
Db 100 LAVADILFLTLFPWAVS 117

RESULT 12
US-09-251-545-1
; Sequence 1, Application US/09251545
; Patent No. 6153441
; GENERAL INFORMATION:
; APPLICANT: Edward R. Appelbaum
; APPLICANT: Henry M. Sarau
; APPLICANT: John R. White
; TITLE OF INVENTION: METHODS OF SCREENING FOR AGONISTS AND
; TITLE OF INVENTION: ANTAGONISTS OF THE INTERACTION BETWEEN HUMAN CCR7 RECEPTOR
; FILE REFERENCE: P50753
; CURRENT APPLICATION NUMBER: US/09/251,545
; CURRENT FILING DATE: 1999-02-17
; EARLIER APPLICATION NUMBER: 60/074,883
; EARLIER FILING DATE: 1998-02-17
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 378
; TYPE: PRT
; ORGANISM: Human
US-09-251-545-1

Query Match 86.7%; Score 78; DB 4; Length 378;

Best Local Similarity 77.8%; Pred. No. 5.2e-05;
Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MAIADILFVLTLFPWFAYS 18
:|:||||:|||||
Db 100 LAVADILFLLTLFPWFAYS 117

RESULT 13

PCT-US93-09636-2

; Sequence 2, Application PC/TUS9309636
; GENERAL INFORMATION:
; APPLICANT: Birkenbach, Mark
; APPLICANT: Kieff, Elliot
; TITLE OF INVENTION: Epstein Barr Virus Induced Genes
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue N.W., Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3934

COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US93/09636
; FILING DATE: herewith

; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540

; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:

; LENGTH: 378 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

PCT-US93-09636-2

Query Match 86.7%; Score 78; DB 5; Length 378;
Best Local Similarity 77.8%; Pred. No. 5.2e-05;
Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MAIADILFVLTLFPWFAYS 18
:|:||||:|||||
Db 100 LAVADILFLLTLFPWFAYS 117

RESULT 14

PCT-US93-11153-15

; Sequence 15, Application PC/TUS9311153
; GENERAL INFORMATION:

; APPLICANT: Godiska, Ronald
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schweikart, Vicki L.

; TITLE OF INVENTION: Novel Seven Transmembrane Receptors
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell

; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago

; STATE: Illinois
; COUNTRY: USA

; ZIP: 60606

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

; INFORMATION FOR SEQ ID NO: 7:

; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/11153
; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/977,452

; FILING DATE: 17-NOV-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Noland, Greta E.

; REGISTRATION NUMBER: 35,302

; REFERENCE/DOCKET NUMBER: 31794

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (312) 474-6300

; TELEFAX: (312) 474-0448

; TELEX: 25-3856

; INFORMATION FOR SEQ ID NO: 15:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 378 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

PCT-US93-11153-15

Query Match 86.7%; Score 78; DB 5; Length 378;

Best Local Similarity 77.8%; Pred. No. 5.2e-05;

Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MAIADILFVLTLFPWFAYS 18

:|:||||:|||||

Db 100 LAVADILFLLTLFPWFAYS 117

RESULT 15

US-08-153-848-7

; Sequence 7, Application US/08153848

; Patent No. 5759804

; GENERAL INFORMATION:

; APPLICANT: Godiska, Ronald

; APPLICANT: Gray, Patrick W.

; APPLICANT: Schweikart, Vicki L.

; TITLE OF INVENTION: No. 5759804el Seven Transmembrane Receptors

; NUMBER OF SEQUENCES: 64

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &

; ADDRESSEE: Bicknell

; STREET: 6300 Sears Tower, 233 South Wacker Drive

; CITY: Chicago

; STATE: Illinois

; COUNTRY: USA

; ZIP: 60606

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/153,848

; FILING DATE:

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/977,452

; FILING DATE: 17-NOV-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: No. 5759804and, Greta E.

; REGISTRATION NUMBER: 35,302

; REFERENCE/DOCKET NUMBER: 31794

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (312) 474-6300

; TELEFAX: (312) 474-0448

; TELEX: 25-3856

; INFORMATION FOR SEQ ID NO: 7:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 410 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-153-848-7

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Query Match      86.7%; Score 78; DB 1; Length 410;
Best Local Similarity 77.8%; Pred. No. 5.7e-05;
Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

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Qy 1 MAIADILFVLTLPFWAYS 18
   :|:||||:|||||||
Db 132 LAVADILFLLTLPFWAYS 149

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Search completed: May 23, 2001, 15:30:05
Job time: 412 sec

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OM protein - protein search, using sw model.

Run on: May 23, 2001, 15:31:59 ; Search time 110.15 Seconds
(without alignments)
11.230 Million cell updates/sec

Title: US-08-887-977-10_COPY_79_96
Perfect score: 90
Sequence: 1 MAIADILFVLTLPFWAVS 18
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 198801 seqs, 68722935 residues

Total number of hits satisfying chosen parameters: 198801

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_67: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	90	100.0	369	2 JC5068	G protein-coupled
2	78	86.7	378	2 A45680	G protein-coupled
3	78	86.7	378	2 B57335	lymphocyte-specific
4	77	85.6	353	2 S28787	neuropeptide Y/pep
5	75	83.3	352	2 A45747	neuropeptide Y/pep
6	72	80.0	352	2 G00048	fusin (LESTRA) - C
7	72	80.0	378	2 A55735	G protein-coupled
8	70	77.8	355	2 J01231	interleukin-8 rece
9	69	76.7	350	2 A39445	interleukin-8 rece
10	69	76.7	360	2 A53611	interleukin-8 rece
11	69	76.7	367	2 J00349	interferon-inducib
12	67	74.4	383	2 S55594	interleukin-8 rece
13	66	73.3	356	2 S42096	interleukin-8 rece
14	66	73.3	358	2 A53752	interleukin-8 rece
15	66	73.3	359	2 A48921	interleukin-8 rece
16	66	73.3	360	2 JC4587	chemokine (C-C) re
17	65	72.2	359	2 JC1104	angiotensin II rec
18	65	72.2	359	2 S44425	angiotensin II rec
19	65	72.2	359	2 JC1194	angiotensin II rec
20	65	72.2	359	2 A48857	angiotensin II rec
21	65	72.2	359	2 A42656	angiotensin II rec
22	65	72.2	359	2 S15403	angiotensin II rec
23	65	72.2	359	2 I39418	angiotensin II rec
24	65	72.2	359	2 JH0621	angiotensin II rec
25	65	72.2	359	2 JC2134	angiotensin II rec
26	64	71.1	350	2 JN0621	G protein-coupled
27	64	71.1	352	2 A43113	chemokine (C-C) re
28	64	71.1	355	2 G02436	chemokine (C-C) re
29	64	71.1	360	2 JC2443	chemokine (C-C) re

30 64 71.1 374 2 I38450 chemokine (C-C) re
31 63 70.0 354 2 I58186 probable G protein
32 63 70.0 355 2 JC4304 orphan G protein-c
33 63 70.0 355 2 A45177 chemokine (C-C) re
34 62 68.9 359 2 J01516 angiotensin II rec
35 62 68.9 360 2 A57160 chemokine (C-C) re
36 62 68.9 380 2 I38435 angiotensin recept
37 61 67.8 177 2 PH1372 angiotensin II rec
38 60 66.7 341 2 S43252 platelet-activatin
39 60 66.7 342 2 S13638 platelet-activatin
40 60 66.7 344 2 JC5942 chemokine receptor
41 60 66.7 359 2 I49341 MIP-1 alpha recept
42 59 65.6 334 2 JC4681 bradykinin BI rece
43 59 65.6 352 2 S60024 bradykinin BI rece
44 59 65.6 353 2 A53858 bradykinin recepto
45 59 65.6 355 2 I49339 macrophage inflamm

ALIGNMENTS

RESULT 1

JC5068
G protein-coupled receptor CKR-L3 - human
C:Species: Homo sapiens (man)
C:Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 21-Jul-2000
C:Accession: JC5068
R:Zaballos, A.; Varona, R.; Gutierrez, J.; Lind, P.; Marquez, G.
Biochem. Biophys. Res. Commun. 227, 846-853, 1996
A:Title: Molecular cloning and RNA expression of two new human chemokine receptor-lik
A:Reference number: JC5067; MUID:97040707
A:Accession: JC5068
A:Molecule type: DNA
A:Residues: 1-369 <ZAB>

A:Cross-references: EMBL:Z79784; NID:gl668737; PIDN:CAB02144.1; PID:gl668738
C:Comment: This protein belongs to the family of alpha chemokine receptors.
C:Genetics:

A:Gene: GDB:CKRB6; STRL22; GPR29; CCR6; CKR-L3; GPR-CY4
A:Cross-references: GDB:5370639; OMIM:601835
A:Map position: 6q27-6q27

C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; transmembrane protein
F:42-68/Domain: transmembrane #status predicted <TM1>
F:79-99/Domain: transmembrane #status predicted <TM2>
F:115-136/Domain: transmembrane #status predicted <TM3>
F:160-180/Domain: transmembrane #status predicted <TM4>
F:212-233/Domain: transmembrane #status predicted <TM5>
F:250-271/Domain: transmembrane #status predicted <TM6>
F:292-315/Domain: transmembrane #status predicted <TM7>

Query Match 100.0%; Score 90; DB 2; Length 369;
Best Local Similarity 100.0%; Pred. No. 2,2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAIADILFVLTLPFWAVS 18
Dd 83 MAIADILFVLTLPFWAVS 100
|||||

RESULT 2

A45680
G protein-coupled peptide receptor EBI 1 - human
C:Species: Homo sapiens (man)
C:Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 24-Nov-1999
C:Accession: A45680
R: Birkenbach, M.; Josefsen, K.; Yalamanchili, R.; Lenoir, G.; Kieff, E.
J. Virol. 67, 2209-2220, 1993
A:Title: Epstein-Barr virus-induced genes: first lymphocyte-specific G protein-couple
A:Reference number: A45680; MUID:93188173
A:Accession: A45680
A>Status: preliminary
A:Molecule type: nucleic acid

CROSS-REFERENCES: EMBL: M86 / 39

Matches 12; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAIADILFVLTLFPWAV 17

:::|||||:|||||

Db 80 LSVADLLFVTLFPWAV 96

RESULT 6

G00048

fusin (LESTRA) - crab-eating macaque

C:Species: Macaca fascicularis (crab-eating macaque)

C>Date: 11-Apr-1997 #sequence_revision 11-Apr-1997 #text_change 26-Aug-1999

C:Accession: G00048

R:Tatsumi, M.

submitted to GenBank, July 1996

A:Reference number: H00048

A:Accession: G00048

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-352 <TAT>

A:Cross-references: GB:D86579; NID:g1468948; PID:g1468949

C:Superfamily: vertebrate rhodopsin

Query Match 80.0%; Score 72; DB 2; Length 352;

Best Local Similarity 64.7%; Pred. No. 0.0002;

Matches 11; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAIADILFVLTLFPWAV 17

:::|||||:|||||

Db 80 LSVADLLYVTLFPWAV 96

RESULT 7

A55735

G protein-coupled receptor EB11 - mouse

C:Species: Mus musculus (house mouse)

C>Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 24-Nov-1999

C:Accession: A55735

R:Schweickart, V.L.; Raport, C.J.; Godiska, R.; Byers, M.G.; Eddy Jr., R.L.; Shows, T.B.

Genomics 23, 643-650, 1994

A:Title: Cloning of human and mouse EB11, a lymphoid-specific G-protein-coupled receptor

A:Reference number: A55735; MUID:95154835

A:Accession: A55735

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-378 <SCH>

A:Cross-references: GB:L31580; NID:g468340; PIDN:AAA74232.1; PID:g468341

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor

Query Match 80.0%; Score 72; DB 2; Length 378;

Best Local Similarity 72.2%; Pred. No. 0.00021;

Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 MAIADILFVLTLFPWAVS 18

:::|||||:|||||

Db 100 LAVADILFLILFPWAVS 117

RESULT 8

JQ1231

interleukin-8 receptor - rabbit

C:Species: Oryctolagus cuniculus (domestic rabbit)

C>Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 05-Nov-1999

C:Accession: JQ1231; A46483

R:Beckmann, M.P.; Munger, W.E.; Kozlosky, C.; VandenBos, T.; Price, V.; Lyman, S.; Gerard

Biochem. Biophys. Res. Commun. 179, 784-789, 1991

A:Title: Molecular characterization of the interleukin-8 receptor.

A:Reference number: JQ1231; MUID:91378994

A:Accession: JQ1231

A:Molecule type: DNA

A:Residues: 1-355 <BEC>

A:Cross-references: GB:M74240; NID:g165438; PIDN:AAA31375.1; PID:g165439

R:Lee, J.; Kuang, W.J.; Rice, G.C.; Wood, W.I.

J. Immunol. 148, 1261-1264, 1992

A:Title: Characterization of complementary DNA clones encoding the rabbit IL-8 receptor

A:Reference number: A46483; MUID:92148149

A:Accession: A46483

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-355 <LEE>

A:Cross-references: GB:M82873; NID:g165440; PIDN:AAA31376.1; PID:g165441

A:Experimental source: neutrophils

A>Note: sequence extracted from NCBI backbone (NCBIN:81526, NCBIIP:81530)

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 77.8%; Score 70; DB 2; Length 355;

Best Local Similarity 66.7%; Pred. No. 0.00043;

Matches 12; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 MAIADILFVLTLFPWAVS 18

:::|||||:|||||

Db 86 LAMADLLFALTMPWAVS 103

RESULT 9

A39445

N:Interleukin-8 receptor type A - human

A:Alternate names: interleukin-8 receptor, high-affinity

C:Species: Homo sapiens (man)

C>Date: 22-Jan-1993 #sequence_revision 12-Apr-1996 #text_change 05-Nov-1999

C:Accession: I37449; I38710; I38711; A39445

R:Mollereau, C.; Muscatelli, F.; Mattei, M.G.; Vassart, G.; Parmentier, M.

Genomics 16, 248-251, 1993

A:Title: The high-affinity interleukin 8 receptor gene (IL8RA) maps to the 2q33-q36 r

A:Reference number: I37449; MUID:93252387

A:Accession: I37449

A:Molecule type: DNA

A:Residues: 1-350 <RES>

A:Cross-references: EMBL:X65858; NID:g312046; PIDN:CAA46688.1; PID:g312047

R:Ahuja, S.K.; Shetty, A.; Tiffany, H.L.; Murphy, P.M.

J. Biol. Chem. 269, 26381-26389, 1994

A:Title: Comparison of the genomic organization and promoter function for human inter

A:Reference number: I37898; MUID:95014476

A:Accession: I38710

A:Molecule type: DNA

A:Residues: 1-350 <RE2>

A:Cross-references: EMBL:U11870; NID:g511804; PIDN:AAA64378.1; PID:g511805

A:Accession: I38711

A:Molecule type: mRNA

A:Residues: 1-16 <RE3>

A:Cross-references: EMBL:U11871; NID:g511806; PIDN:AAA64379.1; PID:g733002

R:Holmes, W.E.; Lee, J.; Kuang, W.J.; Rice, G.C.; Wood, W.I.

Science 253, 1278-1280, 1991

A:Title: Structure and functional expression of a human interleukin-8 receptor.

A:Reference number: A39445; MUID:91368199

A:Accession: A39445

A:Molecule type: mRNA

A:Residues: 1-275, 'T', 277-350 <HOL>

A:Cross-references: GB:M68932; NID:g186369; PIDN:AAA59159.1; PID:g186370

C:Genetics:

A:Gene: GDB:IL8RA

A:Cross-references: GDB:I35039; OMIM:146929

A:Map position: 2q35-2q35

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor; glycoprotein; membrane protein

Query Match 76.7%; Score 69; DB 2; Length 350;

Best Local Similarity 66.7%; Pred. No. 0.00062;

Matches 12; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

A.Molecule type: mRNA
A.Residues: 1-367 <TAM>
A.Cross-references: DDBJ:AB003174; NID:g3798731; PIDN:BAA34045.1; PID:g3798732
C.Comment: This protein is important for lymphocyte trafficking to lymphoid organs.
C.Superfamily: vertebrate rhodopsin

Query Match 76.7%; Score 69; DB 2; Length 367;
Best Local Similarity 70.6%; Pred. No. 0.00064;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 MATADILFVLTLPFWAV 17
DB 94 LAVADVLLVLTPLWAV 110
:|::| | | | | | | |

RESULT 12
S55594
G protein-coupled receptor E1 - equine herpesvirus 2
C.Species: equine herpesvirus 2
C.Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 13-Aug-1999
C.Accession: S55594
R.Fellford, E.A.R.; Watson, M.S.; Aird, H.C.; Perry, J.; Davison, A.J.
J. Mol. Biol. 249, 520-528, 1995
A.Title: The DNA sequence of equine herpesvirus 2.
A.Reference number: S55594; MUID:95302501
A.Accession: S55594
A.Status: preliminary; nucleic acid sequence not shown
A.Molecule type: DNA
A.Residues: 1-383 <TEL>
A.Cross-references: GB:U20824; NID:g695172; PIDN:AAC13788.1; PID:g695173
C.Superfamily: vertebrate rhodopsin
C.Keywords: G protein-coupled receptor

Query Match 74.4%; Score 67; DB 2; Length 383;
Best Local Similarity 73.3%; Pred. No. 0.0014;
Matches 11; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATADILFVLTLPFW 15
DB 114 LAISDLLFLLTLPFW 128
:|::| | | | | | | |

RESULT 13
S42096
Interleukin-8 receptor - rat
C.Species: Rattus norvegicus (Norway rat)
C.Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 26-Aug-1999
C.Accession: S42096
R.Gobl, A.E.; Wang, S.; Zhou, Y.; Oeberg, K.
submitted to the EMBL Data Library, February 1994
A.Description: Molecular cloning of the rat IL8 receptor.
A.Reference number: S42096
A.Accession: S42096
A.Status: preliminary
A.Molecule type: mRNA
A.Residues: 1-356 <GOB>
A.Cross-references: EMBL:X77797
C.Superfamily: vertebrate rhodopsin
C.Keywords: G protein-coupled receptor; transmembrane protein

Query Match 73.3%; Score 66; DB 2; Length 356;
Best Local Similarity 66.7%; Pred. No. 0.002;
Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 MATADILFVLTLPFWAS 18
DB 89 LAIADLFFALTLPWAAAS 106
:|::| | | | | | | |

RESULT 14

Search completed: May 23, 2001, 15:31:59
Job time: 506 sec

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OM protein - protein search, using sw model

Run on: May 23, 2001, 15:36:17 ; Search time 62.39 Seconds
(without alignments)
9.883 Million cell updates/sec

Title: US-08-887-977-10_COPY_79_96

Perfect score: 90

Sequence: 1 MATADILFVTLFPWAVS 18

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	90	100.0	374	1	CKR6_HUMAN
2	83	92.2	367	1	CKR6_MOUSE
3	78	86.7	378	1	CKR7_HUMAN
4	77	85.6	192	1	CCR4_SHEEP
5	77	85.6	353	1	CCR4_BOVIN
6	77	85.6	353	1	CCR4_FELCA
7	75	83.3	349	1	CCR4_RAT
8	75	83.3	352	1	CCR4_CERTO
9	75	83.3	352	1	CCR4_HUMAN
10	75	83.3	352	1	CCR4_MACMU
11	75	83.3	352	1	CCR4_PAPAN
12	75	83.3	356	1	IL8B_CANFA
13	75	83.3	357	1	CKR9_HUMAN
14	75	83.3	359	1	CCR4_MOUSE
15	73	81.1	369	1	CKR9_MOUSE
16	72	80.0	352	1	CCR4_MACFA
17	72	80.0	378	1	CKR7_MOUSE
18	71	78.9	354	1	CKR5_MOUSE
19	71	78.9	354	1	CKR5_RAT
20	71	78.9	373	1	CKR2_MOUSE
21	71	78.9	373	1	CKR2_RAT
22	70	77.8	355	1	IL8A_RABIT
23	69	76.7	350	1	IL8A_GORGO
24	69	76.7	350	1	IL8A_HUMAN
25	69	76.7	350	1	IL8A_PANTR
26	69	76.7	353	1	IL8B_GORGO
27	69	76.7	353	1	IL8B_MACMU
28	69	76.7	353	1	IL8B_PANTR
29	69	76.7	360	1	IL8B_HUMAN
30	69	76.7	367	1	CCR3_MOUSE
31	68	75.6	352	1	CKR5_CERAE
32	68	75.6	352	1	CKR5_CERTO
33	68	75.6	352	1	CKR5_MACMU

34 68 75.6 352 1 CKR5_PAPHA
35 67 74.4 359 1 AG2R_CAVPO
36 66 73.3 349 1 IL8A_RAT
37 66 73.3 358 1 IL8B_RABIT
38 66 73.3 359 1 IL8B_MOUSE
39 66 73.3 359 1 IL8B_MOUSE
40 66 73.3 360 1 CKR4_MOUSE
41 65 72.2 359 1 AG2R_BOVIN
42 65 72.2 359 1 AG2R_CANFA
43 65 72.2 359 1 AG2R_HUMAN
44 65 72.2 359 1 AG2R_MOUSE
45 65 72.2 359 1 AG2R_PIG

P56441 papio hamad
Q9wv26 cavia porce
P70612 rattus norv
P35344 oryctolagus
P35343 mus musculu
P35407 rattus norv
P51680 mus musculu
P25104 bos taurus
P43204 canis famil
P30556 homo sapien
P29794 mus musculu
P30555 sus scrofa

ALIGNMENTS

RESULT 1
ID CKR6_HUMAN STANDARD; PRT; 374 AA.
AC P51684: Q92846; P78553;
DT 01-OCT-1996 (Rel. 34, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DE C-C CHEMOKINE RECEPTOR TYPE 6 (C-C CKR-6) (CC-CKR-6) (CCR-6) (LARC
DE RECEPTOR) (GPR-CY4) (GPCY4) (CHEMOKINE RECEPTOR-LIKE 3) (CKR-L3)
DE (DRV6)
GN CKR6 OR CMKR6 OR STRL22 OR GPR29 OR CKRL3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID:9606;
RN [1]
RP SEQUENCE FROM N.A., AND FUNCTION.
RX MEDLINE:97313465; PubMed:9169459;
RA Baba M., Imai T., Nishimura M., Kakizaki M., Takagi S., Hieshima K.,
RA Nomiya H., Yoshie O.;
RT "Identification of CCR6, the specific receptor for a novel
RT lymphocyte-directed CC chemokine LARC";
RL J. Biol. Chem. 272:14893-14898(1997).
RN [2]
RP SEQUENCE FROM N.A.
RA Lautens L.L., Modi W., Bonner T.I.;
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE:97040707; PubMed:8886020;
RA Zaballo A., Varona R., Gutierrez J., Lind P., Marquez G.;
RT "Molecular cloning and RNA expression of two new human chemokine
RT receptor-like genes";
RL Biochem. Biophys. Res. Commun. 227:846-853(1996).
RN [4]
RP SEQUENCE FROM N.A.
RA McCoy R., Perlmuter D.H.;
RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE:97224503; PubMed:9070937;
RA Liao F., Lee H.-H., Farber J.M.;
RT "Cloning of STRL22, a new human gene encoding a G-protein-coupled
RT receptor related to chemokine receptors and located on chromosome
RT 6q27";
RL Genomics 40:175-180(1997).
CC -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-3-
CC ALPHA/LARC AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE
CC INTRACELLULAR CALCIUM IONS LEVEL.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- TISSUE SPECIFICITY: SPLEEN, LYMPH NODES, APPENDIX, AND FETAL
CC LIVER. EXPRESSED IN LYMPHOCYTES, T CELLS AND B CELLS BUT NOT IN
CC NATURAL KILLER CELLS, MONOCYTES, OR GRANULOCYTES.
CC -!- INDUCTION: INTERLEUKIN-2.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -!- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-6 IS THE INITIATOR.

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 CC -----
 DR EMBL; U45984; AAB62714.1; -;
 DR EMBL; 279784; CAB02144.1; ALT_INIT.
 DR EMBL; U60000; AAB06949.1; -;
 DR EMBL; U68030; AAC51124.1; -;
 DR EMBL; U68032; AAC51125.1; -;
 DR HSSP; P34996; 1DDD.
 DR GCRdb; GCR1037; -;
 DR GCRdb; GCR1075; -;
 DR GCRdb; GCR1306; -;
 DR GCRdb; GCR1919; -;
 DR GCRdb; GCR1941; -;
 DR GCRdb; GCR2110; -;
 DR MIM; 601835; -;
 DR InterPro; IPR000276; -;
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PROSITE; PS00237; G-PROTEIN_RECP_FL_1; 1.
 DR PROSITE; PS0262; G-PROTEIN_RECP_FL_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 47
 FT TRANSMEM 48 74
 FT DOMAIN 75 83
 FT TRANSMEM 84 104
 FT DOMAIN 105 119
 FT TRANSMEM 120 141
 FT DOMAIN 142 159
 FT TRANSMEM 160 180
 FT DOMAIN 181 211
 FT TRANSMEM 212 238
 FT DOMAIN 239 254
 FT TRANSMEM 255 279
 FT DOMAIN 280 303
 FT TRANSMEM 304 321
 FT DOMAIN 322 374
 FT TRANSMEM 375 391
 FT DISULFID 118 197
 FT CARBOHYD 7 7
 FT CARBOHYD 23 23
 FT CONFLICT 60 60
 FT CONFLICT 74 74
 FT CONFLICT 86 86
 FT CONFLICT 164 164
 FT CONFLICT 182 182
 FT CONFLICT 192 192
 FT CONFLICT 206 206
 FT CONFLICT 225 225
 FT CONFLICT 370 374
 SQ SEQUENCE 374 AA; 42494 MW; D7F963534E990BC4 CRC64;

Query Match 100.0%; Score 90; DB 1; Length 374;
 Best Local Similarity 100.0%; Pred. No. 4.9e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAIADILFVLTLPPFWAVS 18
 |||||
 DB 88 MAIADILFVLTLPPFWAVS 105

RESULT 2
 ID_CKR6_MOUSE STANDARD; PRT; 367 AA.
 AC O54689;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 01-OCT-2000 (Rel. 40, Last annotation update)
 GN C-C CHEMOKINE RECEPTOR TYPE 6 (C-C CKR-6) (CCR-6) (KY411).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Yanagihara S., Komura E., Yamaguchi Y.;
 RT "Mouse G-protein-coupled receptor KY411.";
 RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99077268; PubMed=9862452;
 RA Varona R., Zaballós A., Gutierrez J., Martin P., Roncal F.,
 RA Albar J.P., Ardavin C., Marquez G.;
 RT "Molecular cloning, functional characterization and mRNA expression
 RT analysis of the murine chemokine receptor CCR6 and its specific ligand
 RT MIP-3alpha.";
 RL MIP-3alpha.";
 CC FEBS Lett. 440:188-194(1998).
 CC -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-3-
 CC ALPHA/LARC AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE
 CC INTRACELLULAR CALCIUM IONS LEVEL.
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 CC -----
 DR EMBL; AB009369; BAA23776.1; -;
 DR EMBL; AJ222714; CAA10956.1; -;
 DR MGD; MGI:1333797; Cmkbr6.
 DR InterPro; IPR000276; -;
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PROSITE; PS00237; G-PROTEIN_RECP_FL_1; 1.
 DR PROSITE; PS0262; G-PROTEIN_RECP_FL_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 39
 FT TRANSMEM 40 66
 FT DOMAIN 67 75
 FT TRANSMEM 76 96
 FT DOMAIN 97 111
 FT TRANSMEM 112 133
 FT DOMAIN 134 151
 FT TRANSMEM 152 172
 FT DOMAIN 173 203
 FT TRANSMEM 204 230
 FT DOMAIN 231 246
 FT TRANSMEM 247 271
 FT DOMAIN 272 295
 FT TRANSMEM 296 313
 FT DOMAIN 314 367
 FT DISULFID 110 189
 FT CARBOHYD 35 35
 SQ SEQUENCE 367 AA; 42102 MW; 6A309AF833B1117E CRC64;

Query Match 92.2%; Score 83; DB 1; Length 367;
 Best Local Similarity 88.9%; Pred. No. 6e-06;
 Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAIADILFVLTLPPFWAVS 18
 |||||
 DB 80 MAITDILFVLTLPPFWAVT 97

ET	DOMAIN	87	95	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	96	116	2 (POTENTIAL).
FT	DOMAIN	117	130	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	131	152	3 (POTENTIAL).
FT	DOMAIN	153	170	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	171	191	4 (POTENTIAL).
FT	DOMAIN	192	219	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	220	247	5 (POTENTIAL).
FT	DOMAIN	248	263	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	264	289	6 (POTENTIAL).
FT	DOMAIN	290	313	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	314	331	7 (POTENTIAL).
FT	DOMAIN	332	378	CYTOPLASMIC (POTENTIAL).
FT	CARBOHYD	36	36	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	DISULFID	129	210	BY SIMILARITY.
FT	CONFLICT	182	183	IW -> SA (IN REF. 1).
FT	CONFLICT	337	337	L -> I (IN REF. 1).
SO	SEQUENCE	378 AA;	42874 MW;	D4CB4213841A1BD4 CRC64;

Query Match 86.7%; Score 78; DB 1; Length 378;
Best Local Similarity 77.8%; Pred. No. 3.7e-05;
Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy	1	MAIADILEVLTLPFWAYS 18
		: : :
Db	100	LAVADILELTLPFWAYS 117

RESULT 4

CC	RA	CCR4_SHEEP	STANDARD;	PRT;	192 AA.
AC	Q28553;				
DT	15-JUL-1998	(Rel. 36, Created)			
DT	15-JUL-1998	(Rel. 36, Last sequence update)			
DT	15-JUL-1998	(Rel. 36, Last annotation update)			
DE	C-X-C CHEMOKINE RECEPTOR TYPE 4 (CXC-R4)	(CXCR-4) (SDF-1 RECEPTOR)			
DE	(SPROMAL CELL-DERIVED FACTOR 1 RECEPTOR) (FUSIN) (LEUKOCYTE-DERIVED				
DE	SEVEN TRANSMEMBRANE DOMAIN RECEPTOR) (LESTR) (FRAGMENT).				
GN	CXCR4 OR LESTR.				
OS	Ovis aries (Sheep).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;				
OC	Bovidae; Caprinae; Ovis.				
OX	NCBI_TaxID=9940;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Hypothalamus;				
RA	Dyer C.J., Matteri R.L., Keisler D.H.;				
RT	"Development of an ovine Y3 cDNA and expression of the Y3 receptor				
RT	mRNA in the ovine hypothalamus and pituitary.";				
FL	Abstr.- Soc. Neurosci. 21:1890-1890(1995).				
CC	-!- FUNCTION: RECEPTOR FOR THE C-X-C CHEMOKINE SDF-1. TRANSDUCES A				
CC	SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.				
CC	-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.				
CC	-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.				
CC	-!- CAUTION: WAS ORIGINALLY THOUGHT TO BE A RECEPTOR FOR NEUROPEPTIDE				
CC	Y, TYPE 3 (NPY3-R).				

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CC	EMBL;	U38942;	AAA81347.1;	
DR	GCRdb;	GCR 1581;		
DR	InterPro;	IPR000276;		
DR	Pfam;	PF00001;	7tm_1;	1.
DR	PROSITE;	PS00237;	G_PROTEIN_RECEP_F1.1;	1.
DR	PROSITE;	PS50262;	G_PROTEIN_RECEP_F1.2;	1.

KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT NON_TER 1
 FT DOMAIN <1 29
 FT TRANSMEM 30 53
 FT DOMAIN 54 59
 FT TRANSMEM 70 89
 FT DOMAIN 90 100
 FT TRANSMEM 101 122
 FT DOMAIN 123 144
 FT TRANSMEM 145 165
 FT DOMAIN 166 190
 FT TRANSMEM 191 >192
 FT DISULFID 99 176
 FT NON_TER 192 192
 SQ SEQUENCE 192 AA; 22178 MW; A8BCFE303C52BD98 CRC64;

Query Match 85.6%; Score 77; DB 1; Length 192;
 Best Local Similarity 76.5%; Pred. No. 2.9e-05;
 Matches 13; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAIADILFVLTLPFWAV 17
 ::::|||||
 DB 70 LSVADLLFVLTLPFWAV 86

RESULT 5
 ID CCR4_BOVIN STANDARD; PRT; 353 AA.
 AC P25930;

DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE C-X-C CHEMOKINE RECEPTOR TYPE 4 (CXCR-4) (SDF-1 RECEPTOR)
 DE (STROMAL CELL-DERIVED FACTOR 1 RECEPTOR) (FUSIN) (LEUKOCYTE-DERIVED
 SEVEN TRANSMEMBRANE DOMAIN RECEPTOR) (LESTR) (LCR1).

GN CXCR4.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;

RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Locus coeruleus;
 RX MEDLINE=92100053; PubMed=1661837;
 RA Rinland J., Xin W., Sweetnam P., Saijoh K., Nestler E.J., Duman R.S.;
 RT "Sequence and expression of a neuropeptide Y receptor cDNA";
 RL Mol. Pharmacol. 40:869-875(1991).
 RN [2]

RP SHOWS THAT IT IS NOT A NPX3-R.
 RX MEDLINE=94052833; PubMed=8234909;
 RA Jazin E.E., Yoo H., Blomqvist G., Yee F., Weng G., Walker M.W.,
 RA Salon J., Larhammar D., Wahlestedt C.R.;
 RT "A proposed bovine neuropeptide Y (NPY) receptor cDNA clone, or its
 human homologue, confers neither NPY binding sites nor NPY
 responsiveness on transfected cells";
 RL Regul. Pept. 47:247-258(1993).

CC -1- FUNCTION: RECEPTOR FOR THE C-X-C CHEMOKINE SDF-1. TRANSDUCES A
 SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: BRAIN, HEART, KIDNEY, LUNG AND LIVER.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -1- CAUTION: WAS ORIGINALLY (REF.1) THOUGHT TO BE A RECEPTOR FOR
 NEUROPEPTIDE Y, TYPE 3 (NPY3-R).

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CC EMBL; M86739; -, NOT_ANNOTATED_CDS.
 DR PIR; S28787; S28787.
 DR GCRDB; GCR_0180; -.
 DR InterPro; IPR000276; -.
 DR Pfam; PF0001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PRINTS; PR00645; LCR1ORPHAN.
 DR PROSITE; PS00237; G_PROTEIN_REC_F1_1; 1.
 DR PROSITE; PS00262; G_PROTEIN_REC_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 40
 FT TRANSMEM 41 64
 FT DOMAIN 65 80
 FT TRANSMEM 81 100
 FT DOMAIN 101 111
 FT TRANSMEM 112 133
 FT DOMAIN 134 155
 FT TRANSMEM 156 176
 FT DOMAIN 177 201
 FT TRANSMEM 202 221
 FT DOMAIN 222 241
 FT TRANSMEM 242 262
 FT DOMAIN 263 286
 FT TRANSMEM 287 306
 FT DOMAIN 307 353
 FT CARBOHYD 11 11
 FT DISULFID 110 187
 SQ SEQUENCE 353 AA; 39938 MW; 42FFE5BC7545505E CRC64;

Query Match 85.6%; Score 77; DB 1; Length 353;
 Best Local Similarity 76.5%; Pred. No. 5e-05;
 Matches 13; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAIADILFVLTLPFWAV 17
 ::::|||||
 DB 81 LSVADLLFVLTLPFWAV 97

RESULT 6

ID CCR4_FELCA STANDARD; PRT; 353 AA.
 AC P56498; P79172; O02700;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DE C-X-C CHEMOKINE RECEPTOR TYPE 4 (CXCR-4) (SDF-1 RECEPTOR)
 DE (STROMAL CELL-DERIVED FACTOR 1 RECEPTOR) (FUSIN) (LESTR).
 GN CXCR4.
 OS Felis silvestris catus (Cat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
 OX NCBI_TaxID=9685;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97404646; PubMed=9261358;
 RA Willett B.J., Picard L., Hosie M.J., Turner J.D., Adema K.,
 RA Clapham P.R.;
 RT "Shared usage of the chemokine receptor CXCR4 by the feline and human
 immunodeficiency viruses";
 RL J. Virol. 71:6407-6413(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Willett B.J.;
 RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Lerner D.L., Elder J.H.;
 RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: RECEPTOR FOR THE C-X-C CHEMOKINE SDF-1. TRANSDUCES A
 SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.

RT naturally infected in west Africa: a comparison of coreceptor usage
 RT of primary HIV-2, and HIV-1; and HIV-2; and HIV-1; and HIV-2; and HIV-1;
 RL Virology 246:113-124(1998).
 CC -!- FUNCTION: RECEPTOR FOR THE C-X-C CHEMOKINE SDF-1. TRANSDUCES A
 CC SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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 CC
 CC EMBL; AF051906; AAC39834.1; -
 DR InterPro: IPR000276; -
 DR InterPro: IPR001277; -
 DR Pfam; PF000001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCRHHODOPSIN.
 DR PRINTS: PR00645; LCR1ORPHAN.
 DR PROSITE; PS00237; G-PROTEIN RECF_F1.1; 1.
 DR PROSITE; PS00262; G-PROTEIN RECF_F1.2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 39
 FT TRANSMEM 40 63
 FT DOMAIN 64 79
 FT TRANSMEM 80 99
 FT DOMAIN 100 110
 FT TRANSMEM 111 132
 FT DOMAIN 133 154
 FT TRANSMEM 155 175
 FT DOMAIN 176 200
 FT TRANSMEM 201 220
 FT DOMAIN 221 240
 FT TRANSMEM 241 261
 FT DOMAIN 262 285
 FT TRANSMEM 286 305
 FT DOMAIN 306 352
 FT CARBOHYD 11 11
 FT DISULFID 109 186
 SQ SEQUENCE 352 AA; 39648 MW; 4027432B8032F87E CRC64;

Query Match 83.3%; Score 75; DB 1; Length 352;
 Best Local Similarity 70.6%; Pred. No. 0.0001;
 Matches 12; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAIADILVLTLPFWAV 17
 :::::|||||
 Db 80 LSVADLLVLTLPFWAV 96

RESULT 9
 CCR4_HUMAN STANDARD; PRT; 352 AA.
 ID CCR4_HUMAN STANDARD; PRT; 352 AA.
 AC P30991; P56438;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE C-X-C CHEMOKINE RECEPTOR TYPE 4 (CXCR-4) (CXCR-4) (SDF-1 RECEPTOR)
 DE (STROMAL CELL-DERIVED FACTOR 1 RECEPTOR) (FUSIN) (LEUKOCYTE-DERIVED
 DE SEVEN TRANSMEMBRANE DOMAIN RECEPTOR) (LESTR) (LCR1) (FB22) (NPYL)
 DE (HM89).
 DE CCR4.
 GN Homo sapiens (Human), and Pan troglodytes (Chimpanzee).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID=9606, 9598;
 RN [1]
 RN SEQUENCE FROM N.A.
 RC SPECIES=Human; TISSUE=Lung;

RX MEDLINE-93319629; PubMed-8329116;
 RA Herzog H., Hort Y.J., Shine J., Selbie L.A.;
 RT "Molecular cloning, characterization, and localization of the human
 RT homolog to the reported bovine NPY Y3 receptor: lack of NPY binding
 RT and activation.";
 RL DNA Cell Biol. 12:465-471(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC SPECIES=Human; TISSUE=Brain;
 RX MEDLINE-94052833; PubMed-8234909;
 RA Jazin E.E., Yoo H., Blomqvist G., Yee F., Weng G., Walker M.W.,
 RA Salton J., Larhammar D., Wahlstedt C.R.;
 RT "A proposed bovine neuropeptide Y (NPY) receptor cDNA clone, or its
 RT human homologue, confers neither NPY binding sites nor NPY
 RT responsiveness on transfected cells.";
 RL Regul. Pept. 47:247-258(1993).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC SPECIES=Human; TISSUE=Spleen;
 RX MEDLINE-93315164; PubMed-8325644;
 RA Federspiel B., Delaney A.D., Clark-Lewis I., Jirik F., Duncan A.M.,
 RA Schappert K.T., Melhado I.;
 RT "Molecular cloning of the cDNA and chromosomal localization of the
 RT gene for a putative seven-transmembrane segment (7-TMS) receptor
 RT isolated from human spleen.";
 RL Genomics 16:707-712(1993).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC SPECIES=Human; TISSUE=Leukocyte;
 RX MEDLINE-94103215; PubMed-8276799;
 RA Loetscher M., Geiser T., O'Reilly T., Zwahlen R., Baggiolini M.,
 RA Moser B.;
 RT "Cloning of a human seven-transmembrane domain receptor, LESTR, that
 RT is highly expressed in leukocytes.";
 RL J. Biol. Chem. 269:232-237(1994).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC SPECIES=Human; TISSUE=Monocytes;
 RX MEDLINE-94092629; PubMed-7505609;
 RA Nomura H., Nielsen B.W., Matsushima K.;
 RT "Molecular cloning of cDNAs encoding a LD78 receptor and putative
 RT leukocyte chemotactic peptide receptors.";
 RL Int. Immunol. 5:1239-1249(1993).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC SPECIES=Human;
 RA Wegner S.A., Ehrenberg P.K., Chang G., Dayhoff D.E., Michael N.L.;
 RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP SEQUENCE FROM N.A.
 RC SPECIES=Human;
 RX MEDLINE-98258970; PubMed-9599023;
 RA Caruz A., Samsom M., Alonso J.M., Alcamí J., Balleux F.,
 RA Virelizier J.L., Parmentier M., Arenzana-Seisdedos F.;
 RT "Genomic organization and promoter characterization of human CXCR4
 RT gene.";
 RL FEBS Lett. 426:271-278(1998).
 RN [8]
 RP SEQUENCE FROM N.A.
 RC SPECIES=Human;
 RA Xiao L., Weiss S., Qari S., Rudolph D., Hodge T., Lal R.;
 RT "Partial resistance to infection by syncytium-inducing primary HIV-1
 RT in exposed uninfected individuals homozygous for CCR5 32bp
 RT deletion.";
 RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
 RN [9]
 RP SEQUENCE FROM N.A.
 RC SPECIES=Human; TISSUE=Blood;
 RA Frodl R., Moepes B., Gierschik P.;
 RT "Genomic organization and expression pattern of the human chemokine
 RT receptor CXCR4.";
 RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
 RN [10]

OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BEAGLE;
 RA Chang Y.F., Novosel V., Chang C.F.;
 RT "The isolation and sequence of canine interleukin-8 receptor
 homolog.";
 RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: RECEPTOR TO INTERLEUKIN-8, WHICH IS A POWERFUL
 CC NEUTROPHILS CHEMOTACTIC FACTOR. BINDING OF IL-8 TO THE RECEPTOR
 CC CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA A
 CC G-PROTEIN THAT ACTIVATES A PHOSPHATIDYLINOSITOL-CALCIUM SECOND
 CC MESSENGER SYSTEM. THE AFFINITY OF THIS RECEPTOR IS IL-8 >> NAP-2 >
 CC MGSA (GRO).
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC
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 CC
 CC EMBL: AF047047; AAC98968.1; -
 CC InterPro: IPR000057; -
 CC InterPro: IPR000174; -
 CC InterPro: IPR000276; -
 CC InterPro: IPR000355; -
 CC InterPro: IPR001277; -
 CC Pfam: PF00001; 7tm.1; 1.
 CC PRINTS: PR00237; GPCRHHODOPSIN.
 CC PRINTS: PR00427; INTRLEUKIN8R.
 CC PRINTS: PR00573; INTRLEUKIN8R.
 CC PRINTS: PR00645; LCR1ORPHANR.
 CC PRINTS: PR00657; CCHEMOKINER.
 CC PROSITE: PS00237; G-PROTEIN RECEPTOR FL1; 1.
 CC PROSITE: PS0262; G-PROTEIN RECEPTOR FL2; 1.
 CC G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Chemotaxis.
 FT DOMAIN 1 46 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 47 73 1 (POTENTIAL).
 FT DOMAIN 74 82 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 83 103 2 (POTENTIAL).
 FT DOMAIN 104 118 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 119 140 3 (POTENTIAL).
 FT DOMAIN 141 161 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 162 181 4 (POTENTIAL).
 FT DOMAIN 182 206 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 207 229 5 (POTENTIAL).
 FT DOMAIN 230 249 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 250 269 6 (POTENTIAL).
 FT DOMAIN 270 290 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 291 311 7 (POTENTIAL).
 FT DOMAIN 312 356 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 8 8 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT DISULFID 20 20 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT SEQUENCE 117 194 BY SIMILARITY.
 SQ SEQUENCE 356 AA; 40505 MW; 2B67DD4E8DD39B15 CRC64;

Query Match 83.3%; Score 75; DB 1; Length 356;
 Best Local Similarity 77.8%; Pred. No. 0.0001;
 Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 MAIADILFVLTLPFWAS 18
 :|||||:|||||
 Db 88 LAIADLLFALTPIWAS 105

RESULT 13

CKR9_HUMAN
 ID CKR9_HUMAN STANDARD; PRT; 357 AA.
 AC P51686;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE C-C CHEMOKINE RECEPTOR TYPE 9 (C-C CKR-9) (CCR-9) (GPR-9-
 DE 6).
 GN CCR9 OR CMKBR9.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Lautens L.L., Tiffany H.L., Gao J.-L., Modi W., Murphy P.M.,
 RA Bonner T.I.;
 RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
 RL [2]
 CC CHARACTERIZATION.
 CC MEDLINE=99248139; PubMed=10229797;
 CC Zaballos A., Gutierrez J., Varona R., Ardavin C., Marquez G.;
 CC "Cutting edge: identification of the orphan chemokine receptor GPR-9-6
 CC as CCR9, the receptor for the chemokine TECK.";
 CC J. Immunol. 162:5671-5675(1999).
 CC -!- FUNCTION: RECEPTOR FOR CHEMOKINE SCYA25/TECK. SUBSEQUENTLY
 CC TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS
 CC LEVEL.
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN THE THYMUS AND LOW IN
 CC LYMPH NODES AND SPLEEN.
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL: U45982; AAA93319.1; -
 CC MIM: 604738; -
 CC GCRDb: GCR.1943; -
 CC InterPro: IPR000276; -
 CC Pfam: PF00001; 7tm.1; 1.
 CC PRINTS: PR00237; GPCRHHODOPSIN.
 CC PROSITE: PS00237; G-PROTEIN RECEPTOR FL1; 1.
 CC PROSITE: PS0262; G-PROTEIN RECEPTOR FL2; 1.
 CC G-protein coupled receptor; Transmembrane; Glycoprotein.
 KW DOMAIN 1 37 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 38 64 1 (POTENTIAL).
 FT DOMAIN 65 73 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 74 94 2 (POTENTIAL).
 FT DOMAIN 95 108 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 109 130 3 (POTENTIAL).
 FT DOMAIN 131 148 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 149 169 4 (POTENTIAL).
 FT DOMAIN 170 198 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 199 226 5 (POTENTIAL).
 FT DOMAIN 227 242 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 243 268 6 (POTENTIAL).
 FT DOMAIN 269 292 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 293 310 7 (POTENTIAL).
 FT DOMAIN 311 357 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 20 20 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT DISULFID 107 186 BY SIMILARITY.
 SQ SEQUENCE 357 AA; 40713 MW; 96982E0B922F6B31 CRC64;

Query Match 83.3%; Score 75; DB 1; Length 357;
 Best Local Similarity 66.7%; Pred. No. 0.0001;
 Matches 12; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

OY 1 MAIADILFVLTLPFWAVS 18
 DB 78 LAIADLLFVLTLPFWAIA 95

RESULT 14
 CCR4_MOUSE
 ID CCR4_MOUSE STANDARD; PRT; 359 AA.
 AC P70658; P70346; O09062; O09059; P70233;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE C-X-C CHEMOKINE RECEPTOR TYPE 4 (CXCR-4) (SDF-1 RECEPTOR)
 DE (STROMAL CELL-DERIVED FACTOR 1 RECEPTOR) (FUSIN) (LEUKOCYTE-DERIVED
 DE SEVEN TRANSMEMBRANE DOMAIN RECEPTOR) (LESTR).
 GN CXCR4 OR LESTR OR CXCR4 OR SDF1R.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6 X CBA; TISSUE=Thymus;
 RA Moeppe B., Frodl R., Kessler H., Gierschik P.;
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SV;
 RA Heesen M., Berman M.A., Gerard C., Dorf M.E.;
 RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J;
 RA Heesen M., Berman M.A., Benson J.D., Gerard C., Dorf M.E.;
 RL "Cloning of the mouse fusin gene, homologue to a human HIV-1
 RL co-factor.";
 RL J. Immunol. 157:5455-5460(1996).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Bone marrow;
 RA Nagasawa T., Nakajima T., Tachibana K., Iizasa H., Bleul C.C.,
 RA Yoshie O., Matsushima K., Yoshida N., Springer T.A., Kishimoto T.;
 RA "Molecular cloning and characterization of a murine pre-B-cell
 RT growth-stimulating factor/stromal cell-derived factor 1 receptor, a
 RT murine homolog of the human immunodeficiency virus 1 entry coreceptor
 RT fusin.";
 RL Proc. Natl. Acad. Sci. U.S.A. 93:14726-14729(1996).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Thymus;
 RA Suzuki G., Nakata Y., Uzawa A., Shirasawa T., Saito T., Mita K.;
 RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SV; TISSUE=Thymus;
 RA Schubel A., Burgstahler R., Lipp M.;
 RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: RECEPTOR FOR THE C-X-C CHEMOKINE SDF-1. TRANSDUCES A
 CC SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC
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DR EMBL; X99581; CAA67893.1; -
 DR EMBL; X99582; AAB67894.1; -
 DR EMBL; U59760; AAB07725.1; -
 DR EMBL; U65580; AAC52953.1; -
 DR EMBL; D87747; BAA13451.1; -
 DR EMBL; AB00803; BAA19187.1; -
 DR EMBL; Z80111; CAB02201.1; -
 DR EMBL; Z80112; CAB02202.1; -
 DR GCRDB; GCR_1138; -
 DR GCRDB; GCR_1387; -
 DR GCRDB; GCR_1646; -
 DR GCRDB; GCR_1730; -
 DR GCRDB; GCR_2592; -
 DR MGD; MGI:109563; Cmkar4.
 DR InterPro: IPR000276; -
 DR InterPro: IPR001277; -
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRHHODOPS.
 DR PRINTS; PR00645; LCR1ORPHAN.
 DR PROSITE; PS00237; G_PROTEIN_RECP_FL_1; 1.
 DR PROSITE; PS00262; G_PROTEIN_RECP_FL_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 41
 FT TRANSMEM 42 65
 FT DOMAIN 66 81
 FT TRANSMEM 82 101
 FT DOMAIN 102 112
 FT TRANSMEM 113 134
 FT DOMAIN 135 156
 FT TRANSMEM 157 177
 FT DOMAIN 178 207
 FT TRANSMEM 208 227
 FT DOMAIN 228 247
 FT TRANSMEM 248 268
 FT DOMAIN 269 292
 FT TRANSMEM 293 312
 FT DOMAIN 313 359
 FT DISULFID 111 193
 FT CARBOHYD 13 13
 FT CONFLICT 6 7
 FT CONFLICT 216 216 I -> V (IN REF. 1 AND 5).
 SQ SEQUENCE 359 AA; 40426 MW; 33D1B5552A31595B CRC64;

Query Match 83.3%; Score 75; DB 1; Length 359;
 Best Local Similarity 70.6%; Pred. No. 0.00011;
 Matches 12; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

OY 1 MAIADILFVLTLPFWAV 17
 DB 82 LSVADLLFVLTLPFWAV 98

RESULT 15
 CCR9_MOUSE
 ID CCR9_MOUSE STANDARD; PRT; 369 AA.
 AC O9WU7;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE C-C CHEMOKINE RECEPTOR TYPE 9 (C-C CCR-9) (CCR-9)
 DE (CHEMOKINE C-C RECEPTOR 10).
 GN CCR9 OR CCKBR10.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Thymus;
 RA Zaballos A., Gutierrez J., Varona R., Ardavin C., Marquez G.;
 RL MEDLINE=99248139; PubMed=10229797;
 RT "Cutting edge: identification of the orphan chemokine receptor GPR-9-6

RT as CCR9, the receptor for the chemokine TECK.";
RL J. Immunol. 162:5671-5675(1999).
CC -1- FUNCTION: RECEPTOR FOR CHEMOKINE SCYA25/TECK. SUBSEQUENTLY
CC TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS
CC LEVEL.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN THE THYMUS AND LOW IN
CC LYMPH NODES AND SPLEEN.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC -----
DR EMBL; AJ132336; CAB43480.1; -;
DR MGD; MGI:1341902; Cmkbr10.
DR InterPro; IPR000174; -;
DR InterPro; IPR000248; -;
DR InterPro; IPR000276; -;
DR InterPro; IPR000355; -;
DR InterPro; IPR000496; -;
DR InterPro; IPR001277; -;
DR InterPro; IPR001718; -;
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHDOPSN.
DR PRINTS; PR00241; ANGIOTENSINR.
DR PRINTS; PR00425; BRADYKININR.
DR PRINTS; PR00427; INTRLEUKIN8R.
DR PRINTS; PR00641; CHEMOKINER7.
DR PRINTS; PR00645; LCR1ORPHANR.
DR PRINTS; PR00657; CCHEMOKINER.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 49 EXTRACELLULAR (POTENTIAL).
FT TRANSEM 50 76 1 (POTENTIAL).
FT DOMAIN 77 85 CYTOPLASMIC (POTENTIAL).
FT TRANSEM 86 106 2 (POTENTIAL).
FT DOMAIN 107 120 EXTRACELLULAR (POTENTIAL).
FT TRANSEM 121 142 3 (POTENTIAL).
FT DOMAIN 143 160 CYTOPLASMIC (POTENTIAL).
FT TRANSEM 161 181 4 (POTENTIAL).
FT DOMAIN 182 210 EXTRACELLULAR (POTENTIAL).
FT TRANSEM 211 238 5 (POTENTIAL).
FT DOMAIN 239 254 CYTOPLASMIC (POTENTIAL).
FT TRANSEM 255 280 6 (POTENTIAL).
FT DOMAIN 281 304 EXTRACELLULAR (POTENTIAL).
FT TRANSEM 305 322 7 (POTENTIAL).
FT DOMAIN 323 369 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 32 32 N-LINKED (GLCNAC. .) (POTENTIAL).
FT DISULFID 119 198 BY SIMILARITY.
SQ SEQUENCE 369 AA; 41913 MW; 6971F76F0A24B4AE CRC64;

Query Match 81.1%; Score 73; DB 1; Length 369;
Best Local Similarity 66.7%; Pred. No. 0.00022;
Matches 12; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAIADILFVLTPFAVS 18
:|||||:|||||:
Db 90 LAIADLLFLATLPFAIA 107

Search completed: May 23, 2001, 15:36:17
Job time: 648 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 23, 2001, 15:35:12 ; Search time 189.03 Seconds
(without alignments)
11.161 Million cell updates/sec

Title: US-08-887-977-10_COPY_79_96
Perfect score: 90
Sequence: 1 MAIADILFVLTLFPFAVS 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues
Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL15:
1: sp_archaea:
2: sp_bacteria:
3: sp_fungi:
4: sp_human:
5: sp_invertebrate:
6: sp_mammal:
7: sp_mhc:
8: sp_organelle:
9: sp_phase:
10: sp_plant:
11: sp_rodent:
12: sp_unclassified:
13: sp_vertebrate:
14: sp_virus:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	83	92.2	367	11	Q9R1V0	Q9R1V0 mus musculus
2	78	86.7	353	13	Q93247	Q93247 cyprinus ca
3	78	86.7	353	13	Q9PTF7	Q9PTF7 brachydanio
4	77	85.6	357	13	Q42445	Q42445 oncorhynchus
5	75	83.3	334	6	Q9N1P4	Q9N1P4 cercopithec
6	75	83.3	334	6	Q9N1P3	Q9N1P3 hylobates l
7	75	83.3	334	6	Q9N1P2	Q9N1P2 saquinus oe
8	75	83.3	334	6	Q9N130	Q9N130 saimiri bol
9	75	83.3	346	6	Q9MZM4	Q9MZM4 nycticebus
10	75	83.3	346	6	Q9MZM3	Q9MZM3 nycticebus
11	75	83.3	346	6	Q9MZM2	Q9MZM2 nycticebus
12	75	83.3	347	6	Q9MZQ3	Q9MZQ3 pygathrix a
13	75	83.3	347	6	Q9MZQ2	Q9MZQ2 rhinopithec
14	75	83.3	347	6	Q9MZQ1	Q9MZQ1 pygathrix b
15	75	83.3	347	6	Q9MZQ0	Q9MZQ0 pygathrix n
16	75	83.3	347	6	Q9MZP9	Q9MZP9 nasalis lar
17	75	83.3	347	6	Q9MZP8	Q9MZP8 colobus pol
18	75	83.3	347	6	Q9MZP7	Q9MZP7 presbytis s
19	75	83.3	347	6	Q9MZP6	Q9MZP6 presbytis j

20	75	83.3	347	6	Q9MZP5	Q9MZP5 presbytis p
21	75	83.3	347	6	Q9MZP4	Q9MZP4 presbytis f
22	75	83.3	347	6	Q9MZP3	Q9MZP3 presbytis e
23	75	83.3	347	6	Q9MZP2	Q9MZP2 mandrillus
24	75	83.3	347	6	Q9MZP1	Q9MZP1 mandrillus
25	75	83.3	347	6	Q9MZP0	Q9MZP0 macaca assa
26	75	83.3	347	6	Q9MZN9	Q9MZN9 macaca thib
27	75	83.3	347	6	Q9MZN8	Q9MZN8 macaca arct
28	75	83.3	347	6	Q9MZN7	Q9MZN7 macaca neme
29	75	83.3	347	6	Q9MZN6	Q9MZN6 hylobates c
30	75	83.3	347	6	Q9MZN5	Q9MZN5 hylobates h
31	75	83.3	347	6	Q9MZN4	Q9MZN4 hylobates l
32	75	83.3	347	6	Q9MZN3	Q9MZN3 hylobates s
33	75	83.3	347	6	Q9MZN2	Q9MZN2 pongo pygma
34	75	83.3	347	6	Q9MZN1	Q9MZN1 gorilla gor
35	75	83.3	347	6	Q9MZN0	Q9MZN0 alouatta se
36	75	83.3	347	6	Q9MZM9	Q9MZM9 ateles pani
37	75	83.3	347	6	Q9MZM8	Q9MZM8 callithrix
38	75	83.3	347	6	Q9MZM6	Q9MZM6 callicebus
39	75	83.3	347	6	Q9MZM5	Q9MZM5 pithecia pi
40	75	83.3	347	6	Q9MZM1	Q9MZM1 eulemur mac
41	75	83.3	347	6	Q9MZM0	Q9MZM0 perodicticu
42	75	83.3	352	6	O77488	O77488 cercopithec
43	75	83.3	352	6	Q9TSQ8	Q9TSQ8 cercopithec
44	75	83.3	356	4	Q9UKN2	Q9UKN2 homo sapien
45	75	83.3	360	4	O60835	O60835 homo sapien

ALIGNMENTS

RESULT 1
Q9R1V0 PRELIMINARY; PRT; 367 AA.
ID Q9R1V0
AC Q9R1V0
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE CC-CHEMOKINE LARC SPECIFIC RECEPTOR.
GN MCCR6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Tanaka Y.;
RT "Molecular Cloning of Murine Homologue of CCR6, the Specific Receptor
for CC Chemokine LARC."
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB016031; BAA82443.1;
DR INTERPRO: IPR000190;
DR INTERPRO: IPR000276;
DR INTERPRO: IPR000355;
DR PFAM: PF00001; 7tm.1; 1.
DR PRINTS: PR00237; GPCRHHODPSN.
DR PRINTS: PR00635; ANGIOTENSINR.
DR PRINTS: PR00657; CCHEMOKINER.
DR PROSITE: PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
KW Receptor.
SQ SEQUENCE 367 AA; 42082 MW; 207FD98B2F7A6DD3 CRC64;

Query Match 92.2%; Score 83; DB 11; Length 367;
Best Local Similarity 88.9%; Pred. No. 2.2e-05;
Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAIADILFVLTLFPFAVS 18
DB 80 MAITDILFVLTLFPFAVT 97

RESULT 2

O93247
ID O93247 PRELIMINARY; PRT; 353 AA.
AC O93247;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE CXCR4.
OS Cyprinus carpio (Common carp).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Cyprininae; Cyprinus.
OX NCBI_TaxID=7962;
RN [1]
RP SEQUENCE FROM N.A.
RA Fujiki K., Nakao M., Shin D., Yano T.;
RT "cDNA cloning of a carp homologue of mammalian CXCR4.";
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; AB012310; BAA32797.1; -;
DR INTERPRO; IPR000276; -;
DR PFAM; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
SQ SEQUENCE 353 AA; 39633 MW; 84924BE413FB3B3F CRC64;

Query Match 86.7%; Score 78; DB 13; Length 353;
Best Local Similarity 82.4%; Pred. No. 0.00013;
Matches 14; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAIADILFVLTLPFWAV 17
Db 78 LSIADLLFVLTLPFWAV 94
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RESULT 3
Q9PTF7
ID Q9PTF7 PRELIMINARY; PRT; 353 AA.
AC Q9PTF7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE CHEMOKINE RECEPTOR CXCR4.
GN CXCR4.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Rasbora; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Tseng S., Rollins B.J.;
RT "Chemokines and chemokine receptors in zebrafish.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF201451; AAF17561.1; -;
DR INTERPRO; IPR000276; -;
DR PFAM; PF000355; -;
DR INTERPRO; IPR001277; -;
DR PFAM; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PRINTS; PR00645; LCRIORPHANR.
DR PRINTS; PR00657; CCHEMOKINER.
KW PROSITE; PS00237; G_PROTEIN_RECEPTOR; 1.
SQ SEQUENCE 353 AA; 39444 MW; 410F9A7F75D631BE CRC64;

Query Match 86.7%; Score 78; DB 13; Length 353;
Best Local Similarity 82.4%; Pred. No. 0.00013;
Matches 14; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAIADILFVLTLPFWAV 17
Db 78 LSIADLLFVLTLPFWAV 94
:::|||||

RESULT 4
O42445
ID O42445 PRELIMINARY; PRT; 357 AA.
AC O42445;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE CXC CHEMOKINE RECEPTOR.
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE FROM N.A.
RA Daniels G.D., Charlemagne J., Secombes C.J.;
RT "Cloning and sequencing of a rainbow trout, Oncorhynchus mykiss, chemokine receptor homolog.";
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; AJ001039; CAA04493.1; -;
DR INTERPRO; IPR000276; -;
DR PFAM; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
SQ SEQUENCE 357 AA; 39817 MW; 14EC2F0IDA1222C4 CRC64;

Query Match 85.6%; Score 77; DB 13; Length 357;
Best Local Similarity 76.5%; Pred. No. 0.00019;
Matches 13; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAIADILFVLTLPFWAV 17
Db 82 LSVADLLFVLTLPFWAV 98
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RESULT 5
Q9N1P4
ID Q9N1P4 PRELIMINARY; PRT; 334 AA.
AC Q9N1P4;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE CXC CHEMOKINE RECEPTOR 4 (FRAGMENT).
GN CXCR4.
OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9534;
RN [1]
RP SEQUENCE FROM N.A.
RA Zubair S., Metzberg S.;
RT "CXCR4 homologs of Gibbon ape, African green monkey, and Cotton-top marmoset.";
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF178082; AAF42990.1; -;
KW Receptor.
FT NON_TER 1 1
FT NON_TER 334 334
SQ SEQUENCE 334 AA; 37752 MW; 8C91CED8AB54D131 CRC64;

Query Match 83.3%; Score 75; DB 6; Length 334;
Best Local Similarity 70.6%; Pred. No. 0.00037;

Matches 12; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAIADILFVLTLPFWAV 17
:::|||||
Db 67 LSVADLLFVLTLPFWAV 83

RESULT 6

Q9NIP3 ID Q9NIP3 PRELIMINARY; PRT; 334 AA.
AC Q9NIP3;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
DE CXC CHEMOKINE RECEPTOR 4 (FRAGMENT).
GN CXCR4.
OS Hylobates lar (Common gibbon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
OX NCBI_TaxID=9580;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LYMPHOSARCOMA;
RA Zubair S., Metzberg S.;
RT "CXCR4 homologs of Gibbon ape, African green monkey, and Cotton-top marmoset."
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF178083; AAF42991.1; -
KW Receptor.
FT NON_TER 1 1
FT NON_TER 334 334
SQ SEQUENCE 334 AA; 37725 MW; C8813B0CB3CF9A61 CRC64;

Query Match 83.3%; Score 75; DB 6; Length 334;

Best Local Similarity 70.6%; Pred. No. 0.00037;
Matches 12; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAIADILFVLTLPFWAV 17
:::|||||
Db 67 LSVADLLFVLTLPFWAV 83

RESULT 7

Q9NIP2 ID Q9NIP2 PRELIMINARY; PRT; 334 AA.
AC Q9NIP2;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
DE CXC CHEMOKINE RECEPTOR 4 (FRAGMENT).
GN CXCR4.
OS Saguinus oedipus (Cotton-top tamarin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Saguinus.
OX NCBI_TaxID=9490;
RN [1]
RP SEQUENCE FROM N.A.
RA Zubair S., Metzberg S.;
RT "CXCR4 homologs of Gibbon ape, African green monkey, and Cotton-top marmoset."
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF178084; AAF42992.1; -
KW Receptor.
FT NON_TER 1 1
FT NON_TER 334 334
SQ SEQUENCE 334 AA; 37877 MW; EB2362E88D0997C5 CRC64;

Query Match 83.3%; Score 75; DB 6; Length 334;

Best Local Similarity 70.6%; Pred. No. 0.00037;
Matches 12; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAIADILFVLTLPFWAV 17
:::|||||
Db 67 LSVADLLFVLTLPFWAV 83

RESULT 8

Q9N130 ID Q9N130 PRELIMINARY; PRT; 334 AA.
AC Q9N130;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
DE CXCR4 RECEPTOR (FRAGMENT).
OS Saimiri boliviensis (Bolivian squirrel monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Saimiri.
OX NCBI_TaxID=27679;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BLOOD;
RA Zubair S., Metzberg S.;
RT "CXCR4 homologs of Gibbon ape, African green monkey, Cotton-top marmoset, and Bolivian squirrel monkey."
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF229128; AAF37288.1; -
KW Receptor.
FT NON_TER 1 1
FT NON_TER 334 334
SQ SEQUENCE 334 AA; 37943 MW; 277227E898098DB5 CRC64;

Query Match 83.3%; Score 75; DB 6; Length 334;

Best Local Similarity 70.6%; Pred. No. 0.00037;
Matches 12; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAIADILFVLTLPFWAV 17
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Db 67 LSVADLLFVLTLPFWAV 83

RESULT 9

Q9M2M4 ID Q9M2M4 PRELIMINARY; PRT; 346 AA.
AC Q9M2M4;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
DE CHEMOKINE RECEPTOR CXCR4 (FRAGMENT).
GN CXCR4.
OS Nycticebus coucang (Slow loris).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Strepsirhini; Loridae; Nycticebus.
OX NCBI_TaxID=9470;
RN [1]
RP SEQUENCE FROM N.A.
RA Zheng X.-Z., Zhang Y.-P., Geng Z.-C.;
RT "Molecular Evolution of the Chemokine Receptor CXCR4 Gene Sequences in Primates."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF172239; AAF89359.1; -
KW Receptor.
FT NON_TER 1 1
SQ SEQUENCE 346 AA; 39235 MW; BC1766D2E634CCEE CRC64;

Query Match 83.3%; Score 75; DB 6; Length 346;

Best Local Similarity 70.6%; Pred. No. 0.00038;
Matches 12; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAIADILFVLTLPFWAV 17
:::|||||
Db 75 LSVADLLFVLTLPFWAV 91

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RESULT 10
Q9MZM3
ID Q9MZM3 PRELIMINARY; PRT; 346 AA.
AC Q9MZM3;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE CHEMOKINE RECEPTOR CXCR4 (FRAGMENT).
GN CXCR4.
OS Nycticebus intermedius.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Strepsirhini; Loridae; Nycticebus.
OX NCBI_TaxID=101277;
RN [1]
RP SEQUENCE FROM N.A.
RA Zheng X.-Z., Zhang Y.-P., Geng Z.-C.;
RT "Molecular Evolution of the Chemokine Receptor CXCR4 Gene Sequences in
RT Primates.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF172240; AAF89360.1;
KW Receptor.
FT NON_TER
SQ SEQUENCE 346 AA; 39235 MW; BC1766D2E634CCEE CRC64;

Query Match 83.3%; Score 75; DB 6; Length 346;
Best Local Similarity 70.6%; Pred. No. 0.00038;
Matches 12; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAIADILFVLTLPFWAV 17
Db 75 LSVADLLFVLTLPFWAV 91
:::||||:|||||

RESULT 11
Q9MZM2
ID Q9MZM2 PRELIMINARY; PRT; 346 AA.
AC Q9MZM2;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE CHEMOKINE RECEPTOR CXCR4 (FRAGMENT).
GN CXCR4.
OS Nycticebus pygmaeus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Strepsirhini; Loridae; Nycticebus.
OX NCBI_TaxID=101278;
RN [1]
RP SEQUENCE FROM N.A.
RA Zheng X.-Z., Zhang Y.-P., Geng Z.-C.;
RT "Molecular Evolution of the Chemokine Receptor CXCR4 Gene Sequences in
RT Primates.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF172241; AAF89361.1;
KW Receptor.
FT NON_TER
SQ SEQUENCE 346 AA; 39235 MW; BC1766D2E634CCEE CRC64;

Query Match 83.3%; Score 75; DB 6; Length 346;
Best Local Similarity 70.6%; Pred. No. 0.00038;
Matches 12; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAIADILFVLTLPFWAV 17
Db 75 LSVADLLFVLTLPFWAV 91
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RESULT 12
Q9MZQ3
ID Q9MZQ3 PRELIMINARY; PRT; 347 AA.
AC Q9MZQ3;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE CHEMOKINE RECEPTOR CXCR4 (FRAGMENT).
GN CXCR4.
OS Pygathrix avunculus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
OC Pygathrix.
OX NCBI_TaxID=66062;
RN [1]
RP SEQUENCE FROM N.A.
RA Zheng X.-Z., Zhang Y.-P., Geng Z.-C.;
RT "Molecular Evolution of the Chemokine Receptor CXCR4 Gene Sequences in
RT Primates.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF172210; AAF89330.1;
KW Receptor.
FT NON_TER
SQ SEQUENCE 347 AA; 39205 MW; E96B66136541515C CRC64;

Query Match 83.3%; Score 75; DB 6; Length 347;
Best Local Similarity 70.6%; Pred. No. 0.00038;
Matches 12; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAIADILFVLTLPFWAV 17
Db 75 LSVADLLFVLTLPFWAV 91
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RESULT 13
Q9MZQ2
ID Q9MZQ2 PRELIMINARY; PRT; 347 AA.
AC Q9MZQ2;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE CHEMOKINE RECEPTOR CXCR4 (FRAGMENT).
GN CXCR4.
OS Rhinopithecus roxellanae.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
OC Pygathrix.
OX NCBI_TaxID=101279;
RN [1]
RP SEQUENCE FROM N.A.
RA Zheng X.-Z., Zhang Y.-P., Geng Z.-C.;
RT "Molecular Evolution of the Chemokine Receptor CXCR4 Gene Sequences in
RT Primates.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF172211; AAF89331.1;
KW Receptor.
FT NON_TER
SQ SEQUENCE 347 AA; 39205 MW; E96B66136541515C CRC64;

Query Match 83.3%; Score 75; DB 6; Length 347;
Best Local Similarity 70.6%; Pred. No. 0.00038;
Matches 12; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAIADILFVLTLPFWAV 17
Db 75 LSVADLLFVLTLPFWAV 91
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RESULT 14
Q9MZQ1
ID Q9MZQ1 PRELIMINARY; PRT; 347 AA.
AC Q9MZQ1;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE CHEMOKINE RECEPTOR CXCR4 (FRAGMENT).
GN CXCR4.
OS Pygathrix avunculus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
OC Pygathrix.
OX NCBI_TaxID=66062;
RN [1]
RP SEQUENCE FROM N.A.
RA Zheng X.-Z., Zhang Y.-P., Geng Z.-C.;
RT "Molecular Evolution of the Chemokine Receptor CXCR4 Gene Sequences in
RT Primates.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF172211; AAF89331.1;
KW Receptor.
FT NON_TER
SQ SEQUENCE 347 AA; 39205 MW; E96B66136541515C CRC64;

Query Match 83.3%; Score 75; DB 6; Length 347;
Best Local Similarity 70.6%; Pred. No. 0.00038;
Matches 12; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAIADILFVLTLPFWAV 17
Db 75 LSVADLLFVLTLPFWAV 91
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DE CHEMOKINE RECEPTOR CXCR4 (FRAGMENT).
GN CXCR4.
OS Pygathrix bieti (Black snub-nosed monkey) (Rhinopithecus bieti).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae; Colobinae;
OC Pygathrix.
OX NCBI_TaxID=61621;
RN [1]
RP SEQUENCE FROM N.A.
RA Zheng X.-Z., Zhang Y.-P., Geng Z.-C.;
RT "Molecular Evolution of the Chemokine Receptor CXCR4 Gene Sequences in
RT Primates.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF172212; AAF89332.1; -
KW Receptor.
FT NON_TER
SQ SEQUENCE 347 AA; 39205 MW; E96B66136541515C CRC64;

Query Match 83.3%; Score 75; DB 6; Length 347;
Best Local Similarity 70.6%; Pred. No. 0.00038;
Matches 12; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAIADILFVLTLPFWAV 17
   :::::|||||
Db 75 LSVADLLFVTLTPFWAV 91

RESULT 15
Q9MZQ0 PRELIMINARY; PRT; 347 AA.
AC Q9MZQ0;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE CHEMOKINE RECEPTOR CXCR4 (FRAGMENT).
GN CXCR4.
OS Pygathrix nemaeus (Dove langur).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae; Colobinae;
OC Pygathrix.
OX NCBI_TaxID=54133;
RN [1]
RP SEQUENCE FROM N.A.
RA Zheng X.-Z., Zhang Y.-P., Geng Z.-C.;
RT "Molecular Evolution of the Chemokine Receptor CXCR4 Gene Sequences in
RT Primates.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF172213; AAF89333.1; -
KW Receptor.
FT NON_TER
SQ SEQUENCE 347 AA; 39205 MW; E96B66136541515C CRC64;

Query Match 83.3%; Score 75; DB 6; Length 347;
Best Local Similarity 70.6%; Pred. No. 0.00038;
Matches 12; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAIADILFVLTLPFWAV 17
   :::::|||||
Db 75 LSVADLLFVTLTPFWAV 91

Search completed: May 23, 2001, 15:35:12
Job time: 618 sec
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 23, 2001, 15:28:27 ; Search time 184.73 Seconds
(without alignments)
4.332 Million cell updates/sec

Title: US-08-887-977-10_COPY_97_110

Perfect score: 81

Sequence: 1 HATGAWVFSNATCK 14

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 390729 seqs, 57163235 residues

Total number of hits satisfying chosen parameters: 390729

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_0401.*
1: /SID56/qcgdata/geneseq/geneseq/AA1980.DAT.*
2: /SID56/qcgdata/geneseq/geneseq/AA1981.DAT.*
3: /SID56/qcgdata/geneseq/geneseq/AA1982.DAT.*
4: /SID56/qcgdata/geneseq/geneseq/AA1983.DAT.*
5: /SID56/qcgdata/geneseq/geneseq/AA1984.DAT.*
6: /SID56/qcgdata/geneseq/geneseq/AA1985.DAT.*
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22: /SID56/qcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	81	100.0	365	19 W48086	Human dendritic ce
2	81	100.0	365	21 Y97077	Primate (human) ch
3	49	60.5	1455	19 W48663	Fanconi anaemia of
4	47	58.0	360	16 R79166	Human monocyte che
5	47	58.0	360	18 W35833	Human monocyte che
6	47	58.0	374	16 R79165	Human monocyte che
7	45	55.6	415	21 Y90634	Human G protein-co
8	45	55.6	415	21 Y90668	Human mutant G pro
9	44.5	54.9	428	21 Y56887	Human B5 receptor
10	44.5	54.9	430	21 Y93151	Novel human G-prot
11	44.5	54.9	430	21 Y79376	Human neuropeptide

12	44.5	54.9	432	21 Y93146	Novel rat G-protei
13	44.5	54.9	432	21 Y79373	Rat neuropeptide F
14	44.5	54.9	432	21 Y56886	Rat B5 receptor po
15	43	53.1	321	21 G31332	Arabidopsis thalia
16	43	53.1	342	21 G31331	Arabidopsis thalia
17	43	53.1	349	21 G31330	Arabidopsis thalia
18	43	53.1	354	19 W54037	Mouse CC-CRR5 prot
19	42	51.9	131	21 B24020	Arachidonic acid m
20	42	51.9	213	21 Y68859	A kappa3-related o
21	42	51.9	341	21 Y68861	A kappa3-related o
22	42	51.9	343	21 Y68856	A kappa3-related o
23	42	51.9	343	21 Y68860	A kappa3-related o
24	42	51.9	365	21 Y68862	A kappa3-related o
25	42	51.9	367	16 R74298	Mouse kappa-3 Opio
26	42	51.9	367	16 R71968	Rat opioid recepto
27	42	51.9	367	16 R67671	Mouse opioid recep
28	42	51.9	367	16 R76638	Rat opioid recept
29	42	51.9	367	21 B07868	A rat mu opioid re
30	42	51.9	370	21 Y55988	Variant orphan noc
31	42	51.9	663	21 B24019	Arachidonic acid m
32	41	50.6	310	21 G21034	Arabidopsis thalia
33	41	50.6	310	21 G50071	Arabidopsis thalia
34	41	50.6	324	21 G21033	Arabidopsis thalia
35	41	50.6	324	21 G50070	Arabidopsis thalia
36	41	50.6	368	21 G21032	Arabidopsis thalia
37	41	50.6	368	21 G50069	Arabidopsis thalia
38	41	50.6	2150	21 Y53898	Amino acid sequenc
39	40	49.4	66	21 B33299	Pinus radiata tran
40	40	49.4	263	17 W11236	G-protein conjugat
41	40	49.4	263	17 R91233	Rabbit G-protein c
42	40	49.4	362	20 Y06324	Mouse G protein co
43	40	49.4	362	20 W92976	Rat mACHR-6 protei
44	40	49.4	369	17 W06125	Neuropeptide recep
45	40	49.4	370	20 W92977	Rat mACHR-6 protei

ALIGNMENTS

RESULT	1
W48086	
ID	W48086 standard; Protein; 365 AA.
XX	
AC	W48086;
XX	
DT	11-JUN-1998 (first entry)
XX	
DE	Human dendritic cell chemokine receptor.
XX	
DE	Human; thymus expressed chemokine; TECK; MIP-3alpha; MIP-3beta;
KW	receptor; dendritic cell; macrophage; inflammation; asthma.
KW	
XX	
OS	Homo sapiens.
XX	
FH	Key
FT	Misc-difference 193
FT	/note= "encoded by CAN"
XX	
XX	WO9801557-A2.
PN	
XX	
PD	15-JAN-1998.
XX	
PF	02-JUL-1997; 97WO-US10819.
XX	
PR	04-JUN-1997; 97US-0048593.
PR	05-JUL-1996; 96US-0675814.
PR	11-OCT-1996; 96US-0028329.
XX	
XX	(SCHE) SCHERING CORP.
PA	
XX	
PI	Gish KC, Schall TJ, Vicari A, Wang W, Zlotnik A;
XX	
DR	WPI; 1998-101054/09.

DR N-PSDB; V15418.
XX Novel chemokines, e.g. thymus expressed chemokine - used for
PT treating inflammatory conditions including asthma.
PT Claim 3; Page 94-95; 202pp; English.
XX
XX The present sequence represents human dendritic cell chemokine receptor.
CC Antibodies which bind to the protein can be used in detecting or
CC diagnosing various immunological conditions related to expression
CC of the protein. The nucleic acid can be used for screening and
CC isolating DNA clones for the chemokines, especially from other
CC species. The chemokine can be used in the treatment of conditions
CC associated with abnormal physiology or development, including
CC inflammatory conditions such as asthma.
XX
XX Sequence 365 AA;
SQ

Query Match 100.0%; Score 81; DB 19; Length 365;
Best Local Similarity 100.0%; Pred. No. 1.8e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HATGAWFSNATCK 14
Db 97 hatgawfsnatck 110
|||||

RESULT 2
Y97077
ID Y97077 standard; Protein; 365 AA.
XX
XX Y97077;
XX
XX 04-DEC-2000 (first entry)
XX
XX Primate (human) chemokine receptor CCR6.
XX
XX MIP-3-alpha; chemokine; CCR6 receptor; ligand; cytostatic; agonist;
KW antagonist; anti-psoriatic; dermatological; immunosuppressive;
KW anti-inflammatory.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FT Misc-difference 193 /note="Encoded by CAN#"
FT
XX
XX WO200046248-A1.
XX
XX 10-AUG-2000.
XX
XX 02-FEB-2000; 2000WO-US00511.
XX
XX 03-FEB-1999; 99US-0244281.
XX
XX (SCHE) SCHERING CORP.
XX
XX Oldham ER, Homey B, Dieu-Nosjean M, Caux C, Zlotnik A;
XX
XX WPI; 2000-543477/49.
XX
XX N-PSDB; A51971.
XX
XX Novel methods for modulating the migration of cells within or to the
PT skin using MIP-3-alpha or CCR6 agonists or antagonists, useful for
PT treating skin disorders, e.g. cancer
XX
XX Disclosure; Page 53-54; 61pp; English.
XX
XX The MIP-3-alpha chemokine is expressed in inflamed skin cells. This
CC chemokine is the ligand for the CCR6 receptor. MIP-3-alpha or CCR6
CC agonists or antagonists can be used to modulate the migration of a cell
CC within or to the skin of a mammal. MIP-3-alpha can be used to purify a

CC population of cells expressing a MIP-3-alpha receptor. The methods are
CC useful for treating a mammalian subject with a skin disease or condition,
CC e.g. cancer, metastasis, psoriasis, atopic or contact dermatitis,
CC systemic lupus erythematosus and lichen ruber planus, or for treating
CC skin transplants or grafts.
XX
XX Sequence 365 AA;
SQ

Query Match 100.0%; Score 81; DB 21; Length 365;
Best Local Similarity 100.0%; Pred. No. 1.8e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HATGAWFSNATCK 14
Db 97 hatgawfsnatck 110
|||||

RESULT 3
W48663
ID W48663 standard; Protein; 1455 AA.
XX
XX W48663;
AC
XX 28-AUG-1998 (first entry)
DT
XX
XX Fanconi anaemia of complementation group A protein.
XX
XX Fanconi anaemia of complementation group A; FA-A; genetic defect;
KW prenatal FA-A; FA-A carrier detection; disease diagnosis.
XX
XX Homo sapiens.
OS
XX
XX WO9814462-A1.
XX
XX 09-APR-1998.
XX
XX 03-OCT-1997; 97WO-US18010.
XX
XX 04-OCT-1996; 96US-0726012.
PR
XX
XX (FANC-) FANCONI ANEMIA RES FUND INC.
XX
XX Joenje H, Lo Ten Foe JR;
XX
XX WPI; 1998-240012/21.
DR
XX
XX N-PSDB; V18187.
XX
XX DNA for Fanconi Anaemia complementation group A - useful for, e.g.
PT developing products for diagnosis and screening of disease and gene
PT therapy
XX
XX Claim 1; Fig 3; 63pp; English.
XX
XX This sequence is the Fanconi anaemia of complementation group A
CC (FA-A) protein of the invention. The DNA's may be used to complement a
CC genetic defect in a cell (especially the FA-A gene). The products can be
CC used for screening (especially prenatal FA-A), detection of FA-A carriers
CC and FA-A disease diagnosis.
XX
XX Sequence 1455 AA;
SQ

Query Match 60.5%; Score 49; DB 19; Length 1455;
Best Local Similarity 53.8%; Pred. No. 12;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY 1 HATGAWFSNATC 13
Db 204 havgswifnrncc 216
|||||

RESULT 4


```

CC has a mol. wt. of about 41,000 daltons.
XX
SQ Sequence 360 AA;

Query Match 58.0%; Score 47; DB 16; Length 360;
Best Local Similarity 61.5%; Pred. No. 5.9;
Matches 8; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 ATGAWFSNATCK 14
   | ||| || ||
Db 102 aanewvfgnamck 114

RESULT 5
W35833
ID W35833 standard; Protein; 360 AA.
XX
XX W35833;
XX
XX 27-FEB-1998 (first entry)
XX
XX Human monocyte chemoattractant protein 1 receptor.
DE
XX Human; MCP-1; monocyte chemoattractant protein; receptor; tumour;
KW inflammatory disease; viral; allergy; diabetes.
KW
XX Homo sapiens.
OS
XX JP09238688-A.
PN
XX 16-SEP-1997.
PD
XX
XX 11-MAR-1996; 96JP-0053574.
PF
XX
XX 11-MAR-1996; 96JP-0053574.
PR
XX
XX (TAKE ) TAKEDA CHEM IND LTD.
PA
XX
XX WPI: 1997-506557/47.
DR
XX N-PSDB; T96976.
DR
XX
XX DNA encoding human monocyte chemoattractant protein 1 receptor -
PT used to treat tumours and inflammatory, viral, infectious, allergic,
PT diabetic and central nervous system diseases
PT
PT Disclosure; Page 12-14; 15pp; Japanese.
PS
XX
XX The present sequence represents human monocyte chemoattractant protein 1
CC (MCP-1) receptor protein. The MCP-1 receptor protein and encoding DNA
CC are used for the prevention and treatment of tumours and inflammatory,
CC viral, infectious, allergic, diabetic and central nervous system
CC diseases.
CC
SQ Sequence 360 AA;

Query Match 58.0%; Score 47; DB 18; Length 360;
Best Local Similarity 61.5%; Pred. No. 5.9;
Matches 8; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 ATGAWFSNATCK 14
   | ||| || ||
Db 102 aanewvfgnamck 114

RESULT 6
R79165
ID R79165 standard; Protein; 374 AA.
XX
XX R79165;
AC
XX
XX 29-DEC-1995 (first entry)
DT

```

XX Human monocyte chemoattractant protein-1 receptor MCP-1RA.
 XX Monocyte chemoattractant protein-1 receptor; MCP-1R; chemokine.
 XX Homo sapiens.

Key Location/Qualifiers
 FH Domain 49..70
 FT /label= transmembrane
 FT Domain 80..700
 FT /label= transmembrane
 FT Domain 115..136
 FT /label= transmembrane
 FT Domain 154..178
 FT /label= transmembrane
 FT Domain 204..231
 FT /label= transmembrane
 FT Domain 244..268
 FT /label= transmembrane
 FT Domain 295..313
 FT /label= transmembrane
 FT Region 314..375
 FT /label= carboxyl tail
 FT Domain 1..48
 FT /label= extracellular

XX W09519436-A.
 XX 20-JUL-1995.
 XX 11-JAN-1995; 95WO-US00476.
 XX 13-JAN-1994; 94US-0182962.
 XX (REGC) UNIV CALIFORNIA.
 XX Charo I, Coughlin S;
 XX WPI: 1995-263866/34.
 XX N-PSDB; Q96297.

XX DNA encoding monocyte chemo-attractant protein-1 receptor - used partic.
 XX for identifying antagonists and for treating diseases characterised by
 XX monocytic infiltrates

XX Claim 2; Fig 1; 84pp; English.

XX To identify and clone new members of the chemokine receptor gene
 CC family, degenerate oligo primers were designed corresp. to the
 CC conserved sequences R79167 in the second and R79168 in the third
 CC transmembrane domains of the MIP-1alpha/RANTES receptor, the IL-8
 CC receptors and the HMOSTRS orphan receptor (GenBank Accession #M99293).
 CC The degenerate oligo incorporating EcoRI and XhoI sites at their 5',
 CC ends are Q96299 and Q96300. Amplification of cDNA derived from MM6
 CC cells with the primers yielded a number of PCR products. One cDNA
 CC appeared to encode a novel protein. To obtain a full-length version
 CC of this clone, a MM6 cDNA library was constructed in pPROG and probed
 CC with the PCR product. A 2.1 kb cDNA clone was obt'd. Analysis of
 CC additional clones in the MM6 cDNA library revealed a second
 CC sequence that was identical to the 2.1 kb cDNA sequence first obt'd.
 CC from the 5' UTR through the putative seventh transmembrane domain
 CC but contained a different cytoplasmic tail. The second sequence
 CC appears to represent alternative splicing of the carboxyl-terminal
 CC tail of the MCP-1R protein. The two sequences are denoted MCP-1RA
 CC and MCP-1RB (see Q96297/R79165 & Q96298/R79166). Active mature
 CC MCP-1RA has a predicted mol. wt. of about 42,000 daltons. MCP-1RB
 CC has a mol. wt. of about 41,000 daltons.

XX Sequence 374 AA;

Query Match 58.0%; Score 47; DB 16; Length 374;

Best Local Similarity 61.5%; Pred. No. 6.1;
 Matches 8; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 ATGAWVFSNATCK 14
 | | | | | | | |
 Db 102 aanewvfgnamck 114

RESULT 7

Y90634
 ID Y90634 standard; Protein; 415 AA.

XX AC Y90634;

XX DT 21-AUG-2000 (first entry)

XX DE Human G protein-coupled receptor GPR-NGA.

XX KW G protein-coupled receptor; GPCR; constitutively active;
 KW intracellular loop 3; transmembrane domain 6; drug screening;
 KW agonist; antagonist.

XX OS Homo sapiens.

XX PN W0200022129-A1.

XX PD 20-APR-2000.

XX PF 12-OCT-1999; 99WO-US23938.

XX PR 13-OCT-1998; 98US-0170496.

XX PA (AREN-) ARENA PHARM INC.

XX PI Behan DP, Chalmers DT, Liaw CW;

XX DR WPI: 2000-329165/28.

XX DR N-PSDB; A30649.

XX Non-endogenous constitutively activated human G protein-coupled
 PT receptors, useful for identifying agonists for use as pharmaceutical
 PT agents -

XX Example 1; Page 175-176; 341pp; English.

XX The invention relates to constitutively active, non-endogenous versions
 CC of endogenous human orphan G protein-coupled receptors (GPCRs, Y90643-
 CC Y90677 and Y90683-Y90687), and to DNA encoding them (A30709-A30743 and
 CC A30775-A30779). The mutant proteins of the invention contain a
 CC mutation in a portion of the protein comprising intracellular loop 3
 CC (IC3) and transmembrane domain 6 (TM6). A non-endogenous amino acid, X,
 CC is substituted for an endogenous residue in IC3 at a position 16 amino
 CC acids N-terminal of an endogenous proline in TM6 to form a sequence
 CC X-(AA)15-Pro. The endogenous amino acid is selected from Lys, His, Arg or
 CC Ala, and is preferably Lys. When the endogenous residue at this position
 CC is Lys, this residue is replaced by His, Arg or preferably Ala. The 15
 CC amino acid stretch between the substituted amino acid and the Pro may be
 CC endogenous, non-endogenous, or a mixture of endogenous and non-endogenous
 CC residues. The constitutively active GPCRs are useful for identifying
 CC antagonists, agonists and partial agonists for use as pharmaceutical
 CC agents. The mutant proteins are also useful in research settings for
 CC elucidating the roles of the receptors in normal and diseased conditions.
 CC Antagonists for a particular GPCR are useful for treating diseases and
 CC disorders associated with that receptor. Because the novel mutant GPCRs
 CC are constitutively active, they can be used directly for screening of
 CC compounds without the need for endogenous ligands. The present
 CC sequence represents a human wild-type GPCR referred to in an
 CC exemplification of the invention.

XX Sequence 415 AA;

Query Match 55.6%; Score 45; DB 21; Length 415;

Best Local Similarity 58.3%; Pred. No. 14;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 3 TGAWFSNATCK 14
||| :||||
Db 128 tgrwtlgsatck 139

RESULT 8
Y90668
ID Y90668 standard; Protein; 415 AA.
XX
AC Y90668;
XX
XX 21-AUG-2000 (first entry)
XX
XX Human mutant G protein-coupled receptor GPR-NGA (I275K).
DE
XX G protein-coupled receptor; GPCR; constitutively active;
KW intracellular loop 3; transmembrane domain 6; drug screening;
KW agonist; antagonist; mutant; mutein.
XX
XX Homo sapiens.
OS Synthetic.
OS
XX WO200022129-A1.
XX
XX 20-APR-2000.
XX
XX 12-OCT-1999; 99WO-US23938.
XX
XX 13-OCT-1998; 98US-0170496.
XX
XX (AREN-) ARENA PHARM INC.
XX
XX Behan DP, Chalmers DT, Liaw CW;
PI
XX WPI; 2000-329165/28.
DR N-PSDB; A30734.
XX
XX Non-endogenous constitutively activated human G protein-coupled
PT receptors, useful for identifying agonists for use as pharmaceutical
PT agents
PT
PS
XX
XX Example 2; Page 273-274; 34lpp; English.
XX
CC The invention relates to constitutively active, non-endogenous versions
CC of endogenous human orphan G protein-coupled receptors (GPCRs, Y90643-
CC Y90677 and Y90683-Y90687), and to DNA encoding them (A30709-A30743 and
CC A30775-A30779). The mutant proteins of the invention contain a
CC mutation in a portion of the protein comprising intracellular loop 3
CC (IC3) and transmembrane domain 6 (TM6). A non-endogenous amino acid, X,
CC is substituted for an endogenous residue in IC3 at a position 16 amino
CC acids N-terminal of an endogenous proline in TM6 to form a sequence
CC X-(AA)15-Pro. The endogenous amino acid is selected from Lys, His, Arg or
CC Ala, and is preferably Lys. When the endogenous residue at this position
CC is Lys, this residue is replaced by His, Arg or preferably Ala. The 15
CC amino acid stretch between the substituted amino acid and the Pro may be
CC endogenous, non-endogenous, or a mixture of endogenous and non-endogenous
CC residues. The constitutively active GPCRs are useful for identifying
CC antagonists, agonists and partial agonists for use as pharmaceutical
CC agents. The mutant proteins are also useful in research settings for
CC elucidating the roles of the receptors in normal and diseased conditions.
CC Antagonists for a particular GPCR are useful for treating diseases and
CC disorders associated with that receptor. Because the novel mutant GPCRs
CC are constitutively active, they can be used directly for screening of
CC compounds without the need for endogenous ligands. Sequences Y90643-
CC Y90677 and Y90683-Y90687 the mutant human GPCRs of the invention.
XX
SQ Sequence 415 AA;

Query Match 55.6%; Score 45; DB 21; Length 415;

Best Local Similarity 58.3%; Pred. No. 14;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 3 TGAWFSNATCK 14
||| :||||
Db 128 tgrwtlgsatck 139

RESULT 9
Y56887
ID Y56887 standard; Protein; 428 AA.
XX
AC Y56887;
XX
XX 14-APR-2000 (first entry)
XX
XX Human B5 receptor polypeptide.
DE
XX G protein coupled receptor; B5 receptor; intracellular cell signaling;
KW human.
KW
XX Homo sapiens.
OS
XX CA2269192-A1.
PN
XX 16-OCT-1999.
PD
XX 16-APR-1999; 99CA-2269192.
PF
XX 16-APR-1998; 98US-0081995.
PR
XX (ALLX) ALLELIX BIOPHARMACEUTICALS INC.
PA
XX Zastawny RL, McWhinnie EA;
PI
XX WPI; 2000-127208/12.
DR N-PSDB; Z46951.
XX
XX New nucleic acids encoding rat and human G protein coupled receptors,
PT useful in drug screening assays -
PT
PS Claim 3; Fig 2; 60pp; English.
XX
XX The invention provides nucleic acids encoding rat and human G protein
CC coupled receptors, defined as the B5 receptors. The G protein coupled
CC receptors are involved in the intracellular cell signaling mechanism.
CC The B5 receptors are useful for screening candidate ligands which include
CC candidate drug compounds. Expression of the B5 receptor encoding DNA can
CC be used to produce fragments of the receptor in soluble form for
CC structure investigation and for raising antibodies for experimental uses.
CC The present sequence represents the human B5 receptor.
XX
SQ Sequence 428 AA;

Query Match 54.9%; Score 44.5; DB 21; Length 428;
Best Local Similarity 75.0%; Pred. No. 18;
Matches 9; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 3 TGAWFSNATCK 14
||| :||||
Db 105 tg-wpfdnatck 115

RESULT 10
Y93151
ID Y93151 standard; Protein; 430 AA.
XX
AC Y93151;
XX
XX 06-DEC-2000 (first entry)
XX
XX Novel human G-protein coupled receptor h07T022.

XX KW G-protein coupled receptor; human; bovine; nervous system disorder;
 XX rat; mouse; somatostatin excretion.
 XX OS Homo sapiens.
 XX PN WO200029441-A1.
 XX PD 25-MAY-2000.
 XX PF 11-NOV-1999; 99WO-JP06283.
 XX PR 13-NOV-1998; 98JP-0323759.
 XX PR 08-MAR-1999; 99JP-0060030.
 XX PR 14-APR-1999; 99JP-0106812.
 XX PR 14-JUN-1999; 99JP-0166672.
 XX PR 04-AUG-1999; 99JP-0221640.
 XX PR 14-SEP-1999; 99JP-0259818.
 XX PA (TAKE) TAKEDA CHEM IND LTD.
 XX PI Watanabe T, Kikuchi K, Terao Y, Shintani Y, Hinuma S, Fukusumi S;
 XX PI Fujii R, Hosoya M, Kitada C;
 XX DR WPI; 2000-387747/33.
 XX DR N-PSDB; A70507, A70508.
 XX PT G protein coupled receptor protein and antibodies to it for treatment
 XX and diagnosis of nerve diseases
 XX PS Disclosure; Page 178-180; 184pp; Japanese.
 XX CC The invention relates to the isolation of novel G-protein coupled
 CC receptor (GPCR) genes and their encoded proteins. This sequence
 CC represents the protein sequence of a human cPCR encoded by the clone
 CC h077022 which has 2 alleles (A70507 and A70508). The DNAs and proteins
 CC are used for the treatment, prevention and diagnosis of disorders of
 CC the nervous system. The proteins and its fragments are also promoters
 CC of somatostatin excretion.
 XX SQ Sequence 430 AA;

Query Match 54.9%; Score 44.5; DB 21; Length 430;
 Best Local Similarity 75.0%; Pred. No. 18;
 Matches 9; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
 Qy 3 TGAWVFSNATCK 14
 || | | | | | | |
 Db 107 tg-wpfdnatck 117

RESULT 11
 Y79376
 ID Y79376 standard; Protein; 430 AA.
 XX AC Y79376;
 XX DT 01-AUG-2000 (first entry)
 XX DE Human neuropeptide FF (NPFF1) receptor.
 XX KW Neuropeptide FF receptor; NPFF1 receptor; human; antiinflammatory;
 KW antiasthmatic; antidiabetic; immunostimulant; immunosuppressive;
 KW nootropic; neuroprotective; analgesic; anorectic; antipsychotic;
 KW antidiabetic; antilmigraine; hypertensive; hypotensive; cardiant;
 KW antiasthmatic; therapy; G protein coupled receptor.
 XX OS Homo sapiens.
 XX PH Key Location/Qualifiers
 FT Domain 42..68
 FT /note= "transmembrane domain I"

FT Domain 78..102
 FT /note= "transmembrane domain II"
 FT Domain 121..139
 FT /note= "transmembrane domain III"
 FT Domain 158..178
 FT /note= "transmembrane domain IV"
 FT Domain 217..240
 FT /note= "transmembrane domain V"
 FT Domain 268..293
 FT /note= "transmembrane domain VI"
 FT Domain 313..336
 FT /note= "transmembrane domain VII"
 XX WO200018438-A1.
 XX PN 06-APR-2000.
 XX PD 24-SEP-1999; 99WO-US22384.
 XX PF 25-SEP-1998; 98US-0161113.
 XX PR 22-FEB-1999; 99US-0255368.
 XX PA (SYNA-) SYNAPTIC PHARM CORP.
 XX PI Gerald CPG, Jones KA, Bonini JA, Borowsky B;
 XX PI WPI; 2000-293017/25.
 XX DR N-PSDB; 294668.
 XX PT Nucleic acid encoding a mammalian neuropeptide FF (NPFF) receptor,
 PT useful for treatment of e.g pain, obesity, diabetes, hypertension,
 PT hypotension, hypoglycemia, respiratory disorders
 XX Claim 17; Fig 13; 253pp; English.
 XX CC The present sequence is that of a human neuropeptide FF (NPFF1)
 CC receptor full-length polypeptide, as deduced from isolated
 CC cosmid cDNA (see 294668). Expression patterns suggest a modulatory
 CC role for NPFF1 in multiple systems within the central nervous system,
 CC and a role in sensory transmission, modulation of the limbic system,
 CC modulation of feeding/circadian rhythms, and modulation of
 CC extrapyramidal motor systems. High levels in the spinal cord and
 CC thalamus imply a role in sensory transmission or modulation
 CC (including nociception). Expression in the hippocampus and amygdala
 CC suggest involvement in modulation of learning and memory and a role
 CC in regulation of fear and mood. NPFF1 may provide a target for
 CC treatment of depression, anxiety, phobias, mood and movement
 CC disorders. The invention provides rat and human NPFF polypeptides
 CC and polynucleotides, vectors, host cells, antibodies, nucleic acid
 CC probes, antisense oligonucleotides, transgenic animals, methods
 CC of isolating mammalian NPFF receptors, methods of treating an
 CC abnormality associated with NPFF receptor activity, methods of
 CC determining binding of compounds to NPFF receptors, methods of
 CC identifying agonists and antagonists of NPFF receptors, and the
 CC agonists and antagonists obtained. Claimed methods of treating
 CC an abnormality that is alleviated by increasing/decreasing NPFF
 CC activity involve administering an NPFF receptor agonist/antagonist.
 CC The abnormality is a lower urinary tract disorder, an epinephrine
 CC release disorder, a gastrointestinal disorder, irritable bowel
 CC syndrome, a cardiovascular disorder, an electrolyte balance
 CC disorder, diuresis, hypertension, hypotension, diabetes,
 CC hypoglycemia, a respiratory disorder, asthma, a reproductive
 CC function disorder, an immune disorder, an endocrine disorder, a
 CC musculoskeletal disorder, a neuroendocrine disorder, a cognitive
 CC disorder, a memory disorder, a sensory modulation and
 CC transmission disorder, a motor coordination disorder, a sensory
 CC integration disorder, obesity, pain, psychotic behaviour,
 CC morphine tolerance, nicotine addiction, opiate addiction,
 CC affective disorder or migraine (all claimed).
 XX SQ Sequence 430 AA;

Query Match 54.9%; Score 44.5; DB 21; Length 430;
 Best Local Similarity 75.0%; Pred. No. 18;
 Matches 9; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 3 TGAWVFSNATCK 14
 ||| |
 Db 107 tg-wpfdnatck 117

RESULT 12

Y93146
 ID Y93146 standard; Protein; 432 AA.

XX AC Y93146;

XX XX 06-DEC-2000 (first entry)

XX DE Novel rat G-protein coupled receptor #3.

XX KW G-protein coupled receptor; human; bovine; nervous system disorder;
 KW KW rat; mouse; somatostatin excretion.

XX OS Rattus sp.

XX PN WO200029441-A1.

XX PD 25-MAY-2000.

XX PF 11-NOV-1999; 99WO-JP06283.

XX PR 13-NOV-1998; 98JP-0323759.

XX PR 08-MAR-1999; 99JP-0060030.

XX PR 14-APR-1999; 99JP-0106812.

XX PR 14-JUN-1999; 99JP-0166672.

XX PR 04-AUG-1999; 99JP-0221640.

XX PR 14-SEP-1999; 99JP-0259818.

XX PA (TAKE) TAKEDA CHEM IND LTD.

XX PI Watanabe T, Kikuchi K, Terao Y, Shintani Y, Hinuma S, Fukusumi S;

XX PI Fujii R, Hosoya M, Kitada C;

XX XX WPI; 2000-387747/33.
 DR N-PSDB; A70506.

XX PT G protein coupled receptor protein and antibodies to it for treatment
 PT and diagnosis of nerve diseases

XX PS Claim 23; Page 169-170; 184pp; Japanese.

XX CC The invention relates to the isolation of novel G-protein coupled
 CC receptor (GPCR) genes and their encoded proteins. This sequence
 CC represents the protein sequence of a rat GPCR. The DNAs and proteins
 CC are used for the treatment, prevention and diagnosis of disorders of
 CC the nervous system. The proteins and its fragments are also promoters
 CC of somatostatin excretion.

XX SQ Sequence 432 AA;

Query Match 54.9%; Score 44.5; DB 21; Length 432;
 Best Local Similarity 75.0%; Pred. No. 18;
 Matches 9; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 3 TGAWVFSNATCK 14
 ||| |
 Db 107 tg-wpfdnatck 117

RESULT 13

Y79373
 ID Y79373 standard; Protein; 432 AA.

XX

AC Y79373;

XX DT 01-AUG-2000 (first entry)

XX DE Rat neurotrophin-4 (NTR-4) receptor.

XX DE Neurotrophin-4 receptor; NTR-4; rat; anti-inflammatory;
 KW KW antiasthmatic; antidiabetic; immunostimulant; immunosuppressive;
 KW KW nootropic; neuroprotective; analgesic; anorectic; antipsychotic;
 KW KW antiaddictive; antimigraine; hypertensive; hypotensive; cardiatic;
 KW KW antiasthmatic; therapy; G protein coupled receptor.

XX OS Rattus norvegicus.

XX PH key Location/Qualifiers

XX FT Domain 42..69 /note= "transmembrane domain I"

XX FT Domain 78..102 /note= "transmembrane domain II"

XX FT Domain 121..139 /note= "transmembrane domain III"

XX FT Domain 158..178 /note= "transmembrane domain IV"

XX FT Domain 217..240 /note= "transmembrane domain V"

XX FT Domain 270..295 /note= "transmembrane domain VI"

XX FT Domain 313..338 /note= "transmembrane domain VII"

XX FT Modified-site 10 /note= "N-glycosylated"

XX FT Modified-site 18 /note= "N-glycosylated"

XX FT Modified-site 113 /note= "N-glycosylated"

XX FT Modified-site 195 /note= "N-glycosylated"

XX FT Modified-site 154 /note= "O-phosphorylated"

XX FT Modified-site 263 /note= "O-phosphorylated"

XX FT Modified-site 264 /note= "O-phosphorylated"

XX PN WO200018438-A1.

XX XX 06-APR-2000.

XX XX 24-SEP-1999; 99WO-US22384.

XX PR 25-SEP-1998; 98US-0161113.

XX PR 22-FEB-1999; 99US-0255368.

XX PA (SYNA-) SYNAPTIC PHARM CORP.

XX PI Gerald CPG, Jones KA, Bonini JA, Borowsky B;

XX DR WPI; 2000-293017/25.

XX DR N-PSDB; 294665.

XX PT Nucleic acid encoding a mammalian neurotrophin-4 (NTR-4) receptor,
 PT useful for treatment of e.g pain, obesity, diabetes, hypertension,
 PT hypotension, hypoglycemia, respiratory disorders

XX PT Claim 13; Fig 2; 253pp; English.

XX CC The present sequence is that of rat neurotrophin-4 (NTR-4)
 CC receptor, as deduced from a cDNA clone (see 294665) isolated
 CC from a rat hypothalamus cDNA library. Expression patterns suggest
 CC roles for NTR-4 in neuroendocrine regulation, and in regulation of
 CC circadian rhythm, regulation of appetite and other functions
 CC modulated by the hypothalamus. A possible role in modulation of
 CC mood, fear, phobia and anxiety is also suggested, and NTR-4 may

CC provide a target for treatment of depression and other
 CC neuropsychiatric disorders. NPFF1 may also play a role in endocrine
 CC regulation and reproductive function. The invention provides rat
 CC and human NPFF polypeptides and polynucleotides, vectors, host
 CC cells, antibodies, nucleic acid probes, antisense oligonucleotides,
 CC transgenic animals, methods of isolating mammalian NPFF receptors,
 CC methods of treating an abnormality associated with NPFF receptor
 CC activity, methods of determining binding of compounds to NPFF
 CC receptors, methods of identifying agonists and antagonists of NPFF
 CC receptors, and the agonists and antagonists obtained. Claimed
 CC methods of treating an abnormality that is alleviated by
 CC increasing/decreasing NPFF activity involve administering an NPFF
 CC receptor agonist/antagonist. The abnormality is a lower urinary
 CC tract disorder, an epinephrine release disorder, a gastrointestinal
 CC disorder, irritable bowel syndrome, a cardiovascular disorder, an
 CC electrolyte balance disorder, diuresis, hypertension, hypotension,
 CC diabetes, hypoglycemia, a respiratory disorder, asthma, a
 CC reproductive function disorder, an immune disorder, an endocrine
 CC disorder, a musculoskeletal disorder, a neuroendocrine disorder, a
 CC cognitive disorder, a memory disorder, a sensory modulation and
 CC transmission disorder, a motor coordination disorder, a sensory
 CC integration disorder, obesity, pain, psychotic behaviour,
 CC morphine tolerance, nicotine addiction, opiate addiction,
 CC affective disorder or migraine (all claimed).

XX
 SQ Sequence 432 AA;

Query Match 54.9%; Score 44.5; DB 21; Length 432;
 Best Local Similarity 75.0%; Pred. No. 18;
 Matches 9; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 3 TGAWVFSNATCK 14
 || | | | | | | |
 Db 107 tg-wpfdnatck 117

RESULT 14

Y56886
 ID Y56886 standard; Protein; 432 AA.

XX
 AC Y56886;

XX
 DT 14-APR-2000 (first entry)

XX
 DE Rat B5 receptor polypeptide.

XX
 KW G protein coupled receptor; B5 receptor; intracellular cell signaling;
 rat.

XX
 OS Rattus sp.

XX
 PN CA2269192-A1.

XX
 PD 16-OCT-1999.

XX
 PF 16-APR-1999; 99CA-2269192.

XX
 PR 16-APR-1998; 98US-0081995.

XX
 PA (ALIX) ALLELIX BIOPHARMACEUTICALS INC.

XX
 PI Zastawny RL, McWhinnie EA;

XX
 DR WPI; 2000-127208/12.

XX
 DR N-PSDB; 246950.

XX
 PT New nucleic acids encoding rat and human G protein coupled receptors,
 useful in drug screening assays

XX
 PS Claim 1; Fig 1; 60pp; English.

XX
 CC The invention provides nucleic acids encoding rat and human G protein

CC coupled receptors, defined as the B5 receptors. The G protein coupled
 CC receptors are involved in the intracellular cell signaling mechanism.
 CC The B5 receptors are useful for screening candidate ligands which include
 CC candidate drug compounds. Expression of the B5 receptor encoding DNA can
 CC be used to produce fragments of the receptor in soluble form for
 CC structure investigation and for raising antibodies for experimental uses.
 CC The present sequence represents the rat B5 receptor.

XX
 SQ Sequence 432 AA;

Query Match 54.9%; Score 44.5; DB 21; Length 432;
 Best Local Similarity 75.0%; Pred. No. 18;
 Matches 9; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 3 TGAWVFSNATCK 14
 || | | | | | | |
 Db 107 tg-wpfdnatck 117

RESULT 15

G31332
 ID G31332 standard; Protein; 321 AA.

XX
 AC G31332;

XX
 DT 17-OCT-2000 (first entry)

XX
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 37610.

XX
 KW Protein identification; signal transduction pathway; metabolic pathway;
 hybridisation assay; genetic mapping; gene expression control; promoter;
 termination sequence.

XX
 OS Arabidopsis thaliana.

XX
 PN EP1033405-A2.

XX
 PD 06-SEP-2000.

XX
 PF 25-FEB-2000; 2000EP-0301439.

XX
 PR 25-FEB-1999; 99US-0121825.

XX
 PR 05-MAR-1999; 99US-0123180.

XX
 PR 09-MAR-1999; 99US-0123548.

XX
 PR 23-MAR-1999; 99US-0125788.

XX
 PR 25-MAR-1999; 99US-0126284.

XX
 PR 29-MAR-1999; 99US-0126785.

XX
 PR 01-APR-1999; 99US-0127462.

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 PR 06-APR-1999; 99US-0128234.

XX
 PR 08-APR-1999; 99US-0128714.

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 PR 16-APR-1999; 99US-0129845.

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 PR 19-APR-1999; 99US-0130077.

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 PR 21-APR-1999; 99US-0130449.

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 PR 23-APR-1999; 99US-0130510.

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 PR 28-APR-1999; 99US-0130891.

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 PR 30-APR-1999; 99US-0131449.

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 PR 30-APR-1999; 99US-0132048.

XX
 PR 04-MAY-1999; 99US-0132407.

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XX
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XX
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XX
 PR 20-MAY-1999; 99US-0135124.

XX
 PR 21-MAY-1999; 99US-0135353.

PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
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PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
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PR 07-JUN-1999; 99US-0137724.
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PR 10-JUN-1999; 99US-0138540.
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PR 14-JUN-1999; 99US-0139119.
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PR 28-JUN-1999; 99US-0140823.
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PR 01-JUL-1999; 99US-0141842.
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PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
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PR 03-AUG-1999; 99US-0147038.
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PR 06-AUG-1999; 99US-0147303.
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PR 23-AUG-1999; 99US-0149930.
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PR 27-AUG-1999; 99US-0151065.
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PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
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PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
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PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
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PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
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PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.

PR 28-OCT-1999; 99US-0161992.
 PR 28-OCT-1999; 99US-0161993.
 PR 29-OCT-1999; 99US-0162142.

Query Match 53.1%; Score 43; DB 21; Length 321;
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QY 1 HATGAWFESNATC 13
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 Db 205 hcidtwllsnstc 217

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 Job time: 405 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 23, 2001, 15:30:05 ; Search time 95.91 Seconds
(without alignments)
2.804 Million cell updates/sec

Title: US-08-887-977-10_COPY_97_l10
Perfect score: 81
Sequence: 1 HATGAWFSNATCK 14

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Searched: 185757 seqs, 19210857 residues

Total number of hits satisfying chosen parameters: 185757

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	47	58.0	360	1	US-08-450-393A-4
5	47	58.0	360	4	US-08-446-669-4
6	47	58.0	360	5	PCT-US95-00476-4
7	47	58.0	374	1	US-08-450-393A-2
8	47	58.0	374	5	PCT-US95-00476-2
9	47	58.0	374	1	US-08-446-669-2
10	42	51.9	367	2	US-08-147-949A-2
11	42	51.9	367	2	US-08-454-549-2
12	42	51.9	367	3	US-08-454-552-2
13	42	51.9	367	3	US-08-676-351-2
14	42	51.9	367	3	US-08-147-592A-6
15	42	51.9	367	3	US-08-889-108-17
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19	40	49.4	362	2	US-08-985-090-5
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33	40	49.4	445	3	US-09-165-543-5	Sequence 5, Appli
34	40	49.4	445	4	US-09-167-354-7	Sequence 7, Appli
35	39	48.1	257	1	US-07-828-790B-2	Sequence 2, Appli
36	39	48.1	355	1	US-08-012-988A-2	Sequence 2, Appli
37	39	48.1	355	1	US-08-450-393A-5	Sequence 5, Appli
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39	39	48.1	355	5	PCT-US95-00476-5	Sequence 5, Appli
40	38	46.9	269	1	US-08-307-499-30	Sequence 30, Appli
41	38	46.9	373	2	US-08-559-524A-4	Sequence 4, Appli
42	38	46.9	373	3	US-08-749-707-4	Sequence 4, Appli
43	38	46.9	383	3	US-09-045-186-2	Sequence 4, Appli
44	38	46.9	384	1	US-08-232-144-4	Sequence 4, Appli
45	38	46.9	384	2	US-08-555-268A-15	Sequence 15, Appli

ALIGNMENTS

RESULT 1
US-08-726-012B-2
; Sequence 2, Application US/08726012B
; Patent No. 5952190
; GENERAL INFORMATION:
; APPLICANT: Hans Joenje, et al.
; TITLE OF INVENTION: CDNA FOR FANCONI ANEMIA COMPLEMENTATION GROUP A
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klarquist Sparkman Campbell Leigh & Whinston, LLP
; STREET: One World Trade Center, Suite 1600, 121 S.W. Salmon Street
; CITY: Portland
; STATE: OR
; COUNTRY: USA
; ZIP: 97204-2988
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Disk, 3.5-inch
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS DOS
; SOFTWARE: WordPerfect 5.1+, ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/726,012B
; FILING DATE: 10/04/96
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Richard J. Polley
; REGISTRATION NUMBER: 28,107
; REFERENCE/DOCKET NUMBER: 3812-45520/RJP/DJE
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (503) 226-7391
; TELEFAX: (503) 228-9446
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1455
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: Linear
US-08-726-012B-2

Query Match 60.5%; Score 49; DB 2; Length 1455;
Best Local Similarity 53.8%; Pred. No. 5.5;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
Qy: 1 HATGAWFSNATC 13
Db 204 HAVGSWLFNLC 216

RESULT 2
US-08-466-343D-9
; Sequence 9, Application US/08466343D
; Patent No. 6025154
; GENERAL INFORMATION:
; APPLICANT: LI, YI
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING HUMAN G-PROTEIN
; TITLE OF INVENTION: CHEMOKINE RECEPTOR HDGMR10 (AS AMENDED)
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVE., NW, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,343D
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.1150000/EKS/KLM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 344 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-466-343D-9

Query Match 58.0%; Score 47; DB 3; Length 344;
Best Local Similarity 61.5%; Pred. No. 2.6;
Matches 8; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 ATGAWVFSNACK 14
| | | | |
DB 85 AANEVFGNAMCK 97

RESULT 3
US-08-461-244-3
; Sequence 3, Application US/08461244
; Patent No. 5776729
; GENERAL INFORMATION:
; APPLICANT: Soppet, Daniel R.
; APPLICANT: Yi, Li
; APPLICANT: Ruben, Steven M.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: HUMAN G-PROTEIN RECEPTOR HGBR32
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
; ADDRESSEE: STUART & OLSTEIN
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,244
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Ferraro, Gregory D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-445
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 347 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-461-244-3

Query Match 58.0%; Score 47; DB 1; Length 347;
Best Local Similarity 61.5%; Pred. No. 2.6;
Matches 8; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 ATGAWVFSNACK 14
| | | | |
DB 89 AANEVFGNAMCK 101

RESULT 4
US-08-450-393A-4
; Sequence 4, Application US/08450393A
; Patent No. 5707815
; GENERAL INFORMATION:
; APPLICANT: Charo, Israel
; APPLICANT: Coughlin, Shaun
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
; TITLE OF INVENTION: PROTEIN RECEPTORS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
; STREET: 5 Palo Alto Square
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,393A
; FILING DATE: May 25, 1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Cserr, Luann
; REGISTRATION NUMBER: 31,822
; REFERENCE/DOCKET NUMBER: UCAL-237/020US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5165
; TELEFAX: 415-8857-0663
; TELEX: 380816CooLeypA
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 360 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

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; MOLECULE TYPE: protein
US-08-450-393A-4

Query Match          58.0%; Score 47; DB 1; Length 360;
Best Local Similarity 61.5%; Pred. No. 2.7;
Matches 8; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 ATGAWVFSNATCK 14
   | ||| ||| ||
Db 102 AANEWVFGNAMCK 114

RESULT 5
US-08-446-669-4
; Sequence 4, Application US/08446669
; Patent No. 6132987
; GENERAL INFORMATION:
; APPLICANT: Charo, Israel
; APPLICANT: Coughlin, Shaun
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
; TITLE OF INVENTION: PROTEIN RECEPTORS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
; STREET: 5 Palo Alto Square
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446.669
; FILING DATE: May 25, 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Neeley, Richard
; REGISTRATION NUMBER: 30,092
; REFERENCE/DOCKET NUMBER: UCAL-237/0105
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5000
; TELEFAX: 415-857-0663
; TELEX: 380816COOLEYPA
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 360 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-446-669-4

Query Match          58.0%; Score 47; DB 4; Length 360;
Best Local Similarity 61.5%; Pred. No. 2.7;
Matches 8; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 ATGAWVFSNATCK 14
   | ||| ||| ||
Db 102 AANEWVFGNAMCK 114

RESULT 6
PCT-US95-00476-4
; Sequence 4, Application PC/TUS9500476
; GENERAL INFORMATION:
; APPLICANT: The Regents of the University of California
; APPLICANT: MAMMALIAN MONOCYTE CHEMOATTRACTANT
; TITLE OF INVENTION: PROTEIN RECEPTORS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Robbins, Berliner & Carson
; STREET: 201 N. Figueroa Street, 5th Floor
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90012-2628
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/00476
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Berliner, Robert
; REGISTRATION NUMBER: 20,121
; REFERENCE/DOCKET NUMBER: 5555-291
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 310-977-1001
; TELEFAX: 310-977-1003
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 360 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-00476-4

Query Match          58.0%; Score 47; DB 5; Length 360;
Best Local Similarity 61.5%; Pred. No. 2.7;
Matches 8; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 ATGAWVFSNATCK 14
   | ||| ||| ||
Db 102 AANEWVFGNAMCK 114

RESULT 7
US-08-450-393A-2
; Sequence 2, Application US/08450393A
; Patent No. 5707815
; GENERAL INFORMATION:
; APPLICANT: Charo, Israel
; APPLICANT: Coughlin, Shaun
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
; TITLE OF INVENTION: PROTEIN RECEPTORS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
; STREET: 5 Palo Alto Square
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,393A
; FILING DATE: May 25, 1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Cseir, Luann
; REGISTRATION NUMBER: 31,822
; REFERENCE/DOCKET NUMBER: UCAL-237/0205
; TELECOMMUNICATION INFORMATION:
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TELEPHONE: 415-843-5165
 TELEFAX: 415-8857-0663
 TELEX: 380816CoolleyPA
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 374 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-450-393A-2

Query Match 58.0%; Score 47; DB 1; Length 374;
 Best Local Similarity 61.5%; Pred. No. 2.8;
 Matches 8; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 ATGAWVFSNATCK 14
 | ||| || ||
 Db 102 AANEWVFGNAMCK 114

RESULT 8
 US-08-446-669-2
 ; Sequence 2, Application US/08446669
 ; Patent No. 6132987
 ; GENERAL INFORMATION:
 ; APPLICANT: Charo, Israel
 ; APPLICANT: Coughlin, Shaun
 ; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
 ; NUMBER OF SEQUENCES: 14
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
 ; STREET: 5 Palo Alto Square
 ; CITY: Palo Alto
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94306-2155
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/446,669
 ; FILING DATE: May 25, 1995
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Neeley, Richard
 ; REGISTRATION NUMBER: 30,092
 ; REFERENCE/DOCKET NUMBER: UCAL-237/01US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-843-5000
 ; TELEFAX: 415-857-0663
 ; TELEX: 380816CoolleyPA
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 374 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-446-669-2

Query Match 58.0%; Score 47; DB 4; Length 374;
 Best Local Similarity 61.5%; Pred. No. 2.8;
 Matches 8; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 ATGAWVFSNATCK 14
 | ||| || ||
 Db 102 AANEWVFGNAMCK 114

RESULT 9
 PCT-US95-00476-2
 ; Sequence 2, Application PC/TUS9500476
 ; GENERAL INFORMATION:
 ; APPLICANT: The Regents of the University of California
 ; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
 ; NUMBER OF SEQUENCES: 14
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Robbins, Berliner & Carson
 ; STREET: 201 N. Figueroa Street, 5th Floor
 ; CITY: Los Angeles
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 90012-2628
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US95/00476
 ; FILING DATE:
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Berliner, Robert
 ; REGISTRATION NUMBER: 20,121
 ; REFERENCE/DOCKET NUMBER: 5555-291
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 310-977-1001
 ; TELEFAX: 310-977-1003
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 374 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; PCT-US95-00476-2

Query Match 58.0%; Score 47; DB 5; Length 374;
 Best Local Similarity 61.5%; Pred. No. 2.8;
 Matches 8; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 ATGAWVFSNATCK 14
 | ||| || ||
 Db 102 AANEWVFGNAMCK 114

RESULT 10
 US-08-147-949A-2
 ; Sequence 2, Application US/08147949A
 ; Patent No. 5747279
 ; GENERAL INFORMATION:
 ; APPLICANT: Pasternak, Gavrill W.
 ; APPLICANT: Pan, Ying-Xian
 ; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING
 ; TITLE OF INVENTION: KAPPA3 OPIOID RECEPTORS, RECEPTORS
 ; TITLE OF INVENTION: ENCODED THEREBY, AND USES THEREOF
 ; NUMBER OF SEQUENCES: 5
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Cooper & Dunham
 ; STREET: 1185 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10036
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.30

;; CURRENT APPLICATION DATA:
 ;; APPLICATION NUMBER: US/08/147,949A
 ;; FILING DATE: 05-NOV-1993
 ;; ATTORNEY/AGENT INFORMATION:
 ;; NAME: White, John P.
 ;; REGISTRATION NUMBER: 28,678
 ;; REFERENCE/DOCKET NUMBER: 44782/JPW/JKM
 ;; TELECOMMUNICATION INFORMATION:
 ;; TELEPHONE: (212) 278-0400
 ;; TELEFAX: (212) 391-0525
 ;; TELEX: 422523 COOP UI
 ;; INFORMATION FOR SEQ ID NO: 2:
 ;; SEQUENCE CHARACTERISTICS:
 ;; LENGTH: 367 amino acids
 ;; TYPE: amino acid
 ;; TOPOLOGY: linear
 ;; MOLECULE TYPE: protein
 ;; US-08-147-949A-2

Query Match 51.9%; Score 42; DB 1; Length 367;
 Best Local Similarity 63.6%; Pred. No. 17;
 Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 GAWVFSNATCK 14
 | | | | |
 Db 111 GFWPFGNALCK 121

RESULT 11
 US-08-454-549-2
 ; Sequence 2, Application US/08454549
 ; Patent No. 5866324
 ; GENERAL INFORMATION:
 ; APPLICANT: EPPLER, C. Mark
 ; APPLICANT: OZENBERGER, Bradley A.
 ; APPLICANT: HULMES, Jeffrey D.
 ; TITLE OF INVENTION: CDNA'S ENCODING PROTEINS CLOSELY RELATED
 ; TITLE OF INVENTION: TO OPIOID RECEPTORS
 ; NUMBER OF SEQUENCES: 13
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Darby & Darby, P.C.
 ; STREET: 805 Third Avenue
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10022
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/454,549
 ; FILING DATE: 30-MAY-1995
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Robinson, Joseph R.
 ; REGISTRATION NUMBER: 33,448
 ; REFERENCE/DOCKET NUMBER: 0646/1A818-US5
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 527-7700
 ; TELEFAX: (212) 753-6237
 ; TELEX: 236687
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 367 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: not relevant
 ; TOPOLOGY: not relevant
 ; MOLECULE TYPE: protein
 ; ORIGINAL SOURCE:
 ; ORGANISM: Rat

US-08-454-549-2

Query Match 51.9%; Score 42; DB 2; Length 367;
 Best Local Similarity 63.6%; Pred. No. 17;
 Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 GAWVFSNATCK 14
 | | | | |
 Db 111 GFWPFGNALCK 121

RESULT 12
 US-08-454-552-2
 ; Sequence 2, Application US/08454552
 ; Patent No. 6005072
 ; GENERAL INFORMATION:
 ; APPLICANT: EPPLER, C. Mark
 ; APPLICANT: OZENBERGER, Bradley A.
 ; APPLICANT: HULMES, Jeffrey D.
 ; TITLE OF INVENTION: CDNA'S ENCODING PROTEINS CLOSELY RELATED
 ; TITLE OF INVENTION: TO OPIOID RECEPTORS
 ; NUMBER OF SEQUENCES: 13
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Darby & Darby, P.C.
 ; STREET: 805 Third Avenue
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10022
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/454,552
 ; FILING DATE: 30-MAY-1995
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Robinson, Joseph R.
 ; REGISTRATION NUMBER: 33,448
 ; REFERENCE/DOCKET NUMBER: 0646/1A818-US4
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 527-7700
 ; TELEFAX: (212) 753-6237
 ; TELEX: 236687
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 367 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: not relevant
 ; TOPOLOGY: not relevant
 ; MOLECULE TYPE: protein
 ; ORIGINAL SOURCE:
 ; ORGANISM: Rat
 ; US-08-454-552-2

Query Match 51.9%; Score 42; DB 3; Length 367;
 Best Local Similarity 63.6%; Pred. No. 17;
 Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 GAWVFSNATCK 14
 | | | | |
 Db 111 GFWPFGNALCK 121

RESULT 13
 US-08-676-351-2
 ; Sequence 2, Application US/08676351C
 ; Patent No. 6046026
 ; GENERAL INFORMATION:

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; APPLICANT: EPPLER, CECIL
; APPLICANT: OZENBERGER, BRADLEY
; APPLICANT: HULMES, JEFFREY
; TITLE OF INVENTION: CDNAS ENCODING PROTEINS CLOSELY RELATED
; TITLE OF INVENTION: TO OPIOID RECEPTORS
; FILE REFERENCE: 0646/1A818US1
; CURRENT APPLICATION NUMBER: US/08/676,351C
; CURRENT FILING DATE: 1996-09-12
; EARLIER APPLICATION NUMBER: PCT/US95/00939
; EARLIER FILING DATE: 1995-01-20
; EARLIER APPLICATION NUMBER: US 08/185,360
; EARLIER FILING DATE: 1994-01-21
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 367
; TYPE: PRT
; ORGANISM: Rat
US-08-676-351-2

Query Match          51.9%; Score 42; DB 3; Length 367;
Best Local Similarity 63.6%; Pred. No. 17;
Matches 7; Conservative 0; Mismatches 4; Indels 4; Gaps 0;

QY      4 GAWVFSNATCK 14
      | | | | |
Db      111 GFWPFGNALCK 121

RESULT 14
US-08-147-592A-6
; Sequence 6, Application US/08147592A
; Patent No. 6096513
; GENERAL INFORMATION:
; APPLICANT: Bell, Graeme I
; APPLICANT: Reisine, Terry
; APPLICANT: Yasuda, Kazuki
; TITLE OF INVENTION: Opioid Receptor Genes,
; TITLE OF INVENTION: Compositions and Methods
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/147,592A
; FILING DATE: 05-NOV-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/100,694
; FILING DATE: 30-JUL-1993
; CLASSIFICATION: 435
; APPLICATION NUMBER: 08/066,296
; FILING DATE: 20-MAY-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilson, Mark B.
; REGISTRATION NUMBER: 37,259
; REFERENCE/DOCKET NUMBER: ARCD:105
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 6:
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 367 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-147-592A-6

Query Match          51.9%; Score 42; DB 3; Length 367;
Best Local Similarity 63.6%; Pred. No. 17;
Matches 7; Conservative 0; Mismatches 4; Indels 4; Gaps 0;

QY      4 GAWVFSNATCK 14
      | | | | |
Db      111 GFWPFGNALCK 121

RESULT 15
US-08-889-108-17
; Sequence 17, Application US/08889108
; Patent No. 6103492
; GENERAL INFORMATION:
; APPLICANT: Yu, Lei
; TITLE OF INVENTION: Mu Opioid Receptors: Compositions and Methods
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P. O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/889,108
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/305,518
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilson, Mark B.
; REGISTRATION NUMBER: 37,259
; REFERENCE/DOCKET NUMBER: INDA005\WIM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 367 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-889-108-17

Query Match          51.9%; Score 42; DB 3; Length 367;
Best Local Similarity 63.6%; Pred. No. 17;
Matches 7; Conservative 0; Mismatches 4; Indels 4; Gaps 0;

QY      4 GAWVFSNATCK 14
      | | | | |
Db      111 GFWPFGNALCK 121

Search completed: May 23, 2001, 15:30:06
Job time: 413 sec
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 23, 2001, 15:31:59 ; Search time 110.15 Seconds
(without alignments)
8.735 Million cell updates/sec

Title: US-08-887-977-10_COPY_97_110

Perfect score: 81

Sequence: 1 HATGAWFSNATCK 14

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 19801 seqs, 68722935 residues

Total number of hits satisfying chosen parameters: 198801

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_67:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	81	100.0	369	2 JC5068	G protein-coupled
2	49	60.5	660	2 T02755	fanconi anemia com
3	47	58.0	356	2 I49340	Mip-1 alpha recept
4	47	58.0	360	2 JC2443	chemokine (C-C) re
5	47	58.0	374	2 I38450	chemokine (C-C) re
6	45	55.6	415	2 S74237	probable G protein
7	45	55.6	452	1 S14332	rhodopsin - northe
8	44	54.3	319	2 S34806	hypothetical prote
9	44	54.3	526	2 T13484	frizzled protein h
10	44	54.3	1073	1 T08228	plasmid replicatio
11	43	53.1	349	2 T06680	hypothetical prote
12	43	53.1	5627	2 C83339	hypothetical prote
13	42	51.9	98	2 A83339	hypothetical prote
14	42	51.9	209	2 H83133	hypothetical prote
15	42	51.9	367	2 I49022	kappa opioid recep
16	42	51.9	367	2 JC2421	opioid receptor ho
17	42	51.9	367	2 I56520	G protein-coupled
18	42	51.9	370	2 S43087	orphan opioid rece
19	42	51.9	412	2 S37906	translation elonga
20	42	51.9	663	1 A38283	arachidonate 12-11
21	41	50.6	103	2 S69712	hypothetical prote
22	41	50.6	126	2 B82448	hypothetical prote
23	41	50.6	487	2 T49211	hypothetical prote
24	41	50.6	646	2 E82133	ATP-dependent heli
25	41	50.6	2165	2 T21371	hypothetical prote
26	40	49.4	297	2 T21898	hypothetical prote
27	40	49.4	346	2 T21398	hypothetical prote
28	40	49.4	352	1 S27357	complement C5a ana
29	40	49.4	407	1 EDBEQ3	immediate-early pr

30	40	49.4	426	2 T16340	hypothetical prote
31	40	49.4	721	2 JC4643	lanosterol synthas
32	39	48.1	190	2 S07000	modulation protein
33	39	48.1	257	1 S13642	thyroxine deiodina
34	39	48.1	276	2 A69437	dehydrase homolog
35	39	48.1	352	2 S74238	probable G protein
36	39	48.1	355	2 A45177	chemokine (C-C) re
37	39	48.1	365	2 T06693	hypothetical prote
38	39	48.1	398	2 A57510	mu opioid receptor
39	39	48.1	417	2 T04955	hypothetical prote
40	39	48.1	440	1 S60755	rhodopsin - Allote
41	39	48.1	480	2 T15839	hypothetical prote
42	39	48.1	488	2 T15941	hypothetical prote
43	39	48.1	495	2 B71360	hypothetical prote
44	39	48.1	507	1 XYOFS	site-specific DNA-
45	39	48.1	557	2 S21596	extracellular prot

ALIGNMENTS

RESULT 1

JC5068

G protein-coupled receptor CKR-L3 - human

C:Species: Homo sapiens (man)

C:Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 21-Jul-2000

C:Accession: JC5068

R:Zaballos, A.; Varona, R.; Gutierrez, J.; Lind, P.; Marquez, G.

Biochem. Biophys. Res. Commun. 227, 846-853, 1996

A:Title: Molecular cloning and RNA expression of two new human chemokine receptor-lik

A:Reference number: JC5067; MUID:97040707

A:Accession: JC5068

A:Molecule type: DNA

A:Residues: 1-369 <ZAB>

A:Cross-references: EMBL:279784; NID:gl668737; PIDN:CAB02144.1; PID:gl668738

C:Comment: This protein belongs to the family of alpha chemokine receptors.

C:Genetics:

A:Gene: GDB:CMKBR6; STRL22; GPR29; CCR6; CKR-L3; GPR-CV4

A:Cross-references: GDB:5370639; OMIM:601835

A:Map position: 6q27-6q27

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor; transmembrane protein

F:42-68/Domain: transmembrane #status predicted <TM1>

F:79-99/Domain: transmembrane #status predicted <TM2>

F:115-136/Domain: transmembrane #status predicted <TM3>

F:160-180/Domain: transmembrane #status predicted <TM4>

F:212-233/Domain: transmembrane #status predicted <TM5>

F:250-271/Domain: transmembrane #status predicted <TM6>

F:292-315/Domain: transmembrane #status predicted <TM7>

Query Match 100.0%; Score 81; DB 2; Length 369;

Best Local Similarity 100.0%; Pred. NO. 4.5e-06;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HATGAWFSNATCK 14

Db 101 HATGAWFSNATCK 114

RESULT 2

T02755

fanconi anemia complementation group A protein - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 24-Mar-1999

C:Accession: T02755

R:Ricke, D.O.; Bruce, D.; Mundt, M.; Doggett, N.; Munk, C.; Saunders, E.; Robinson, D

re, J.; White, S.; Deng, S.; Fatum, O.; Campbell, C.; Fawcett, J.; Maltbie, M.; Deave

submitted to the EMBL Data Library, August 1998

A:Description: Sequencing of human fanconi anemia complementation group A gene genom

A:Reference number: Z14721

A:Accession: T02755

A>Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA
 A:Residues: 1-660 <CRIC>
 A:Cross-references: EMBL:AC005567; NID:g3493327; PID:g3493328
 C:Genetics:
 A:Gene: FAA
 A:Map position: 16
 A:Note: Intron positions not resolved (incomplete sequence)

Query Match 60.5%; Score 49; DB 2; Length 660;
 Best Local Similarity 53.8%; Pred. No. 1.7;
 Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 HATGAWVFSNATC 13
 I I I I I I I
 Db 30 HAVGSLFNLCC 42

RESULT 3
 I49340
 Mip-1 alpha receptor like-1 - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 13-Aug-1999
 C:Accession: I49340
 R:Gao, J.L.; Murphy, P.M.
 J. Biol. Chem. 270, 17494-17501, 1995
 A:Title: Cloning and differential tissue-specific expression of three mouse beta chemokine
 A:Reference number: I49339; MUID:95340546
 A:Accession: I49340
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 1-356 <RES>
 A:Cross-references: EMBL:U28405; NID:g881549; PIDN:AA89154.1; PID:g881550
 C:Superfamily: vertebrate rhodopsin

Query Match 58.0%; Score 47; DB 2; Length 356;
 Best Local Similarity 63.6%; Pred. No. 2;
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 4 GAWVFSNATCK 14
 I I I I I I I
 Db 98 GDWIFGNAMCK 108

RESULT 4
 JC2443
 chemokine (C-C) receptor 2, splice form B - human
 N:Alternate names: C-C CKR-2; monocyte chemoattractant protein 1 receptor; monocyte chem
 C:Species: Homo sapiens (man)
 C:Date: 21-Feb-1995 #sequence_revision 05-Apr-1995 #text_change 20-Jun-2000
 C:Accession: JC2443; I38463
 R:Yanagami, S.; Tokuda, Y.; Ishii, K.; Tanaka, H.; Endo, N.
 Biochem. Biophys. Res. Commun. 202, 1156-1162, 1994
 A:Title: cDNA cloning and functional expression of a human monocyte chemoattractant prot
 A:Reference number: JC2443; MUID:94324942
 A:Accession: JC2443
 A:Molecule type: mRNA
 A:Residues: 1-360 <YAM>
 A:Cross-references: DBJ:J29984; NID:g531246; PIDN:BAA06253.1; PID:g531247
 R:Charo, I.F.; Myers, S.J.; Herman, A.; Franci, C.; Connolly, A.J.; Coughlin, S.R.
 Proc. Natl. Acad. Sci. U.S.A. 91, 2752-2756, 1994
 A:Title: Molecular cloning and functional expression of two monocyte chemoattractant pr
 A:Reference number: A53477; MUID:94195821
 A:Accession: I38463
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-360 <RES>
 A:Cross-references: EMBL:U03905; NID:g472557; PIDN:AAA19120.1; PID:g472558
 C:Genetics:
 A:Gene: GDB:CMKBR2
 A:Cross-references: GDB:337364; OMIM:601267
 A:Map position: 3p21-3p21

C:Superfamily: vertebrate rhodopsin
 C:Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; transmembr
 F:43-70/Domain: transmembrane #status predicted <TM1>
 F:81-100/Domain: transmembrane #status predicted <TM2>
 F:115-136/Domain: transmembrane #status predicted <TM3>
 F:154-178/Domain: transmembrane #status predicted <TM4>
 F:207-226/Domain: transmembrane #status predicted <TM5>
 F:244-268/Domain: transmembrane #status predicted <TM6>
 F:287-309/Domain: transmembrane #status predicted <TM7>
 F:14/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:113-190/Disulfide bonds: #status predicted

Query Match 58.0%; Score 47; DB 2; Length 360;
 Best Local Similarity 61.5%; Pred. No. 2;
 Matches 8; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 ATGAWVFSNATCK 14
 I I I I I I I
 Db 102 AANWVFGNAMCK 114

RESULT 5
 I38450
 chemokine (C-C) receptor 2, splice form A - human
 N:Alternate names: C-C CKR-2; monocyte chemoattractant protein 1 receptor; monocyte c
 C:Species: Homo sapiens (man)
 C:Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 13-Aug-1999
 C:Accession: I38450
 R:Charo, I.F.; Myers, S.J.; Herman, A.; Franci, C.; Connolly, A.J.; Coughlin, S.R.
 Proc. Natl. Acad. Sci. U.S.A. 91, 2752-2756, 1994
 A:Title: Molecular cloning and functional expression of two monocyte chemoattractant
 A:Reference number: A53477; MUID:94195821
 A:Accession: I38450
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-374 <RES>
 A:Cross-references: EMBL:U03882; NID:g472555; PIDN:AAA19119.1; PID:g472556
 C:Genetics:
 A:Gene: GDB:CMKBR2
 A:Cross-references: GDB:337364; OMIM:601267
 A:Map position: 3p21-3p21
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; transmembr
 F:44-68/Domain: transmembrane #status predicted <TM1>
 F:115-136/Domain: transmembrane #status predicted <TM2>
 F:154-178/Domain: transmembrane #status predicted <TM3>
 F:208-226/Domain: transmembrane #status predicted <TM4>
 F:244-265/Domain: transmembrane #status predicted <TM5>
 F:292-309/Domain: transmembrane #status predicted <TM6>
 F:14/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:32-277,113-190/Disulfide bonds: #status predicted

Query Match 58.0%; Score 47; DB 2; Length 374;
 Best Local Similarity 61.5%; Pred. No. 2.1;
 Matches 8; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 ATGAWVFSNATCK 14
 I I I I I I I
 Db 102 AANWVFGNAMCK 114

RESULT 6
 S74237
 probable G protein-coupled receptor - human
 N:Alternate names: GPR-NGA
 C:Species: Homo sapiens (man)
 C:Date: 29-Jan-1998 #sequence_revision 13-Feb-1998 #text_change 20-Apr-2000
 C:Accession: S74237; G02628
 R:O'Dowd, B.F.; Nguyen, T.; Lynch, K.R.; Kolakowski, L.F.; Thompson, M.; Cheng, R.; M
 FEBS Lett. 394, 325-329, 1996

A:Title: A novel gene codes for a putative G protein-coupled receptor with an abundant
A:Reference number: S74237; MUID:96427280
A:Accession: S74237
A>Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-415 <ODD>
A:Cross-references: EMBL:U64871; NID:gl1575512
R:Bonner, T.
submitted to the EMBL Data Library, April 1996
A:Reference number: H01502
A:Accession: G02628
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-305,'K',307-415 <BON>
A:Cross-references: EMBL:U55312; NID:gl1323695; PIDN:AAB00316.1; PID:gl1323696
C:Genetics:

A:Gene: GDB:GPR19
A:Cross-references: GDB:3770734
A:Map position: 12pter-12qter
A:Introns: #status absent
C:Superfamily: neurokinin 1 receptor
C:Keywords: G protein-coupled receptor; transmembrane protein
F:45-87/Domain: transmembrane #status predicted <TM1>
F:102-124/Domain: transmembrane #status predicted <TM2>
F:140-161/Domain: transmembrane #status predicted <TM3>
F:183-204/Domain: transmembrane #status predicted <TM4>
F:223-243/Domain: transmembrane #status predicted <TM5>
F:277-298/Domain: transmembrane #status predicted <TM6>
F:310-329/Domain: transmembrane #status predicted <TM7>

Query Match 55.6%; Score 45; DB 2; Length 415;
Best Local Similarity 58.3%; Pred. No. 5;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 3 TGAWVFSNATCK 14
||| :|||
Db 128 TGRWTLGSATCK 139

RESULT 7
S14332
rhodopsin - northern European squid
C:Species: Loligo forbesi (northern European squid)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 22-Jun-1999
C:Accession: S14332
R:Hall, M.D.; Hoon, M.A.; Ryba, N.J.P.; Pottinger, J.D.D.; Keen, J.N.; Saibil, H.R.; Fin
Biochem. J. 274, 35-40, 1991
A:Title: Molecular cloning and primary structure of squid (Loligo forbesi) rhodopsin, a
A:Reference number: S14332; MUID:91158727
A:Accession: S14332
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-452 <HAL>
A:Cross-references: EMBL:X56788; NID:g95113; PIDN:CAA40108.1; PID:g603851
C:Superfamily: octopus rhodopsin

C:Keywords: chromoprotein; color vision; G protein-coupled receptor; glycoprotein; lipop
F:36-60/Domain: transmembrane #status predicted <TM1>
F:73-97/Domain: transmembrane #status predicted <TM2>
F:106-130/Domain: transmembrane #status predicted <TM3>
F:153-176/Domain: transmembrane #status predicted <TM4>
F:200-223/Domain: transmembrane #status predicted <TM5>
F:262-285/Domain: transmembrane #status predicted <TM6>
F:301-322/Domain: transmembrane #status predicted <TM7>
F:8/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:305/Binding site: retinal (Lys) (covalent) #status predicted
F:336,337/Binding site: palmitate (Cys) (covalent) #status predicted

Query Match 55.6%; Score 45; DB 1; Length 452;
Best Local Similarity 77.8%; Pred. No. 5.4;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 TGAWVFSNATCK 14
||| :|||
Db 128 TGRWTLGSATCK 139

RESULT 7
S14332
rhodopsin - northern European squid
C:Species: Loligo forbesi (northern European squid)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 22-Jun-1999
C:Accession: S14332
R:Hall, M.D.; Hoon, M.A.; Ryba, N.J.P.; Pottinger, J.D.D.; Keen, J.N.; Saibil, H.R.; Fin
Biochem. J. 274, 35-40, 1991
A:Title: Molecular cloning and primary structure of squid (Loligo forbesi) rhodopsin, a
A:Reference number: S14332; MUID:91158727
A:Accession: S14332
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-452 <HAL>
A:Cross-references: EMBL:X56788; NID:g95113; PIDN:CAA40108.1; PID:g603851
C:Superfamily: octopus rhodopsin

C:Keywords: chromoprotein; color vision; G protein-coupled receptor; glycoprotein; lipop
F:36-60/Domain: transmembrane #status predicted <TM1>
F:73-97/Domain: transmembrane #status predicted <TM2>
F:106-130/Domain: transmembrane #status predicted <TM3>
F:153-176/Domain: transmembrane #status predicted <TM4>
F:200-223/Domain: transmembrane #status predicted <TM5>
F:262-285/Domain: transmembrane #status predicted <TM6>
F:301-322/Domain: transmembrane #status predicted <TM7>
F:8/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:305/Binding site: retinal (Lys) (covalent) #status predicted
F:336,337/Binding site: palmitate (Cys) (covalent) #status predicted

Query Match 55.6%; Score 45; DB 2; Length 415;
Best Local Similarity 58.3%; Pred. No. 5;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 3 TGAWVFSNATCK 14
||| :|||
Db 128 TGRWTLGSATCK 139

RESULT 7
S14332
rhodopsin - northern European squid
C:Species: Loligo forbesi (northern European squid)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 22-Jun-1999
C:Accession: S14332
R:Hall, M.D.; Hoon, M.A.; Ryba, N.J.P.; Pottinger, J.D.D.; Keen, J.N.; Saibil, H.R.; Fin
Biochem. J. 274, 35-40, 1991
A:Title: Molecular cloning and primary structure of squid (Loligo forbesi) rhodopsin, a
A:Reference number: S14332; MUID:91158727
A:Accession: S14332
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-452 <HAL>
A:Cross-references: EMBL:X56788; NID:g95113; PIDN:CAA40108.1; PID:g603851
C:Superfamily: octopus rhodopsin

C:Keywords: chromoprotein; color vision; G protein-coupled receptor; glycoprotein; lipop
F:36-60/Domain: transmembrane #status predicted <TM1>
F:73-97/Domain: transmembrane #status predicted <TM2>
F:106-130/Domain: transmembrane #status predicted <TM3>
F:153-176/Domain: transmembrane #status predicted <TM4>
F:200-223/Domain: transmembrane #status predicted <TM5>
F:262-285/Domain: transmembrane #status predicted <TM6>
F:301-322/Domain: transmembrane #status predicted <TM7>
F:8/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:305/Binding site: retinal (Lys) (covalent) #status predicted
F:336,337/Binding site: palmitate (Cys) (covalent) #status predicted

Query Match 55.6%; Score 45; DB 1; Length 452;
Best Local Similarity 77.8%; Pred. No. 5.4;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 TGAWVFSNATCK 14
||| :|||
Db 128 TGRWTLGSATCK 139

RESULT 7
S14332
rhodopsin - northern European squid
C:Species: Loligo forbesi (northern European squid)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 22-Jun-1999
C:Accession: S14332
R:Hall, M.D.; Hoon, M.A.; Ryba, N.J.P.; Pottinger, J.D.D.; Keen, J.N.; Saibil, H.R.; Fin
Biochem. J. 274, 35-40, 1991
A:Title: Molecular cloning and primary structure of squid (Loligo forbesi) rhodopsin, a
A:Reference number: S14332; MUID:91158727
A:Accession: S14332
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-452 <HAL>
A:Cross-references: EMBL:X56788; NID:g95113; PIDN:CAA40108.1; PID:g603851
C:Superfamily: octopus rhodopsin

C:Keywords: chromoprotein; color vision; G protein-coupled receptor; glycoprotein; lipop
F:36-60/Domain: transmembrane #status predicted <TM1>
F:73-97/Domain: transmembrane #status predicted <TM2>
F:106-130/Domain: transmembrane #status predicted <TM3>
F:153-176/Domain: transmembrane #status predicted <TM4>
F:200-223/Domain: transmembrane #status predicted <TM5>
F:262-285/Domain: transmembrane #status predicted <TM6>
F:301-322/Domain: transmembrane #status predicted <TM7>
F:8/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:305/Binding site: retinal (Lys) (covalent) #status predicted
F:336,337/Binding site: palmitate (Cys) (covalent) #status predicted

Query Match 55.6%; Score 45; DB 1; Length 452;
Best Local Similarity 77.8%; Pred. No. 5.4;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 TGAWVFSNATCK 14
||| :|||
Db 128 TGRWTLGSATCK 139

RESULT 7
S14332
rhodopsin - northern European squid
C:Species: Loligo forbesi (northern European squid)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 22-Jun-1999
C:Accession: S14332
R:Hall, M.D.; Hoon, M.A.; Ryba, N.J.P.; Pottinger, J.D.D.; Keen, J.N.; Saibil, H.R.; Fin
Biochem. J. 274, 35-40, 1991
A:Title: Molecular cloning and primary structure of squid (Loligo forbesi) rhodopsin, a
A:Reference number: S14332; MUID:91158727
A:Accession: S14332
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-452 <HAL>
A:Cross-references: EMBL:X56788; NID:g95113; PIDN:CAA40108.1; PID:g603851
C:Superfamily: octopus rhodopsin

C:Keywords: chromoprotein; color vision; G protein-coupled receptor; glycoprotein; lipop
F:36-60/Domain: transmembrane #status predicted <TM1>
F:73-97/Domain: transmembrane #status predicted <TM2>
F:106-130/Domain: transmembrane #status predicted <TM3>
F:153-176/Domain: transmembrane #status predicted <TM4>
F:200-223/Domain: transmembrane #status predicted <TM5>
F:262-285/Domain: transmembrane #status predicted <TM6>
F:301-322/Domain: transmembrane #status predicted <TM7>
F:8/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:305/Binding site: retinal (Lys) (covalent) #status predicted
F:336,337/Binding site: palmitate (Cys) (covalent) #status predicted

Qy 6 WFFSNATCK 14
||| |||
Db 101 WFFGNAACK 109

RESULT 8
S34806

hypothetical protein 2 [imported] - Halobacterium salinarum plasmid pHH1
C:Species: Halobacterium salinarum
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 03-Nov-2000
C:Accession: S34806
R:Preifer, F.; Ghahraman, P.
Mol. Gen. Genet. 238, 193-200, 1993
A:Title: Plasmid pHH1 of Halobacterium salinarum: characterization of the replicon r
A:Reference number: S34806; MUID:93241154
A:Accession: S34806
A>Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-319 <PPE>
A:Cross-references: EMBL:X67101; NID:g297409; PID:g297410
A:Note: the source is designated as Halobacterium salinarum
C:Comment: this ORF is considered not to be required for plasmid replication [validat
PNRCL00.
C:Genetics:
A:Genome: plasmid pHH1

Query Match 54.3%; Score 44; DB 2; Length 319;
Best Local Similarity 58.3%; Pred. No. 5.7;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 HATGAWVFSNAT 12
||| :|||
Db 59 HLTASWVFSGST 70

RESULT 9
T13484

frizzled protein homolog - fruit fly (Drosophila melanogaster)
N:Alternate names: hypothetical protein EG:34F3.6
C:Species: Drosophila melanogaster
C:Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000
C:Accession: T13484
R:Valenti, P.; Salles, C.; Campbell, L.; Glover, D.
submitted to the EMBL Data Library, April 1999
A:Description: Sequencing the distal X chromosome of Drosophila melanogaster.
A:Reference number: Z17685
A:Accession: T13484
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-526 <PHI>
A:Cross-references: EMBL:AL031583; PIDN:CAA20896.1
C:Genetics:
A:Cross-references: FlyBase:FBgn0025623
A:Introns: 18/3
A:Note: EG:34F3.6

Query Match 54.3%; Score 44; DB 2; Length 526;
Best Local Similarity 58.3%; Pred. No. 9.3;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 3 TGAWVFSNATCK 14
||| |||
Db 449 TGLWVWSKTCE 460

RESULT 10
T08228

plasmid replication protein repH [validated] - Halobacterium sp. (strain NRC-1) plasm
N:Alternate names: hypothetical protein H0136
C:Species: Halobacterium sp.
A:Variety: strain NRC-1

C;Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 18-Feb-2000
 C;Accession: T08228; A40600
 R;Ng, W.V.; Clufo, S.A.; Smith, T.M.; Bumgarner, R.E.; Baskin, D.; Faust, J.; Hall, B.;
 Genome Res. 8, 1131-1141, 1998
 A;Title: Snapshot of a large dynamic replicon in a halophilic Archaeon: megaplasmid or
 A;Reference number: Z16408; MUID:99063795
 C;Accession: T08228
 A;Status: translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-1073 <NGW>
 A;Cross-references: EMBL:AF016485; NID:g2822278; PID:g2822289; HALOSP:H0136
 A;Experimental source: strain NRC-1
 R;Ng, W.L.; DasSarma, S.
 J. Bacteriol. 175, 4584-4596, 1993
 A;Title: Minimal replication origin of the 200-kilobase Halobacterium plasmid pNRC100.
 A;Reference number: A40600; MUID:93328662
 C;Accession: A40600
 A;Molecule type: DNA
 A;Residues: 65-806; 'PPGRGD', 807-1073 <NGA>
 A;Cross-references: GB:LI9296
 A;Note: the source is designated as Halobacterium halobium
 C;Genetics:
 A;Gene: repH; H0136
 A;Genome: plasmid pNRC100
 C;Function:
 A;Description: required for replication of plasmid pNRC100 [validated; MUID:93328662]
 C;Superfamily: Halobacterium plasmid pNRC100 replication protein repH
 C;Keywords: plasmid replication

Query Match 54.3%; Score 44; DB 1; Length 1073;
 Best Local Similarity 58.3%; Pred. No. 18;
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 HATGAWFVSNAAT 12
 ||| :|||| :|
 Db 722 HLTASWVFGST 733

RESULT 11
 T06680
 hypothetical protein T17F15.100 - Arabidopsis thaliana
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 02-Sep-2000
 C;Accession: T06680
 R;Quetier, F.; Choisme, N.; Robert, C.; Brottier, P.; Wincker, P.; Cattolico, L.; Artig
 Submitted to the Protein Sequence Database, April 1999
 A;Reference number: Z15793
 A;Accession: T06680
 A;Molecule type: DNA
 A;Residues: 1-349 <QUE>
 A;Cross-references: EMBL:AL049658; GSPDB:GN00061; ATSP:T17F15.100
 A;Experimental source: cultivar Columbia; BAC clone T17F15
 C;Genetics:
 A;Gene: ATSP:T17F15.100
 A;Map position: 3
 A;Introns: 26/1; 81/2
 C;Superfamily: RING finger homology
 F;203-254/Domain: RING finger homology <RRN>

Query Match 53.1%; Score 43; DB 2; Length 349;
 Best Local Similarity 46.2%; Pred. No. 9.2;
 Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 HATGAWFVSNAATC 13
 | :| :||| :|
 Db 233 HCIDTWLLSNSTC 245

RESULT 12
 C83339
 hypothetical protein PA2462 [imported] - Pseudomonas aeruginosa (strain PA01)

C;Species: Pseudomonas aeruginosa
 C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
 C;Accession: C83339
 R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.;
 adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L
 ; Lory, S.; Olson, M.V.
 Nature 406, 959-964, 2000
 A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa
 A;Reference number: A82950; MUID:20437337
 A;Accession: C83339
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-5627 <STO>
 A;Cross-references: GB:AE004673; GB:AE004091; NID:g9948501; PIDN:AAG05850.1; GSPDB:GN
 A;Experimental source: strain PA01
 C;Genetics:
 A;Gene: PA2462

Query Match 53.1%; Score 43; DB 2; Length 5627;
 Best Local Similarity 80.0%; Pred. No. 1.3e+02;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 TGAWFVSNAAT 12
 ||||| |||
 Db 5313 TGAWVAGNAT 5322

RESULT 13
 A83339
 hypothetical protein PA2460 [imported] - Pseudomonas aeruginosa (strain PA01)
 C;Species: Pseudomonas aeruginosa
 C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
 C;Accession: A83339
 R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.;
 adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L
 ; Lory, S.; Olson, M.V.
 Nature 406, 959-964, 2000
 A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa
 A;Reference number: A82950; MUID:20437337
 A;Accession: A83339
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-98 <STO>
 A;Cross-references: GB:AE004673; GB:AE004091; NID:g9948501; PIDN:AAG05848.1; GSPDB:GN
 A;Experimental source: strain PA01
 C;Genetics:
 A;Gene: PA2460

Query Match 51.9%; Score 42; DB 2; Length 98;
 Best Local Similarity 80.0%; Pred. No. 4;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 TGAWFVSNAAT 12
 ||||| |||
 Db 35 TGAWVARNAT 44

RESULT 14
 H83133
 hypothetical protein PA4103 [imported] - Pseudomonas aeruginosa (strain PA01)
 C;Species: Pseudomonas aeruginosa
 C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
 C;Accession: H83133
 R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.;
 adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L
 ; Lory, S.; Olson, M.V.
 Nature 406, 959-964, 2000
 A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa
 A;Reference number: A82950; MUID:20437337
 A;Accession: H83133
 A;Status: preliminary

A:Molecule type: DNA
A:Residues: 1-209 <STO>
A:Cross-references: GB:AE004826; GB:AE004091; NID:g9950296; PIDN:AAG07490.1; GSPDB:GN001
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA4103

Query Match 51.9%; Score 42; DB 2; Length 209;
Best Local Similarity 46.2%; Pred. No. 8.2;
Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 HATGAWFVSATC 13
|:|:|:|:
Db 153 HSTGTWVLGIFC 165

RESULT 15.
I49022
kappa opioid receptor 3 - mouse
C:Species: Mus musculus (house mouse)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 19-May-2000
C:Accession: I49022
R;Pan, Y.X.; Cheng, J.; Xu, J.; Rossi, G.; Jacobson, E.; Ryan-Moro, J.; Brooks, A.I.; De
Mol. Pharmacol. 47, 1180-1188, 1995
A:Title: Cloning and functional characterization through antisense mapping of a kappa 3-
A:Reference number: I49022; MUID:95327076
A:Accession: I49022
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-367 <RES>
A:Cross-references: EMBL:U09421; NID:g551484; PIDN:AAA81333.1; PID:g551485
C:Superfamily: vertebrate rhodopsin

Query Match 51.9%; Score 42; DB 2; Length 367;
Best Local Similarity 63.6%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 GAWVFSNATCK 14
|:|:|:|:
Db 111 GFWPFGNALCK 121

Search completed: May 23, 2001, 15:32:00
Job time: 507 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 23, 2001, 15:36:17 ; Search time 62.39 Seconds
(without alignments)

7.687 Million cell updates/sec

Title: US-08-887-977-10_COPY_97_110

Perfect score: 81

Sequence: 1 HATGANVFSNATCK 14

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	81	100.0	374	1	CKR6_HUMAN
2	60	74.1	367	1	CKR6_MOUSE
3	49	60.5	1455	1	FACA_HUMAN
4	47	58.0	356	1	CKRV_MOUSE
5	47	58.0	374	1	CKR2_HUMAN
6	45	55.6	415	1	GPRJ_HUMAN
7	45	55.6	452	1	OPSD_LOLFO
8	44	54.3	354	1	CKR5_RAT
9	44	54.3	373	1	CKR2_MOUSE
10	44	54.3	373	1	CKR2_RAT
11	43	53.1	354	1	CKR5_MOUSE
12	42	51.9	367	1	OPRX_MOUSE
13	42	51.9	367	1	OPRX_RAT
14	42	51.9	370	1	OPRX_HUMAN
15	42	51.9	370	1	OPRX_PIG
16	42	51.9	412	1	ERH_YEAST
17	42	51.9	662	1	LOXP_HUMAN
18	41	50.6	355	1	CKR1_MACMU
19	40	49.4	352	1	C3AR_CANFA
20	40	49.4	371	1	NY6R_MOUSE
21	40	49.4	407	1	IE68_HSVSA
22	40	49.4	416	1	OXIR_RAT
23	40	49.4	425	1	OXIR_HUMAN
24	40	49.4	721	1	ERG7_SCHPO
25	39	48.1	190	1	NODL_RHLV
26	39	48.1	257	1	IODI_RAT
27	39	48.1	352	1	GPRJ_RAT
28	39	48.1	355	1	CKR1_HUMAN
29	39	48.1	355	1	CKR3_CERAE
30	39	48.1	355	1	CKR3_MACMU
31	39	48.1	371	1	NY6R_RABIT
32	39	48.1	398	1	OPRM_MOUSE
33	39	48.1	409	1	GPRJ_MOUSE

RESULT 1

ID	CKR6_HUMAN	STANDARD;	PRT;	374 AA.
AC	P51684: Q92846; P78553;			
DT	01-OCT-1996 (Rel. 34, Created)			
DT	15-JUL-1998 (Rel. 36, Last sequence update)			
DT	01-OCT-2000 (Rel. 40, Last annotation update)			
DE	C-C CHEMOKINE RECEPTOR TYPE 6 (C-C CKR-6) (CCR-6) (IARC RECEPTOR) (GPR-CV4) (GPCV4) (CHEMOKINE RECEPTOR-LIKE 3) (CKR-L3) (DRY6).			
DE	CCR6 OR CMKBR6 OR STRL22 OR GPR29 OR CKRL3.			
GN	Homo sapiens (Human).			
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OC	NCBI_TaxID=9606;			
OX	[1]			
RN	SEQUENCE FROM N.A., AND FUNCTION.			
RP	MEDLINE=97313465; PubMed=9169459;			
RX	Baba M., Imai T., Nishimura M., Kakizaki M., Takagi S., Hieshima K., Nomiyama H., Yoshie O.;			
RA	"Identification of CCR6, the specific receptor for a novel lymphocyte-directed CC chemokine IARC."			
RT	J. Biol. Chem. 272:14893-14898(1997).			
RL	[2]			
RN	SEQUENCE FROM N.A.			
RP	Lautens L.L., Modi W., Bonner T.I.;			
RA	Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.			
RL	[3]			
RN	SEQUENCE FROM N.A.			
RP	MEDLINE=97040707; PubMed=8886020;			
RX	Zaballos A., Varona R., Gutierrez J., Lind P., Marquez G.;			
RA	"Molecular cloning and RNA expression of two new human chemokine receptor-like genes."			
RT	Biochem. Biophys. Res. Commun. 227:846-853(1996).			
RL	[4]			
RN	SEQUENCE FROM N.A.			
RP	McCoy R., Perlmuter D.H.;			
RA	Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.			
RL	[5]			
RN	SEQUENCE FROM N.A.			
RP	MEDLINE=97224503; PubMed=9070937;			
RX	Liao F., Lee H.-H., Farber J.M.;			
RA	"Cloning of STRL22, a new human gene encoding a G-protein-coupled receptor related to chemokine receptors and located on chromosome 6q27."			
RT	Genomics 40:175-180(1997).			
RL				
CC	-1- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-3-ALPHA/LARC AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.			
CC	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.			
CC	-1- TISSUE SPECIFICITY: SPLEEN, LYMPH NODES, APPENDIX, AND FETAL LIVER. EXPRESSED IN LYMPHOCYTES, T CELLS AND B CELLS BUT NOT IN NATURAL KILLER CELLS, MONOCYTES, OR GRANULOCYTES.			
CC	-1- INDUCTION: INTERLEUKIN-2.			
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.			
CC	-1- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-6 IS THE INITIATOR.			

Q17094 loligo subu
Q19084 caenorhabdi
P00474 providencia
O75748 homo sapien
P97468 mus musculu
O35786 rattus norv
Q99788 homo sapien
O95867 homo sapien
Q92194 mus musculu
P32229 swinepox vi
P37925 salmonella
P56484 mus musculu

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DR EMBL; U45984; AAB62714.1; -
 DR EMBL; 279784; CAB02144.1; ALT_INIT.
 DR EMBL; U60000; AAB06949.1; -
 DR EMBL; U68030; AAC51124.1; -
 DR EMBL; U68032; AAC51125.1; -
 DR HSSP; P34996; 1DDD.
 DR GCRDb; GCR_1037; -
 DR GCRDb; GCR_1075; -
 DR GCRDb; GCR_1906; -
 DR GCRDb; GCR_1919; -
 DR GCRDb; GCR_1941; -
 DR GCRDb; GCR_2110; -
 DR MIM; 601835; -
 DR InterPro; IPR000276; -
 DR Pfam; PF00001; 7tm1; 1.
 DR PRINTS; PR00237; GPCRHHODOPSN.
 DR PROSITE; PS00237; G-PROTEIN_RECEP_FL_1; 1.
 DR PROSITE; PS0262; G-PROTEIN_RECEP_FL_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 47
 FT TRANSMEM 48 74
 FT DOMAIN 75 83
 FT TRANSMEM 84 104
 FT DOMAIN 105 119
 FT TRANSMEM 120 141
 FT DOMAIN 142 159
 FT TRANSMEM 160 180
 FT DOMAIN 181 211
 FT TRANSMEM 212 238
 FT DOMAIN 239 254
 FT TRANSMEM 255 279
 FT DOMAIN 280 303
 FT TRANSMEM 304 321
 FT DOMAIN 322 374
 FT DISULFID 118 197
 FT CARBOHYD 7 7
 FT CARBOHYD 23 23
 FT CONFLICT 60 60
 FT CONFLICT 74 74
 FT CONFLICT 86 86
 FT CONFLICT 164 164
 FT CONFLICT 182 182
 FT CONFLICT 192 192
 FT CONFLICT 206 206
 FT CONFLICT 225 225
 FT CONFLICT 370 374
 FT CONFLICT 374 374
 FT SEQUENCE 374 AA; 42494 MW; D7F963534E990BC4 CRC64;
 Query Match 100.0%; Score 81; DB 1; Length 374;
 Best Local Similarity 100.0%; Pred. No. 4.2e-06;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 HATGAWFSNATCK 14
 Db 106 HATGAWFSNATCK 119
 RESULT 2
 ID CRR6_MOUSE STANDARD; PRT; 367 AA.
 AC O54689;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE C-C CHEMOKINE RECEPTOR TYPE 6 (C-C CKR-6) (CCR-6) (KY411).
 GN CCR6 OR CMKBR6.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Yanagihara S., Komura E., Yamaguchi Y.;
 RT "Mouse G protein-coupled receptor KY411";
 RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99077268; PubMed=9862452;
 RA Varona R., Zaballos A., Gutierrez J., Martin P., Roncal F.,
 RA Albar J.P., Ardavin C., Marquez G.;
 RT "Molecular cloning, functional characterization and mRNA expression
 RT analysis of the murine chemokine receptor CCR6 and its specific ligand
 RT MIP-3alpha";
 RL FEBS Lett. 440:188-194(1998).
 CC -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-3-
 CC ALPHA/LARC AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE
 CC INTRACELLULAR CALCIUM IONS LEVEL.
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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DR EMBL; AB009369; BAA33776.1; -
 DR EMBL; AJ222714; CAA10956.1; -
 DR MGD; MGI:1333797; Cmkbr6.
 DR InterPro; IPR000276; -
 DR Pfam; PF00001; 7tm1; 1.
 DR PRINTS; PR00237; GPCRHHODOPSN.
 DR PROSITE; PS00237; G-PROTEIN_RECEP_FL_1; 1.
 DR PROSITE; PS0262; G-PROTEIN_RECEP_FL_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 39
 FT TRANSMEM 40 66
 FT DOMAIN 67 75
 FT TRANSMEM 76 96
 FT DOMAIN 97 111
 FT TRANSMEM 112 133
 FT DOMAIN 134 151
 FT TRANSMEM 152 172
 FT DOMAIN 173 203
 FT TRANSMEM 204 230
 FT DOMAIN 231 246
 FT TRANSMEM 247 271
 FT DOMAIN 272 295
 FT TRANSMEM 296 313
 FT DOMAIN 314 367
 FT DISULFID 110 189
 FT CARBOHYD 2 2
 FT CARBOHYD 35 35
 FT SEQUENCE 367 AA; 42102 MW; 6A309AF83B1117E CRC64;
 Query Match 74.1%; Score 60; DB 1; Length 367;
 Best Local Similarity 71.4%; Pred. No. 0.01;
 Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 HATGAWFSNATCK 14
 Db 98 HATNTWFSNALCK 111

RESULT 3
FACA_HUMAN
ID FACA_HUMAN STANDARD: PRT: 1455 AA.
AC O15360; Q92497; Q75266; Q9Y6M2;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE FANCONI ANEMIA GROUP A PROTEIN (FACA PROTEIN).
GN FANCA OR FAA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97312685; PubMed=9169126;
RA Ianzano L., D'Apollito M., Centra M., Savino M., Levran O.,
RA Auerbach A.D., Cleton-Jansen A.M., Doggett N.A., Pronk J.C.,
RA Tipping A.J., Gibson R.A., Mathew C.G., Whitmore S.A., Apostolou S.,
RA Callen F.C., Zelante L., Savoia A.;
RT "The genomic organization of the Fanconi anemia group A (FAA) gene";
RL Genomics 41:309-314(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX TISSUE=Lymphoblast;
RC MEDLINE=97051928; PubMed=8996563;
RA Lo Ten Foe J.R., Rooimans M.A., Bosnyan-Collins L., Alon N.,
RA Wijker M., Parker L., Lightfoot J., Carreau M., Callen D.F.,
RA Savoia A., Cheng N.C., van Berkel C.G.M., Strunk M.H.P., Gilie J.J.P.,
RA Pals G., Kruyt F.A.E., Pronk J.C., Arwert F., Buchwald M., Joenje H.;
RT "Expression cloning of a cDNA for the major Fanconi anaemia gene,
RT FAA";
RL Nat. Genet. 14:320-323(1996).
RN [3]
RP SEQUENCE OF 175-834 FROM N.A.
RX Ricke D.O., Bruce D., Mundt M., Doggett N., Munk C., Saunders E.,
RA Robinson D., Jones M., Buckingham J., Chasteen L., Thompson S.,
RA Goodwin L., Bryant J., Tesmer J., Meincke L., Longmire J., White S.,
RA Deng S., Ratum O., Campbell C., Fawcett J., Maltbie M., Deaven L.;
RT "Sequencing of human Fanconi anemia complementation group A gene
RT genomic region";
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 491-542 FROM N.A.
RX MEDLINE=98375690; PubMed=9711872;
RA Levran O., Doggett N.A., Auerbach A.D.;
RT "Identification of Alu-mediated deletions in the Fanconi anemia gene
RT FAA";
RL Hum. Mutat. 12:145-152(1998).
RN [5]
RP SUBCELLULAR LOCATION, AND MUTAGENESIS.
RX MEDLINE=98414611; PubMed=9742112;
RA Naef D., Kupfer G.M., Suliman A., Lambert K., D'Andrea A.D.;
RT "Functional activity of the Fanconi anemia protein FAA requires FAC
RT binding and nuclear localization";
RL Mol. Cell. Biol. 18:5952-5960(1998).
RN [6]
RP PHOSPHORYLATION.
RX MEDLINE=99007271; PubMed=9789045;
RA Yamashita T., Kupfer G.M., Naf D., Suliman A., Joenje H., Asano S.,
RA D'Andrea A.D.;
RT "The Fanconi anemia pathway requires FAA phosphorylation and FAA/FAC
RT nuclear accumulation";
RL Proc. Natl. Acad. Sci. U.S.A. 95:13085-13090(1998).
RN [7]
RP VARIANTS FA, AND VARIANTS.
RX MEDLINE=98058767; PubMed=9371798;
RA Levran O., Erlich T., Magdalen N., Gregory J.J., Batish S.D.,
RA Verlender P.C., Auerbach A.D.;
RT "Sequence variation in the Fanconi anemia gene FAA";
RL Proc. Natl. Acad. Sci. U.S.A. 94:13051-13056(1997).
RN [8]
RP DNA repair; Nuclear protein; Phosphorylation; Disease mutation;
Polymorphism.

VARIANTS FA PRO-1110 AND GLY-1117.
MEDLINE=99225041; PubMed=10210316;
Kupfer G., Naef D., Garcia-Higuera I., Wasik J., Cheng A.,
Yamashita T., Tipping A., Morgan N., Mathew C.G., D'Andrea A.D.;
RT "A patient-derived mutant form of the Fanconi anemia protein, FANCA,
RT is defective in nuclear accumulation";
RL Exp. Hematol. 27:587-593(1999).
CC -!- FUNCTION: DNA REPAIR PROTEIN THAT MAY OPERATE IN A POSTREPLICATION
CC REPAIR OR A CELL CYCLE CHECKPOINT FUNCTION. MAY BE IMPLICATED IN
CC INTERSTRAND DNA CROSS-LINK REPAIR AND IN THE MAINTENANCE OF NORMAL
CC CHROMOSOME STABILITY.
CC -!- SUBUNIT: BELONGS TO A MULTISUBUNIT COMPLEX COMPOSED OF FANCA,
CC FANCC AND FANCG PROTEINS.
CC -!- SUBCELLULAR LOCATION: NUCLEAR (MAJOR) AND CYTOPLASMIC (MINOR).
CC -!- PTM: PHOSPHORYLATED PRIMARILY ON SERINE RESIDUES. PHOSPHORYLATION
CC IS REQUIRED FOR THE FORMATION OF THE NUCLEAR COMPLEX. NOT
CC PHOSPHORYLATED IN CELLS DERIVED FROM GROUPS A, B, C, E, F, G, AND
CC H.
CC -!- DISEASE: DEFECTS IN FANCA ARE THE CAUSE OF ONE OF THE 8
CC COMPLEMENTATION GROUPS OF FANCONI ANEMIA (FA), AN AUTOSOMAL
CC RECESSIVE DISORDER CHARACTERIZED BY PROGRESSIVE PANCYTOPAENIA, A
CC DIVERSE ASSORTMENT OF CONGENITAL MALFORMATIONS, AND A
CC PREDISPOSITION TO THE DEVELOPMENT OF MALIGNANCIES. AT THE CELLULAR
CC LEVEL IT IS ASSOCIATED WITH HYPERSENSITIVITY TO DNA-DAMAGING
CC AGENTS, CHROMOSOMAL INSTABILITY (INCREASED CHROMOSOME BREAKAGE),
CC AND DEFECTIVE DNA REPAIR. FANCA DEFECTS ACCOUNT FOR 65 % OF FA.
CC -!- DATABASE: NAME-Fanconi Anemia Mutation Database;
CC WWW="http://www.rockefeller.edu/fanconi/mutate/";
CC
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CC EMBL; Z83068; CAB05445.1; JOINED.
CC EMBL; Z83069; CAB05445.1; JOINED.
CC EMBL; Z83070; CAB05445.1; JOINED.
CC EMBL; Z83071; CAB05445.1; JOINED.
CC EMBL; Z83072; CAB05445.1; JOINED.
CC EMBL; Z83073; CAB05445.1; JOINED.
CC EMBL; Z83074; CAB05445.1; JOINED.
CC EMBL; Z83075; CAB05445.1; JOINED.
CC EMBL; Z83076; CAB05445.1; JOINED.
CC EMBL; Z83077; CAB05445.1; JOINED.
CC EMBL; Z83078; CAB05445.1; JOINED.
CC EMBL; Z83079; CAB05445.1; JOINED.
CC EMBL; Z83080; CAB05445.1; JOINED.
CC EMBL; Z83081; CAB05445.1; JOINED.
CC EMBL; Z83082; CAB05445.1; JOINED.
CC EMBL; Z83083; CAB05445.1; JOINED.
CC EMBL; Z83084; CAB05445.1; JOINED.
CC EMBL; Z83085; CAB05445.1; JOINED.
CC EMBL; Z83086; CAB05445.1; JOINED.
CC EMBL; Z83087; CAB05445.1; JOINED.
CC EMBL; Z83088; CAB05445.1; JOINED.
CC EMBL; Z83089; CAB05445.1; JOINED.
CC EMBL; Z83090; CAB05445.1; JOINED.
CC EMBL; Z83091; CAB05445.1; JOINED.
CC EMBL; Z83092; CAB05445.1; JOINED.
CC EMBL; Z83093; CAB05445.1; JOINED.
CC EMBL; Z83094; CAB05445.1; JOINED.
CC EMBL; Z83095; CAB05445.1; JOINED.
CC EMBL; Z83151; CAB05445.1; JOINED.
CC EMBL; X92226; CAA67610.1; JOINED.
CC EMBL; AC005567; AAC33401.1; JOINED.
CC EMBL; AF054569; AAC28331.1; JOINED.
CC MIM: 227650.
KW DNA repair; Nuclear protein; Phosphorylation; Disease mutation;
KW Polymorphism.

```
FT DOMAIN 18 34 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT VARIANT 6 6 V -> D.
FT VARIANT 8 8 /FTIG-VAR_009637.
FT POLYMORPHISM).
FT /FTIG-VAR_009638.
FT A -> V (IN FA A).
FT /FTIG-VAR_009639.
FT L -> F (IN FA A).
FT /FTIG-VAR_009640.
FT D -> G (IN FA A).
FT /FTIG-VAR_009641.
FT R -> C (IN FA A).
FT /FTIG-VAR_009642.
FT H -> R (IN FA A).
FT /FTIG-VAR_009643.
FT S -> G.
FT /FTIG-VAR_009644.
FT P -> L.
FT /FTIG-VAR_009645.
FT G -> D.
FT /FTIG-VAR_009646.
FT L -> P (IN FA A).
FT /FTIG-VAR_009647.
FT L -> P (IN FA A).
FT /FTIG-VAR_009648.
FT R -> L (IN FA A).
FT /FTIG-VAR_009649.
FT H -> P (IN FA A; LOSS OF FUNCTION).
FT /FTIG-VAR_009650.
FT R -> G (IN FA A; LOSS OF FUNCTION).
FT /FTIG-VAR_009651.
FT O -> E (IN FA A).
FT /FTIG-VAR_009652.
FT T -> A (IN FA A).
FT /FTIG-VAR_009653.
FT MISSING (IN FA A).
FT /FTIG-VAR_009654.
FT V -> I.
FT /FTIG-VAR_009655.
FT W -> R (IN FA A).
FT /FTIG-VAR_009656.
FT T -> A.
FT /FTIG-VAR_009657.
FT H -> D (IN FA A).
FT /FTIG-VAR_009658.
FT M -> I (IN REF. 2).
FT CONFLICT 717 717
SQ SEQUENCE 1455 AA; 162804 MW; DB43BEDB29DF5C0E CRC64;
```

Query Match 60.5%; Score 49; DB 1; Length 1455;
Best Local Similarity 53.8%; Pred. No. 2.3;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 HATGAWVFSNATC 13
|||:|:|:|
Db 204 HAVGWSLERNLCC 216

RESULT 4
ID CKRV_MOUSE STANDARD; PRT; 356 AA.
AC P51676;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE C-C CHEMOKINE RECEPTOR (MACROPHAGE INFLAMMATORY PROTEIN-1 ALPHA
DE RECEPTOR-LIKE 1).
GN CMKBR1L1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;

```
RN SEQUENCE FROM N.A.
RP STRAIN=129/SVJ;
RX MEDLINE=95340546; PubMed=7542241;
RA Gao J.-L., Murphy P.M.;
RT "Cloning and differential tissue-specific expression of three mouse
RT beta chemokine receptor-like genes, including the gene for a
RT functional macrophage inflammatory protein-1 alpha receptor.";
RL J. Biol. Chem. 270:17494-17501(1995).
CC -!- FUNCTION: PROBABLE RECEPTOR FOR A C-C TYPE CHEMOKINE.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- TISSUE SPECIFICITY: DETECTED IN THE SPLEEN, LIVER AND LEUKOCYTES.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U28405; AAA89154.1; -
DR GCRDB; GCR_1696; -
DR MGD; MGI:104617; Cmkbr1l1.
DR InterPro; IPR000276; -
DR InterPro; IPR000355; -
DR Pfam; PF00001; 7tm1.1; 1
DR PRINTS; PR00237; GPCRHHODOPSIN.
DR PRINTS; PR00657; CCHEMOKINER.
DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane.
FT DOMAIN 1 32
FT TRANSMEM 33 60
FT DOMAIN 61 67
FT TRANSMEM 68 92
FT DOMAIN 93 108
FT TRANSMEM 109 130
FT DOMAIN 131 147
FT TRANSMEM 148 172
FT DOMAIN 173 198
FT TRANSMEM 199 224
FT DOMAIN 225 240
FT TRANSMEM 241 265
FT DOMAIN 266 282
FT TRANSMEM 283 306
FT DOMAIN 307 356
FT DISULFID 107 184
SQ SEQUENCE 356 AA; 40934 MW; 58C01ABA8D7D4B06 CRC64;
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Query Match 58.0%; Score 47; DB 1; Length 356;
Best Local Similarity 63.6%; Pred. No. 1.3;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 4 GAWVFSNATCK 14
|:|:|:|:|
Db 98 GDWIFGNAMCK 108

RESULT 5
ID CKR2_HUMAN STANDARD; PRT; 374 AA.
AC P41597;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE C-C CHEMOKINE RECEPTOR TYPE 2 (C-C CKR-2) (CC-CKR-2) (CCR2)
DE (MONOCYTE CHEMOATTRACTANT PROTEIN 1 RECEPTOR) (MCP-1-R) (CCR2).
GN CCR2 OR CMKBR2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN NCBI_TaxID=9606;
 [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94195821; PubMed=8146186;
 RA Charo I.F., Myers S.J., Herman A., Franci C., Connolly A.J.,
 RA Coughlin S.R.;
 RT "Molecular cloning and functional expression of two monocyte
 RT chemoattractant protein 1 receptors reveals alternative splicing of
 RT the carboxyl-terminal tails.";
 RL Proc. Natl. Acad. Sci. U.S.A. 91:2752-2756(1994).
 [2]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=94324942; PubMed=8048929;
 RX Yamagami S., Tokuda Y., Ishii K., Tamaka H., Endo N.;
 RA "cDNA cloning and functional expression of a human monocyte
 RT chemoattractant protein 1 receptor.";
 RL Biochem. Biophys. Res. Commun. 202:1156-1162(1994).
 [3]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=97150864; PubMed=8995400;
 RX Wong L.-M., Myers S.J., Tsou C.-L., Gosling J., Arai H., Charo I.F.;
 RA "Organization and differential expression of the human monocyte
 RT chemoattractant protein 1 receptor gene. Evidence for the role of the
 RT carboxyl-terminal tail in receptor trafficking.";
 RL J. Biol. Chem. 272:1038-1045(1997).
 [4]
 RN SEQUENCE FROM N.A.
 RP McCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D.,
 RA Nham M., Parnell L., Dedhia N., Ansari A., Mardis E., Schutz K.,
 RA Guoj L., la Bastide M., Kaplan N., Greco T., Touchman J.,
 RA Muzny D., Chen C.N., Evans C., Fitzgerald M., See L.H., Tang M.,
 RA Porcel B.M., Dragan Y., Giacalone J., Pae A., Powell E.,
 RA Solinsky K.A., Desilva U., Diaz-Perez S., Zhou X., Yu Y.,
 RA Watanabe M., Doggett N., Garcia D., Sagripanti J.L.;
 RA Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
 RL FUNCTION: RECEPTOR FOR THE MCP-1, MCP-3 AND MCP-4 CHEMOKINES.
 CC TRANSDUCE A SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS
 CC LEVEL.
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A (SHOWN HERE) AND B; ARE
 CC PRODUCED BY ALTERNATIVE SPLICING.
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 CC -----
 CC EMBL; U03882; AAA19119.1; -
 DR EMBL; U03905; AAA19120.1; -
 DR EMBL; D29984; BAA06253.1; -
 DR EMBL; U80924; AAC51637.1; -
 DR EMBL; U80924; AAC51636.1; -
 DR EMBL; U95626; AAB57791.1; -
 DR EMBL; U95626; AAB57792.1; -
 DR GCRdb; GCR_0970; -
 DR GCRdb; GCR_0989; -
 DR GCRdb; GCR_1827; -
 DR GCRdb; GCR_2700; -
 DR GCRdb; GCR_2701; -
 DR MIM; 601267; -
 DR InterPro; IPR000276; -
 DR InterPro; IPR000355; -
 DR InterPro; IPR002237; -
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PRINTS; PR00657; CCHEMOKINER.
 DR PRINTS; PR01107; CCHEMOKINER2.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_FL1; 1.

DR PROSITE; PS50262; G_PROTEIN_RECEP_FL2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Alternative splicing.
 FT DOMAIN 1 42 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 43 70 1 (POTENTIAL).
 FT DOMAIN 71 80 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 81 100 2 (POTENTIAL).
 FT DOMAIN 101 114 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 115 136 3 (POTENTIAL).
 FT DOMAIN 137 153 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 154 178 4 (POTENTIAL).
 FT DOMAIN 179 206 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 207 226 5 (POTENTIAL).
 FT DOMAIN 227 243 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 244 268 6 (POTENTIAL).
 FT DOMAIN 269 285 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 286 309 7 (POTENTIAL).
 FT DOMAIN 310 374 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 14 14 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARSPLIC 314 374 BY SIMILARITY.
 SLPHIALGCRIPALQKVCVCGPGVRCGNKVVTOGLDGR
 GKSGISGRAPASLDKQEGA -> RYLSVFRKHITRRFCK
 QCPVYRETVDGVSTNTPTSTGGEQEVSAGL (IN
 ISOFORM B).
 SQ SEQUENCE 374 AA; 41914 MW; F865E0D39E74CF0F CRC64;
 Query Match 58.0%; Score 47; DB 1; Length 374;
 Best Local Similarity 61.5%; Pred. No. 1.4;
 Matches 8; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 2 ATGAWFVSNTACK 14
 Db 102 AANEWFGNAMCK 114
 RESULT 6
 GPRJ_HUMAN STANDARD; PRT; 415 AA.
 ID GPRJ_HUMAN
 AC Q15760;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE PROBABLE G PROTEIN-COUPLED RECEPTOR GPR19 (GPR-NGA).
 GN GPR19.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Bonner T.I., Matsuda L.A.;
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96427280; PubMed=8830667;
 RA O'Dowd B.F., Nguyen T., Lynch K.R., Kolakowski L.F. Jr., Thompson M.,
 RA Cheng R., Marchese A., Ng G.Y.K., Heng H.H.Q., George S.R.;
 RT "A novel gene codes for a putative G protein-coupled receptor with an
 RT abundant expression in brain.";
 RL FEBS Lett. 394:325-329(1996).
 CC -!- FUNCTION: ORPHAN RECEPTOR.
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -!- TISSUE SPECIFICITY: ABUNDANT EXPRESSION IN THE BRAIN.
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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CC EMBL; U55312; AAB00316.1;
CC EMBL; U54871; AAB49751.1;
CC GCRDB; GCR_1914;
CC GCRDB; GCR_1926;
CC MIM; 602927;
CC InterPro; IPR000276;
CC Pfam; PF00001; 7tm_1; 1.
CC PRINTS; PR00237; GPCRHHODOPSN.
CC PROSITE; PS00237; G_PROTEIN_RECEP_FL_1; 1.
CC PROSITE; PS0262; G_PROTEIN_RECEP_FL_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 69 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 70 90 1 (POTENTIAL).
FT DOMAIN 91 102 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 103 123 2 (POTENTIAL).
FT DOMAIN 124 143 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 144 161 3 (POTENTIAL).
FT DOMAIN 162 182 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 183 203 4 (POTENTIAL).
FT DOMAIN 204 221 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 222 242 5 (POTENTIAL).
FT DOMAIN 243 277 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 278 298 6 (POTENTIAL).
FT DOMAIN 299 309 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 310 325 7 (POTENTIAL).
FT DOMAIN 326 415 CYTOPLASMIC (POTENTIAL).
FT DISULFID 138 210 BY SIMILARITY.
FT CARBOHYD 25 25 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 52 52 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 415 AA; 47700 MW; 238619E007152ADF CRC64;

Query Match 55.6%; Score 45; DB 1; Length 415;
Best Local Similarity 58.3%; Pred. No. 3.2;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 3 TGAWFSNATCK 14
   ||| :|||
Db 128 TGRWTLGSATCK 139

RESULT 7
OPSD_LOLFO STANDARD; PRT; 452 AA.
AC P24603;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE RHODOPSIN.
GN RHO.
OS Loligo forbesi (Northern European squid).
OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Teuthoidea;
OC Myopsida; Loliginidae; Loligo.
OX NCBI_TaxID=6618;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Retina;
RX MEDLINE=91158727; PubMed=1900420;
RA Hall M.D., Hoon M.A., Ryba N.J.P., Pottinger J.D.D., Keen J.N.,
RA Saibil H.R., Findlay J.B.C.;
RT "Molecular cloning and primary structure of squid (Loligo forbesi)
RT rhodopsin, a phospholipase C-directed G-protein-linked receptor.";
RL Biochem. J. 274:35-40(1991).
CC -!- FUNCTION: VISUAL PIGMENTS ARE THE LIGHT-ABSORBING MOLECULES THAT
CC MEDIANE VISION. THEY CONSIST OF AN APOPROTEIN, OPSIN, COVALENTLY
CC LINKED TO CIS-RETINAL. THIS RECEPTOR IS COUPLED TO THE ACTIVATION
CC OF PHOSPHOLIPASE C.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- PTM: SOME OR ALL OF THE CARBOXYL-TERMINAL SER OR THR RESIDUES MAY
CC BE PHOSPHORYLATED.
CC -!- MISCELLANEOUS: THIS RHODOPSIN HAS AN ABSORPTION MAXIMA AT 494 NM.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

OPSIN SUBFAMILY.
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EMBL; X56788; CAA40108.1;
PIR; S14332; S14332.
GCRDB; GCR_0239;
InterPro; IPR000216;
InterPro; IPR000276;
InterPro; IPR001760;
Pfam; PF00001; 7tm_1; 1.
PRINTS; PR00237; GPCRHHODOPSN.
PRINTS; PR00238; RHODOPSNTAIL.
PROSITE; PS00237; G_PROTEIN_RECEP_FL_1; 1.
PROSITE; PS0262; G_PROTEIN_RECEP_FL_2; 1.
PROSITE; PS00238; OPSIN; 1.
KW Photoreceptor; Retinal protein; Transmembrane; Glycoprotein; Vision;
KW Phosphorylation; Lipoprotein; Palmitate; G-protein coupled receptor.
FT DOMAIN 1 33 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 34 58 1 (POTENTIAL).
FT DOMAIN 59 70 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 71 97 2 (POTENTIAL).
FT DOMAIN 98 111 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 112 131 3 (POTENTIAL).
FT DOMAIN 132 151 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 152 175 4 (POTENTIAL).
FT DOMAIN 176 199 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 200 227 5 (POTENTIAL).
FT DOMAIN 228 261 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 262 285 6 (POTENTIAL).
FT DOMAIN 286 294 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 295 318 7 (POTENTIAL).
FT DOMAIN 319 452 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 8 8 N-LINKED (GLCNAC...) (PROBABLE).
FT DISULFID 108 186 BY SIMILARITY.
FT BINDING 305 305 RETINAL CHROMOPHORE (BY SIMILARITY).
FT LIPID 336 336 PALMITATE (BY SIMILARITY).
FT LIPID 337 337 PALMITATE (BY SIMILARITY).
FT DOMAIN 370 380 MET-RICH.
FT DOMAIN 381 452 GLN/PRO-RICH.
SQ SEQUENCE 452 AA; 50576 MW; 6AA9E26DE4C4DFA4 CRC64;

Query Match 55.6%; Score 45; DB 1; Length 452;
Best Local Similarity 77.8%; Pred. No. 3.4;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 WVFNSNATCK 14
   ||| |||
Db 101 WVFNGNACK 109

RESULT 8
CKR5_RAT
ID CKR5_RAT STANDARD; PRT; 354 AA.
AC O08556;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35; Last sequence update)
DT 30-MAY-2000 (Rel. 39; Last annotation update)
DE C-C CHEMOKINE RECEPTOR TYPE 5 (C-C CKR-5) (CC-CKR-5) (MIP-1
DE ALPHA RECEPTOR).
DE CCR5 OR CMKR5.
GN Rattus norvegicus (Rat).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;

```

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[1] SEQUENCE FROM N.A.
RN RP STRAIN=WISTAR; TISSUE=Brain;
RC RC MEDLINE=98334064; PubMed=9670989;
RX RX Speliss O., Gourmal N., Boddeke H.W.G.M., Sauter A., Fiebich B.L.,
RA RA Berger M., Gebicke-Haerter P.J.;
RT "Cloning of rat HIV-1-chemokine coreceptor CXR5 from microglia and
RT upregulation of its mRNA in ischemic and endotoxemic rat brain.";
RL J. Neurosci. Res. 53:16-28(1998).
RN [2]
RN RP SEQUENCE FROM N.A.
RN RP STRAIN=SPRAGUE-DAWLEY;
RC RC MEDLINE=98318173; PubMed=9655467;
RX RX Jiang Y., Calafra M.N., Adhikari S., Xia Y., Feng L., Sonntag M.K.,
RA RA Defebvre C.M., Pennell N.A., Streit W.J., Harrison J.K.;
RT "Chemokine receptor expression in cultured glia and rat experimental
RT allergic encephalomyelitis.";
RL J. Neuroimmunol. 86:1-12(1998).
RN CC -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
CC MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
CC INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.
RN CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC -----
RN CC EMBL; Y12009; CAA72737.1; -
DR DR EMBL; U77350; AAC03243.1; -
DR DR GCRDb; GCR_1470; -
DR DR InterPro; IPR000276; -
DR DR InterPro; IPR000355; -
DR DR InterPro; IPR002240; -
DR DR Pfam; PF00001; 7tm_1; 1.
DR DR PRINTS; PR00237; GPCRHHODOPSN.
DR DR PRINTS; PR00657; CCHEMOKINER.
DR DR PRINTS; PR01110; CHEMOKINERS.
DR DR PROSITE; PS00237; G-PROTEIN_RECEP_Fl_1; 1.
DR DR PROSITE; PS00262; G-PROTEIN_RECEP_Fl_2; 1.
RN KW G-protein coupled receptor; Transmembrane; Glycoprotein.
RN FT DOMAIN 1 32 EXTRACELLULAR (POTENTIAL).
FT FT TRANSMEM 33 60 1 (POTENTIAL).
FT FT DOMAIN 61 70 CYTOPLASMIC (POTENTIAL).
FT FT TRANSMEM 71 91 2 (POTENTIAL).
FT FT DOMAIN 92 104 EXTRACELLULAR (POTENTIAL).
FT FT TRANSMEM 105 126 3 (POTENTIAL).
FT FT DOMAIN 127 143 CYTOPLASMIC (POTENTIAL).
FT FT TRANSMEM 144 168 4 (POTENTIAL).
FT FT DOMAIN 169 200 EXTRACELLULAR (POTENTIAL).
FT FT TRANSMEM 201 220 5 (POTENTIAL).
FT FT DOMAIN 221 237 CYTOPLASMIC (POTENTIAL).
FT FT TRANSMEM 238 262 6 (POTENTIAL).
FT FT DOMAIN 263 279 EXTRACELLULAR (POTENTIAL).
FT FT TRANSMEM 280 303 7 (POTENTIAL).
FT FT DOMAIN 304 354 CYTOPLASMIC (POTENTIAL).
FT FT DISULFID 103 180 BY SIMILARITY.
FT FT CARBOHYD 270 270 N-LINKED (GLCNAC. . .) (POTENTIAL).
RN SQ SEQUENCE 354 AA; 41030 MW; 77EDB368AA4C868D CRC64;

```

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Query Match      54.3%; Score 44; DB 1; Length 354;
Best Local Similarity 50.0%; Pred. NO. 4;
Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY      1  HATGAWVFSNATCK 14
      :  |||  ||
Db      91  YAANWVFGNIMCK 104

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RESULT 9

CKR2_MOUSE STANDARD; PRT; 373 AA.

ID CKR2_MOUSE

AC P51683; Q61172;

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE C-C CHEMOKINE RECEPTOR TYPE 2 (C-C CKR-2) (CCR-2) (CCR2)

DE (JE/FIC RECEPTOR) (MCP-1 RECEPTOR).

DE CCR2 OR CMKBR2.

GN GN

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBI_TaxID=10090;

[1]

RN SEQUENCE FROM N.A.

RX MEDLINE=96205938; PubMed=8631787;

RA Boring L., Gosling J., Montecarlo F.S., Lusis A.J., Tsou C.-L., Charo I.F.;

RA "Molecular cloning and functional expression of murine JE (monocyte chemoattractant protein 1) and murine macrophage inflammatory protein 1alpha receptors: evidence for two closely linked C-C chemokine receptors on chromosome 9.";

RT J Biol. Chem. 271:7551-7558 (1996).

RN [2]

RN SEQUENCE FROM N.A.

RC STRAIN-BALB/C;

RX MEDLINE=96216064; PubMed=8662823;

RA Kurihara T., Bravo R.;

RT "cloning and functional expression of mCCR2, a murine receptor for the C-C chemokines JE and FIC.";

RL J. Biol. Chem. 271:11603-11606 (1996).

RN [3]

RN SEQUENCE FROM N.A.

RX MEDLINE=97026720; PubMed=8872898;

RA Heesen M., Tanabe S., Berman M.A., Yoshizawa I., Luo Y., Kim R., Post T.W., Gerard C., Dorf M.E.;

RA "Mouse astrocytes respond to the chemokines MCP-1 and KC, but reverse transcribe tyrosine kinase chain reaction does not detect mRNA for the KC or new MCP-1 receptor.";

RL J. Neurosci. Res. 45:382-391 (1996).

CC -1- FUNCTION: RECEPTOR FOR THE MCP-1 (JE), MCP-3 (FIC) AND MCP-5 CHEMOKINES. TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.

CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

CC -1- TISSUE SPECIFICITY: DETECTED IN MONOCYTE/MACROPHAGE CELL LINES, BUT NOT IN NONHEMATOPOIETIC CELL LINES.

CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

CC -----

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CC -----

CC EMBL; U47035; AAC52453.1; -

DR EMBL; U51717; AAC52557.1; -

DR EMBL; U56819; AAC52784.1; -

DR GCRDB; GCR_1649; -

DR GCRDB; GCR_1651; -

DR GCRDB; GCR_1657; -

DR MGI; 106185; Cmkbr2.

DR InterPro; IPR000276; -

DR InterPro; IPR000355; -

DR InterPro; IPR002237; -

DR Pfam; PF00001; 7tm1.1; 1.

DR PRINTS; PR00237; GPCRHHODPSN.

DR PRINTS; PR00657; GCEHEMOKINER.

DR PRINTS; PR01107; CHEMOKINER2.

DR PROSITE; PS00237; G PROTEIN RECEPTOR FAMILY 1.

RN [3]

RL J. Biol. Chem. 271:14449

RL J. Biol. Chem. 271:14445-14451(1996).

RL J. Biol. Chem. 271:14445-14451(1996).

RL J. Biol. Chem. 271:14445-14451(1996).

RP SEQUENCE FROM N.A.
 RC STRAIN=129/OLA;
 RA Kuziel W.A., Beck M.A., Dawson T.C., Maeda N.;
 RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6, AND NIH/SWISS; TISSUE=Liver, Kidney, and Spleen;
 RX MEDLINE=98001387; PubMed=9343222;
 RA Kubmann S.E., Platt E.J., Kozak S.L., Kabat D.;
 RT "Polymorphisms in the CCR5 genes of African green monkeys and mice
 RT implicate specific amino acids in infections by simian and human
 RT immunodeficiency viruses.";
 RL J. Virol. 71:8642-8656(1997).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129;
 RX MEDLINE=97404635; PubMed=9261347;
 RA Doranz B.J., Lu Z.H., Rucker J., Zhang T.Y., Sharron M., Cen Y.H.,
 RA Wang Z.X., Guo H.H., Du J.G., Accavitti M.A., Doms R.W., Peiper S.C.;
 RT "Two distinct CCR5 domains can mediate coreceptor usage by human
 RT immunodeficiency virus type 1.";
 RL J. Virol. 71:6305-6314(1997).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC Guo B., Kuno K., Harada A., Matsushima K.;
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 CC !- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
 CC MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
 CC INCREASING THE INTRACELLULAR CALCIUM ION LEVEL.
 CC !- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC !- TISSUE SPECIFICITY: DETECTED IN MONOCYTE/MACROPHAGE CELL LINES,
 CC BUT NOT IN NONHEMATOPOIETIC CELL LINES.
 CC !- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; U47036; AAC52454.1; -;
 DR EMBL; X94151; CAA63867.1; -;
 DR EMBL; U68565; AAB37273.1; -;
 DR EMBL; U83327; AAC53386.1; -;
 DR EMBL; AF022990; AAC53389.1; -;
 DR EMBL; AF019772; AAB71183.1; -;
 DR EMBL; D83648; BAAL2024.1; -;
 DR GCRDb; GCR_1150; -;
 DR GCRDb; GCR_1645; -;
 DR GCRDb; GCR_1656; -;
 DR GCRDb; GCR_1729; -;
 DR GCRDb; GCR_2449; -;
 DR GCRDb; GCR_2540; -;
 DR GCRDb; GCR_2554; -;
 DR MGD; MGI:107182; Cmkbr5.
 DR InterPro; IPR000276; -;
 DR InterPro; IPR000355; -;
 DR InterPro; IPR002240; -;
 DR Pfam; PF00001; 7tm.1; 1.
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PRINTS; PR00657; CCEMOKINER.
 DR PRINTS; PR01110; CCEMOKINER.
 DR PROSITE; PS00237; G_PROTEIN_RECP_FL_1; 1.
 DR PROSITE; PS0262; G_PROTEIN_RECP_FL_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Polymorphism.
 FT DOMAIN 1 32 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 33 60 1 (POTENTIAL).
 FT DOMAIN 61 70 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 71 91 2 (POTENTIAL).
 FT DOMAIN 92 104 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 105 126 3 (POTENTIAL).

FT DOMAIN 127 143 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 144 168 4 (POTENTIAL).
 FT DOMAIN 169 200 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 201 220 5 (POTENTIAL).
 FT DOMAIN 221 237 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 238 262 6 (POTENTIAL).
 FT DOMAIN 263 279 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 280 303 7 (POTENTIAL).
 FT DOMAIN 304 354 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 103 180 BY SIMILARITY.
 FT CARBOHYD 270 270 N-LINKED (GLUCNAC. . .) (POTENTIAL).
 FT VARIANT 11 11 I -> S.
 FT VARIANT 62 62 K -> R.
 FT VARIANT 66 66 V -> M.
 FT VARIANT 97 97 I -> V.
 FT VARIANT 109 109 V -> L.
 FT VARIANT 156 156 V -> A.
 FT VARIANT 160 160 F -> S.
 FT VARIANT 185 185 P -> L.
 FT VARIANT 213 213 I -> V.
 FT VARIANT 318 318 I -> M.
 FT VARIANT 337 337 V -> A.
 FT CONFLICT 3 3 F -> L (IN REF. 2).
 FT CONFLICT 80 80 L -> F (IN REF. 2).
 FT CONFLICT 190 190 H -> Y (IN REF. 3).
 FT CONFLICT 208 208 P -> S (IN REF. 1).
 FT CONFLICT 145 145 N -> I (IN REF. 5).
 SQ SEQUENCE 354 AA; 40863 MW; B4A6B942E88F9CF0 CRC64;
 Query Match 53.1%; Score 43; DB 1; Length 354;
 Best Local Similarity 42.9%; Pred No. 5.8;
 Matches 6; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
 Qy 1 HATGAWFSNATCK 14
 Db 91 YAANEWIFGNMCK 104
 RESULT 12
 OPRX_MOUSE
 ID OPRX_MOUSE STANDARD; PRT; 367 AA.
 AC P35377; Q60645;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE NOCICEPTIN RECEPTOR (ORPHANIN FQ RECEPTOR) (KAPPA-TYPE 3 OPIOID
 DE RECEPTOR) (KOR-3) (ORGC) (K3 OPIATE RECEPTOR).
 GN OPR11 OR OPR1 OR OOR.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6N; TISSUE=Brain;
 RA Yasuda K., Jones E., Reisine T., Bell G.I.;
 RL Submitted (JAN-1994) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95100967; PubMed=7802669;
 RA Nishi M., Takeshima H., Mori M., Nakagawara K.I., Takeuchi T.;
 RT "Structure and chromosomal mapping of genes for the mouse
 RT kappa-opioid receptor and an opioid receptor homologue (MOR-C).";
 RL Biochem. Biophys. Res. Commun. 205:1353-1357(1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=96387345; PubMed=8794880;
 RA Matthes H.W.D., Seward E.P., Kieffer B., North R.A.;
 RT "Functional selectivity of orphanin FQ for its receptor coexpressed
 RT with potassium channel subunits in Xenopus laevis oocytes.";
 RL Mol. Pharmacol. 50:447-450(1996).

[4] SEQUENCE FROM N.A.
 RA Pan Y.-X., Xu J., Pasternak G.W.;
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 [5]
 RN SEQUENCE FROM N.A.
 RA MEDLINE=95327076; PubMed=7603458;
 RX Pan Y.-X., Cheng J., Xu J., Rossi G., Jacobson E., Ryan-Moro J.,
 RA Brooks A.I., Dean G.E., Standiford K.M., Pasternak G.W.;
 RT "Cloning and functional characterization through antisense mapping of
 RT a kappa 3-related opioid receptor";
 RL Mol. Pharmacol. 47:1180-1188(1995).
 [6]
 RN SEQUENCE OF 1-357 FROM N.A.
 RP STRAIN=BALB/C; TISSUE=Spleen;
 RX MEDLINE=95318231; PubMed=7797625;
 RA Halford W.P., Gebhardt B.M., Carr D.J.J.;
 RT "Functional role and sequence analysis of a lymphocyte orphan opioid
 RT receptor";
 RL J. Neuroimmunol. 59:91-101(1995).
 CC -1- FUNCTION: RECEPTOR FOR THE NEUROPEPTIDE NOCICEPTIN/ORPHANIN FQ.
 CC HAS A POTENTIAL ROLE IN MODULATING A NUMBER OF BRAIN FUNCTIONS,
 CC INCLUDING INSTINCTIVE BEHAVIORS AND EMOTIONS. THE ACTIVITY OF
 CC THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH INHIBITS ADENYLATE
 CC CYCLASE.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC
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 CC
 DR EMBL; U04952; AAA03730.1; -
 DR EMBL; D31667; BAA06509.1; -
 DR EMBL; D31666; BAA06509.1; JOINED.
 DR EMBL; X91813; CA862922.1; -
 DR EMBL; U32932; AAC52669.1; -
 DR EMBL; U32928; AAC52669.1; JOINED.
 DR EMBL; U32930; AAC52669.1; JOINED.
 DR EMBL; U09421; AAA81333.1; -
 DR EMBL; U14165; AAA87899.1; -
 DR HSP; P34996; IDDD.
 DR GCRDb; GCR_0891; -
 DR GCRDb; GCR_1715; -
 DR GCRDb; GCR_1716; -
 DR GCRDb; GCR_1728; -
 DR GCRDb; GCR_1731; -
 DR MGD; MGI:97440; Oprl.
 DR InterPro; IPR000276; -
 DR InterPro; IPR001418; -
 DR InterPro; IPR001420; -
 DR Pfam; PF00001; 7tm1.1; 1.
 DR PRINTS; PR00237; GPCRHOPOSPN.
 DR PRINTS; PR00384; OPIOIDR.
 DR PRINTS; PR00547; OPIOIDR.
 DR PROSITE; PS00237; G_PROTEIN_RECP_F1.1; 1.
 DR PROSITE; PS00262; G_PROTEIN_RECP_F1.2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW phosphorylation; Lipoprotein; Palmitate.
 FT DOMAIN 1 47
 FT TRANSMEM 48 74
 FT DOMAIN 75 84
 FT CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 85 106
 FT DOMAIN 107 121
 FT EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 122 143
 FT DOMAIN 144 162
 FT CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 163 185
 FT DOMAIN 186 208
 FT EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 209 233

FT DOMAIN 234 261
 FT TRANSMEM 262 285
 FT DOMAIN 286 297
 FT TRANSMEM 298 319
 FT DOMAIN 320 367
 FT DISULFID 120 137
 FT LIPID 331 331
 FT CARBOHYD 21 21
 FT CARBOHYD 26 26
 FT CARBOHYD 36 36
 FT CONFLICT 348 349
 SQ SEQUENCE 367 AA; 40491 MW; E498CA9FE5276026 CRC64;
 Query Match 51.9%; Score 42; DB 1; Length 367;
 Best Local Similarity 63.6%; Pred. No. 8.7;
 Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 4 GAWVFSNATCK 14
 DB 111 GFWPFGNALCK 121
 RESULT 13
 OPRX_RAT
 ID OPRX_RAT STANDARD; PRT; 367 AA.
 AC P35370;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE NOCICEPTIN RECEPTOR (ORPHANIN FQ RECEPTOR) (KAPPA-TYPE 3 OPIOID
 DE RECEPTOR) (KOR-3) (ROR-C) (XOR1).
 GN OPR1 OR OOR.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=WISTAR; TISSUE=Brain;
 RX MEDLINE=94215703; PubMed=8163014;
 RA Fukuda K., Kato S., Mori K., Nishi M., Takeshima H., Iwabe N.,
 RA Miyata T., Houtani T., Sugimoto T.;
 RT "cDNA cloning and regional distribution of a novel member of the
 RT opioid receptor family";
 RL FEBS Lett. 343:42-46(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Hippocampus;
 RA Meng F., Xie G., Alfred M., Thompson R., Hoversten M., Watson S.,
 RA Akil H.;
 RL Submitted (JAN-1994) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Brain;
 RX MEDLINE=94307401; PubMed=8034019;
 RA Bunzow J.R., Saez C., Mortrud M., Bouvier C., Williams J.T., Low M.,
 RA Grandy D.K.;
 RT "Molecular cloning and tissue distribution of a putative member of
 RT the rat opioid receptor gene family that is not a mu, delta or kappa
 RT opioid receptor type";
 RL FEBS Lett. 347:284-288(1994).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94307400; PubMed=8034018;
 RA Chen Y., Fan Y., Liu J., Mestek A., Tian M., Kozak C.A., Yu L.;
 RT "Molecular cloning, tissue distribution and chromosomal localization
 RT of a novel member of the opioid receptor gene family";
 RL FEBS Lett. 347:279-283(1994).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=95096849; PubMed=7798930;

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EMBL: X77130; CAA54386.1; -
DR EMBL: U30185; AA84913.1; -
DR EMBL: L40949; AA96251.1; -
DR PIR: S43087; S43087.
DR HSSP: P34996; 1DDD.
DR GCRDB: GCR_0987; -
DR GCRDB: GCR_1988; -
DR MIM: 602548; -
DR InterPro: IPR000276; -
DR InterPro: IPR001418; -
DR InterPro: IPR001420; -
DR Pfam: PF00001; 7tm.1; 1.
DR PRINTS: PR00237; GPCRHHODPSN.
DR PRINTS: PR00384; OPIOIDR.
DR PRINTS: PR00547; XOPIDR.
DR PROSITE: PS00237; G_PROTEIN_RECF_F1_1; 1.
DR PROSITE: PS0262; G_PROTEIN_RECF_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Phosphorylation; Lipoprotein; Palmitate.
FT DOMAIN 1 50 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 51 77 1 (POTENTIAL).
FT DOMAIN 78 87 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 88 109 2 (POTENTIAL).
FT DOMAIN 110 124 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 125 146 3 (POTENTIAL).
FT DOMAIN 147 165 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 166 188 4 (POTENTIAL).
FT DOMAIN 189 211 5 (POTENTIAL).
FT TRANSMEM 212 236 6 (POTENTIAL).
FT DOMAIN 237 264 7 (POTENTIAL).
FT TRANSMEM 265 288 8 (POTENTIAL).
FT DOMAIN 289 300 9 (POTENTIAL).
FT TRANSMEM 301 322 10 (POTENTIAL).
FT DOMAIN 323 370 11 (POTENTIAL).
FT LIPID 334 334 PALMITATE (POTENTIAL).
FT CARBOHYD 21 21 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 28 28 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 39 39 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 370 AA; 40693 MW; 613700C0B4D093BA CRC64;

Query Match 51.9%; Score 42; DB 1; Length 370;
Best Local Similarity 63.6%; Pred. No. 8.8;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 GAWFVSNTACK 14
| | | | |
Db 114 GFWPFGNALCK 124

RESULT 15
OPRX_PIG STANDARD; PRT; 370 AA.
AC P79292;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE NOCICEPTIN RECEPTOR (ORPHANIN FQ RECEPTOR) (KAPPA-TYPE 3 OPIOID
DE RECEPTOR) (KOR-3) (ORGC) (K3 OPIATE RECEPTOR).
GN OPR1.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.

NCBI_TaxID=9823;
[1]
RN SEQUENCE FROM N.A.
RP TISSUP-Brain cortex;
RC Osinski M.A., Pampusch M.S., Brown D.R., Murtaugh M.P.;
RA Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RL FUNCTION: RECEPTOR FOR THE NEUROPEPTIDE NOCICEPTIN/ORPHANIN FQ.
CC HAS A POTENTIAL ROLE IN MODULATING A NUMBER OF BRAIN FUNCTIONS,
CC INCLUDING INSTINCTIVE BEHAVIORS AND EMOTIONS. THE ACTIVITY OF
CC THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH INHIBITS ADENYLYL
CC CYCLASE (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

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EMBL: U72758; AAB39702.1; -
DR HSSP: P34996; 1DDD.
DR GCRDB: GCR_1519; -
DR InterPro: IPR000276; -
DR InterPro: IPR001418; -
DR InterPro: IPR001420; -
DR Pfam: PF00001; 7tm.1; 1.
DR PRINTS: PR00237; GPCRHHODPSN.
DR PRINTS: PR00384; OPIOIDR.
DR PRINTS: PR00547; XOPIDR.
DR PROSITE: PS00237; G_PROTEIN_RECF_F1_1; 1.
DR PROSITE: PS0262; G_PROTEIN_RECF_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Phosphorylation; Lipoprotein; Palmitate.
FT DOMAIN 1 50 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 51 77 1 (POTENTIAL).
FT DOMAIN 78 87 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 88 109 2 (POTENTIAL).
FT DOMAIN 110 124 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 125 146 3 (POTENTIAL).
FT DOMAIN 147 165 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 166 188 4 (POTENTIAL).
FT DOMAIN 189 211 5 (POTENTIAL).
FT TRANSMEM 212 236 6 (POTENTIAL).
FT DOMAIN 237 264 7 (POTENTIAL).
FT TRANSMEM 265 288 8 (POTENTIAL).
FT DOMAIN 289 300 9 (POTENTIAL).
FT TRANSMEM 301 322 10 (POTENTIAL).
FT DOMAIN 323 370 11 (POTENTIAL).
FT LIPID 334 334 PALMITATE (POTENTIAL).
FT CARBOHYD 21 21 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 28 28 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 39 39 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 370 AA; 40610 MW; 48E4F3E6DA223BCD CRC64;

Query Match 51.9%; Score 42; DB 1; Length 370;
Best Local Similarity 63.6%; Pred. No. 8.8;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 GAWFVSNTACK 14
| | | | |
Db 114 GFWPFGNALCK 124

Search completed: May 23, 2001, 15:36:18
Job time: 649 sec

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OM protein - protein search, using sw model

Run on: May 23, 2001, 15:35:12 ; Search time 189.03 Seconds
(without alignments)
8.681 Million cell updates/sec

Title: US-08-887-977-10_COPY_97_110

Perfect score: 81
Sequence: 1 HATGAWVFSNATCK 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_unclassified:*
- 13: sp_vertebrate:*
- 14: sp_virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	60	74.1	367	11	Q9R1V0	Q9R1V0 mus musculus
2	49	60.5	236	4	Q9UEA5	Q9UEA5 homo sapien
3	49	60.5	1455	4	O15360	O15360 homo sapien
4	47	58.0	360	6	O18793	O18793 macaca mula
5	44	54.3	319	1	Q07069	Q07069 halobacteri
6	44	54.3	334	10	Q9M7R3	Q9M7R3 phaeodactyl
7	44	54.3	355	6	Q9MYJ8	Q9MYJ8 callithrix
8	44	54.3	373	11	O55193	O55193 rattus norv
9	44	54.3	526	5	O77438	O77438 drosophila
10	44	54.3	581	5	Q9W5D5	Q9W5D5 drosophila
11	44	54.3	581	5	Q9U902	Q9U902 drosophila
12	44	54.3	581	5	Q9NIU0	Q9NIU0 drosophila
13	44	54.3	1009	1	Q07971	Q07971 halobacteri
14	44	54.3	1073	1	O51965	O51965 halobacteri
15	43	53.1	349	10	Q9SU66	Q9SU66 arabidopsis
16	42	51.9	112	4	O95569	O95569 homo sapien
17	42	51.9	213	11	Q9QUT5	Q9QUT5 mus musculu
18	42	51.9	362	11	Q9JIN4	Q9JIN4 rattus norv
19	41	50.6	103	3	Q04069	Q04069 saccharomyc

20	41	50.6	126	2	Q9KM54	Q9KM54 vibrio chol
21	41	50.6	334	6	O97724	O97724 felis silve
22	41	50.6	351	6	O97774	O97774 felis silve
23	41	50.6	408	10	Q9SF00	Q9SF00 arabidopsis
24	41	50.6	487	10	Q9LY46	Q9LY46 arabidopsis
25	41	50.6	501	10	Q9XEE7	Q9XEE7 arabidopsis
26	41	50.6	646	2	Q9KQK8	Q9KQK8 vibrio chol
27	41	50.6	1998	5	Q9V7A5	Q9V7A5 drosophila
28	41	50.6	2165	5	O19791	O19791 caenorhabdi
29	40	49.4	85	8	O35796	O35796 spharagemon
30	40	49.4	297	14	Q9YW65	Q9YW65 melanoplus
31	40	49.4	316	6	Q9TUV7	Q9TUV7 saguinus sp
32	40	49.4	339	6	Q9TUV2	Q9TUV2 saguinus sp
33	40	49.4	339	6	Q9TUV1	Q9TUV1 saguinus sp
34	40	49.4	339	6	Q9TUV0	Q9TUV0 saguinus sp
35	40	49.4	339	6	Q9TUV9	Q9TUV9 saguinus sp
36	40	49.4	339	6	Q9TUV8	Q9TUV8 saguinus sp
37	40	49.4	339	6	Q9TUV6	Q9TUV6 saguinus sp
38	40	49.4	339	6	Q9TUV5	Q9TUV5 saguinus sp
39	40	49.4	339	6	Q9TUV4	Q9TUV4 callithrix
40	40	49.4	339	6	Q9TUV3	Q9TUV3 callithrix
41	40	49.4	339	6	Q9TUV2	Q9TUV2 alouatta ca
42	40	49.4	339	6	Q9TUV1	Q9TUV1 aotus trivi
43	40	49.4	339	6	Q9TUV0	Q9TUV0 aotus trivi
44	40	49.4	339	6	Q9TUV5	Q9TUV5 alouatta ca
45	40	49.4	339	6	Q9TQV5	Q9TQV5 saguinus sp

ALIGNMENTS

RESULT 1
Q9R1V0
ID Q9R1V0 PRELIMINARY: PRT: 367 AA.
AC Q9R1V0;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE CC CHEMOKINE LARC SPECIFIC RECEPTOR.
GN MCCR6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Tanaka Y.;
RT "Molecular Cloning of Murine Homologue of CCR6, the Specific Receptor for CC Chemokine LARC";
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB016031; BAA02443.1;
DR INTERPRO; IPR000190;
DR INTERPRO; IPR000355;
DR PRAM; PF00001; 7tm.1.1;
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PRINTS; PR00635; ANGIOTENSINR.
DR PRINTS; PR00657; CCEMOKINER.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
KW Receptor.
SQ SEQUENCE 367 AA; 42082 MW; 207FD98B2F7A6DD3 CRC64;

Query Match 74.1%; Score 60; DB 11; Length 367;
Best Local Similarity 71.4%; Pred. No. 0.016;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 HATGAWVFSNATCK 14
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Db 98 HATNTWVFSALCK 111

RESULT 2


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DR EMBL; Z83076; CAB05445.1; JOINED.
DR EMBL; Z83077; CAB05445.1; JOINED.
DR EMBL; Z83078; CAB05445.1; JOINED.
DR EMBL; Z83079; CAB05445.1; JOINED.
DR EMBL; Z83080; CAB05445.1; JOINED.
DR EMBL; Z83081; CAB05445.1; JOINED.
DR EMBL; Z83082; CAB05445.1; JOINED.
DR EMBL; Z83083; CAB05445.1; JOINED.
DR EMBL; Z83084; CAB05445.1; JOINED.
DR EMBL; Z83085; CAB05445.1; JOINED.
DR EMBL; Z83086; CAB05445.1; JOINED.
DR EMBL; Z83087; CAB05445.1; JOINED.
DR EMBL; Z83088; CAB05445.1; JOINED.
DR EMBL; Z83089; CAB05445.1; JOINED.
DR EMBL; Z83090; CAB05445.1; JOINED.
DR EMBL; Z83091; CAB05445.1; JOINED.
DR EMBL; Z83092; CAB05445.1; JOINED.
DR EMBL; Z83093; CAB05445.1; JOINED.
DR EMBL; Z83094; CAB05445.1; JOINED.
DR EMBL; Z83095; CAB05445.1; JOINED.
DR EMBL; Z83151; CAB05445.1; JOINED.
DR EMBL; X99226; CRA67610.1; -.
DR EMBL; AC005567; AAC33401.1; -.
DR EMBL; AF054569; AAC28331.1; -.
DR MIN; Z27650; -.
KW DNA repair; Nuclear protein; Coiled coil; Phosphorylation;
KW Disease mutation; Polymorphism.
FT DOMAIN 18 34 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT DOMAIN 38 65 COILED COIL (POTENTIAL).
FT DOMAIN 1069 1090 LEUCINE-ZIPPER (POTENTIAL).
FT DOMAIN 1235 1258 COILED COIL (POTENTIAL).
FT VARIANT 6 6 V -> D.
FT VARIANT 8 8 N -> K.
FT VARIANT 435 435 R -> C.
FT VARIANT 492 492 H -> R.
FT VARIANT 817 817 L -> P.
FT VARIANT 845 845 L -> P.
FT VARIANT 1055 1055 R -> L.
FT VARIANT 1128 1128 Q -> E.
FT VARIANT 1131 1131 T -> A.
FT VARIANT 1302 1302 W -> D.
FT VARIANT 1417 1417 H -> R.
FT VARIANT 181 181 A -> V.
FT VARIANT 244 244 L -> F.
FT VARIANT 252 252 D -> G.
FT VARIANT 1110 1110 H -> P (IN FA; LOSS OF FUNCTION).
FT VARIANT 1117 1117 R -> G (IN FA; LOSS OF FUNCTION).
FT CONFLICT 717 717 M -> I (IN REF. 2).
FT CONFLICT 501 501 S -> G (IN REF. 3 AND 4).
SQ SEQUENCE 1455 AA; 162803 MW; DB43EEDB29DF5C0E CRC64;

Query Match 60.5%; Score 49; DB 4; Length 1455;
Best Local Similarity 53.8%; Pred. No. 4.7;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 HATGAWVFSNATC 13
||:|:|:|:|
DB 204 HAVGSLFRNLCC 216

RESULT 4
OL18793 PRELIMINARY; PRT; 360 AA.
AC OL18793;
DT 01-JAN-1998 (TRENBLrel. 05, Created)
DT 01-MAY-1999 (TRENBLrel. 10, Last sequence update)
DT 01-JUN-2000 (TRENBLrel. 14, Last annotation update)
DE CHEMOKINE RECEPTOR.
GN CCR2B.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;

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OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RA Hauer D.A., Margulies B.J., Clements J.E.;
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF013958; AAD11572.1; -.
DR INTERPRO; IPR000248; -.
DR INTERPRO; IPR000276; -.
DR INTERPRO; IPR000355; -.
DR INTERPRO; IPR001277; -.
DR INTERPRO; IPR002236; -.
DR INTERPRO; IPR002237; -.
DR INTERPRO; IPR002240; -.
DR PFAM; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PRINTS; PR00241; ANGIOTENSINR.
DR PRINTS; PR00645; LCR1ORPHANR.
DR PRINTS; PR00657; CCHEMOKINER.
DR PRINTS; PR01106; CHEMOKINER1.
DR PRINTS; PR01107; CHEMOKINER2.
DR PRINTS; PR01110; CHEMOKINER5.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
SQ SEQUENCE 360 AA; 41139 MW; 4B2552BCE913FE9F CRC64;

Query Match 58.0%; Score 47; DB 6; Length 360;
Best Local Similarity 61.5%; Pred. No. 2.6;
Matches 8; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 ATGAWVFSNATCK 14
| | | | | | |
DB 102 AANEWVFGNAMCK 114

RESULT 5
QO7069 PRELIMINARY; PRT; 319 AA.
AC QO7069;
ID QO7069;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-MAY-2000 (TRENBLrel. 13, Last annotation update)
DE HYPOTHETICAL 36.7 KDA PROTEIN.
OS Halobacterium salinarum.
OG Plasmid PHH1.
OC Archaea; Euryarchaeota; Halobacteriales; Halobacteriaceae;
OC Halobacterium.
OX NCBI_TaxID=2242;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93241154; PubMed=8386798;
RA Pfeiffer F., Ghahraman P.;
RT "Plasmid pHH1 of Halobacterium salinarum: characterization of the
RT replicon region, the gas vesicle gene cluster and insertion
RT elements.";
RL Mol. Gen. Genet. 238:193-200(1993).
DR EMBL; X67101; CAA47475.1; -.
DR Hypothetical protein; Plasmid.
SQ SEQUENCE 319 AA; 36662 MW; 430F749412F5B082 CRC64;

Query Match 54.3%; Score 44; DB 1; Length 319;
Best Local Similarity 58.3%; Pred. No. 7.4;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 HATGAWVFSNAT 12
| | | | | | |
DB 59 HLTASWVFGSGT 70

RESULT 6
QO9W7R3 PRELIMINARY; PRT; 334 AA.
ID QO9W7R3

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AC Q9M7R3;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
 DE CYTOSOLIC GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE.
 GN GAPC2
 OS Phaeodactylum tricornutum.
 OC Eukaryota; stramenopiles; Bacillariophyta; Bacillariophyceae;
 OC Bacillariophycidae; Naviculales; Phaeodactylaceae; Phaeodactylum.
 OX NCBI_TaxID=2850;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Liand M.-F., Lichtle C., Apt K., Martin W., Cerff R.;
 RT "Compartment-Specific Isoforms of TPI and GAPDH are Imported into
 RT Mitochondria as a Fusion Protein: Evidence in Favor of a
 RT Mitochondrial Origin of the Eukaryotic Glycolytic Pathway.";
 RL Mol. Biol. Evol. 17:213-223(2000).
 DR EMBL; AF063805; AAF34325.1; -.
 SQ SEQUENCE 334 AA; 35533 MW; 66E1E6821B75F30A CRC64;

Query Match 54.3%; Score 44; DB 10; Length 334;
 Best Local Similarity 66.7%; Pred. No. 7.7;
 Matches 10; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

Qy 1 HAT--GAWFSNATC 13
 I I I I I I I I I
 Db 136 HTTSGATVFSNASC 150

RESULT 7
 Q9MYJ8 PRELIMINARY; PRT; 355 AA.
 AC Q9MYJ8;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
 DE CHEMOKINE RECEPTOR.
 GN CCRI
 OS Callitrix jacchus (Common marmoset).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Callitrix.
 OX NCBI_TaxID=9483;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20153429; PubMed=10686294;
 RA Liang M., Rosser M.P., Ng H.P., May K., Bauman J.G., Islam I.,
 RA Ghanam A., Kretscher P.J., Pu H., Dunning L., Snider R.M.,
 RA Morrissey M.M., Hesselgesser J., Perez H.D., Horuk R.;
 RT "Species selectivity of a small molecule antagonist for the CCR1
 RT chemokine receptor.";
 RL Eur. J. Pharmacol. 389:41-49(2000).
 DR EMBL; AF127528; AAF36453.1; -.
 KW Receptor.
 SQ SEQUENCE 355 AA; 40928 MW; 2B01C47E9874A2C1 CRC64;

Query Match 54.3%; Score 44; DB 6; Length 355;
 Best Local Similarity 77.8%; Pred. No. 8.2;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 WVFNSNATCK 14
 I I I I I I I I
 Db 99 WVFNGAMCK 107

RESULT 8
 O55193 PRELIMINARY; PRT; 373 AA.
 ID O55193;
 AC O55193;
 DT 01-JUN-1998 (TrEMBLrel. 06, Created)
 DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)

DE Q9M7R3;
 GN CMKBR2.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=SPRAGUE DAWLEY;
 RX MEDLINE=98318173; PubMed=9655467;
 RA Jiang Y., Salafranca M.N., Adhikari S., Xia Y., Feng L., Sonntag M.K.,
 RA deGebre C.M., Pennell N.A., Streit W.J., Harrison J.K.;
 RT "Chemokine receptor expression in cultured glia and rat experimental
 RT allergic encephalomyelitis.";
 RL J. Neuroimmunol. 86:1-12(1998).
 CC -1- FUNCTION: RECEPTOR FOR THE MCP-1 (JE), MCP-3 (FIC) AND MCP-5
 CC CHEMOKINES. TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR
 CC CALCIUM IONS LEVEL (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN LUNG, SPLEEN, KIDNEY, THYMUS AND
 CC MACROPHAGES.
 CC -1- INDUCTION: IN ANIMALS IN WHICH EXPERIMENTAL ALLERGIC
 CC ENCEPHALOMYELITIS (EAE) HAS BEEN INDUCED.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 DR EMBL; U77349; AAC03242.1; -.
 DR INTERPRO; IPR000276; -.
 DR INTERPRO; IPR000355; -.
 DR INTERPRO; IPR002237; -.
 DR PFAM; PF00001; 7tm1.1; 1.
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PRINTS; PR00657; CCHEMOKINER.
 DR PRINTS; PR01107; CHEMOKINER2.
 DR PROSITE; PS00237; G-PROTEIN RECEPTOR; UNKNOWN_1.
 KW G-protein coupled receptor; Transmembrane.
 FT DOMAIN 1 60 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 61 81 POTENTIAL.
 FT DOMAIN 82 91 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 92 112 POTENTIAL.
 FT DOMAIN 113 128 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 129 149 POTENTIAL.
 FT DOMAIN 150 170 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 171 191 POTENTIAL.
 FT DOMAIN 192 220 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 221 241 POTENTIAL.
 FT DOMAIN 242 256 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 257 277 POTENTIAL.
 FT DOMAIN 278 301 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 302 322 POTENTIAL.
 FT DOMAIN 323 373 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 126 203 BY SIMILARITY.
 SQ SEQUENCE 373 AA; 42763 MW; 2E7BB012F5D6FD09 CRC64;

Query Match 54.3%; Score 44; DB 11; Length 373;
 Best Local Similarity 50.0%; Pred. No. 8.6;
 Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 1 HATGAWFSNATCK 14
 I I I I I I I I
 Db 114 YAANEWFGNIMCK 127

RESULT 9
 O77438 PRELIMINARY; PRT; 526 AA.
 ID O77438;
 AC O77438;
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
 DE EG:34F3.6 PROTEIN.
 GN EG:34F3.6.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 RN NCBI_TaxID=7227;
 RP SEQUENCE FROM N.A.
 RA Salles C., Valenti P., Darlamitsou A., Henderson N., Campbell L.,
 RA Glover D.;
 RT "Sequencing the distal x chromosome of Drosophila melanogaster."
 RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
 RN (2)
 RP SEQUENCE FROM N.A.
 RA Benos P.;
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL031583; CAA20896.1; -
 DR INTERPRO; IPR000024; -
 DR INTERPRO; IPR000539; -
 DR INTERPRO; IPR000832; -
 DR PFAM; PF01392; Fz; 1.
 DR PFAM; PF01534; Frizzled; 2.
 SQ SEQUENCE 526 AA; 58064 MW; 02C225F7740E6152 CRC64;

Query Match 54.3%; Score 44; DB 5; Length 526;
 Best Local Similarity 58.3%; Pred. No. 12;
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 TGAWFSNATCK 14
 |||||
 Db 449 TGLWWSRKTC 460

RESULT 10
 Q9W5D5
 ID Q9W5D5 PRELIMINARY; PRT; 581 AA.
 AC Q9W5D5;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DE 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
 GN F23 PROTEIN.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 RN NCBI_TaxID=7227;
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Randell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers J.H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster."
 RL Science 287:2185-2195(2000).
 DR EMBL; AE003418; AAF45547.1; -
 DR FLYBASE; FBgn0027343; Fz3.
 DR INTERPRO; IPR000024; -
 DR INTERPRO; IPR000539; -
 DR INTERPRO; IPR000832; -
 DR PFAM; PF01392; Fz; 1.
 DR PFAM; PF01534; Frizzled; 2.
 DR PRINTS; PR00489; FRIZZLED.
 SQ SEQUENCE 581 AA; 63380 MW; 07A30B442A993938 CRC64;

Query Match 54.3%; Score 44; DB 5; Length 581;
 Best Local Similarity 58.3%; Pred. No. 13;
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 TGAWFSNATCK 14
 |||||
 Db 504 TGLWWSRKTC 515

RESULT 11
 Q9U902
 ID Q9U902 PRELIMINARY; PRT; 581 AA.
 AC Q9U902;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DE 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
 GN DFRIZZLED-3 PROTEIN.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 RN NCBI_TaxID=7227;
 RP SEQUENCE FROM N.A.
 RA Sato A., Kojima T., Ui-Tei K., Miyata Y., Saigo K.;
 RT "Dfrizzled-3, a new Drosophila Wnt receptor, acting as an attenuator
 of Wingless signaling in wingless hypomorphic mutants.";
 RL Development 126:4421-4430(1999).
 DR EMBL; AB018565; BAA84677.1; -
 DR INTERPRO; IPR000024; -
 DR INTERPRO; IPR000539; -
 DR INTERPRO; IPR000832; -
 DR PFAM; PF01392; Fz; 1.
 DR PFAM; PF01534; Frizzled; 2.
 DR PRINTS; PR00489; FRIZZLED.
 SQ SEQUENCE 581 AA; 63303 MW; 97CDA856A10A976E CRC64;

Query Match 54.3%; Score 44; DB 5; Length 581;
 Best Local Similarity 58.3%; Pred. No. 13;
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 TGAWFSNATCK 14
 |||||
 Db 504 TGLWWSRKTC 515

```

RESULT 12
Q9NIU0 ID Q9NIU0 PRELIMINARY; PRT; 581 AA.
AC Q9NIU0;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE FRIZZLED 3.
GN FZ3.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RA Sivasankaran R., Calleja M., Morata G., Basler K.;
RT "The Wingless target gene Dfz3 encodes a new member of the Drosophila
RT Frizzled family.";
RL Mech. Dev. 91:427-431(2000).
DR EMBL: AF195242; AAF63250.1; -.
SQ SEQUENCE 581 AA; 63251 MW; 07A8BBFF2A9E3F93 CRC64;

Query Match 54.3%; Score 44; DB 5; Length 581;
Best Local Similarity 58.3%; Pred. No. 13;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 TCAGWFSNATCK 14
DB 504 TGLWVMSRKTCE 515

RESULT 13
Q07971 ID Q07971 PRELIMINARY; PRT; 1009 AA.
AC Q07971;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE REPH PROTEIN.
GN REPH.
OS Halobacterium halobium.
OG Plasmid pNRC100.
OC Archaea; Euryarchaeota; Halobacteriales; Halobacteriaceae;
OC Halobacterium
OX NCBI_TaxID=2241;
RN [1]
RP SEQUENCE FROM N.A.
RA Ng W.L., Dassarma S.;
RX STRAIN=NRC-1;
RX MEDLINE=93328662; PubMed=8335618;
RT "Minimal replication origin of the 200-kilobase Halobacterium plasmid
RT pNRC100.";
RL J. Bacteriol. 175:4584-4596(1993).
DR EMBL: L19296; AAA72017.1; -.
KW Plasmid.
SQ SEQUENCE 1009 AA; 113442 MW; A723BDE83FAF7EE1 CRC64;

Query Match 54.3%; Score 44; DB 1; Length 1009;
Best Local Similarity 58.3%; Pred. No. 23;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 HATGAWFSNAT 12
DB 658 HLTASWVFGST 669

RESULT 14
O51965 ID O51965 PRELIMINARY; PRT; 1073 AA.
AC O51965;

```

```

DT 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DT 01-JUN-1998 (TREMBlrel. 06, Last annotation update)
DE SIMILARITY 100.0.
OS Halobacterium sp.
OG Plasmid pNRC100.
OC Archaea; Euryarchaeota; Halobacteriales; Halobacteriaceae;
OC Halobacterium.
OX NCBI_TaxID=2243;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NRC-1;
RX MEDLINE=88201675; PubMed=3448465;
RA Dassarma S., Damerval T., Jones J.G., Tandeau de Marsac N.;
RT "A plasmid-encoded gas vesicle protein gene in a halophilic
RT archaeobacterium.";
RL Mol. Microbiol. 1:365-370(1987).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=NRC-1;
RX MEDLINE=90016863; PubMed=2552415;
RA Jones J.G., Hackett N.R., Halladay J.T., Scothorn D.J., Yang C.F.,
RA Ng W.L., Dassarma S.;
RT "Analysis of insertion mutants reveals two new genes in the pNRC100
RT gas vesicle gene cluster of Halobacterium halobium.";
RL Nucleic Acids Res. 17:7785-7793(1989).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=NRC-1;
RX MEDLINE=91267967; PubMed=2050644;
RA Ng W.L., Kothakota S., Dassarma S.;
RT "Structure of the gas vesicle plasmid in Halobacterium halobium
RT inversion isomers, inverted repeats, and insertion sequences.";
RL J. Bacteriol. 173:3933-3933(1991).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=NRC-1;
RX MEDLINE=91323716; PubMed=1864501;
RA Jones J.G., Young D.C., Dassarma S.;
RT "Structure and organization of the gas vesicle gene cluster on the
RT Halobacterium halobium plasmid pNRC100.";
RL Gene 102:117-122(1991).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=NRC-1;
RX MEDLINE=93012964; PubMed=1398080;
RA Halladay J.T., Ng W.L., Dassarma S.;
RT "Genetic transformation of a halophilic archaeobacterium with a gas
RT vesicle gene cluster restores its ability to float.";
RL Gene 119:131-136(1992).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=NRC-1;
RX MEDLINE=93139036; PubMed=8423144;
RA Halladay J.T., Jones J.G., Lin F., MacDonald A.B., Dassarma S.;
RT "The rightward gas vesicle operon in Halobacterium plasmid pNRC100:
RT identification of the gvpA and gvpC gene products by use of antibody
RT probes and genetic analysis of the region downstream of gvpC.";
RL J. Bacteriol. 175:684-692(1993).
RN [7]
RP SEQUENCE FROM N.A.
RC STRAIN=NRC-1;
RX MEDLINE=93327890; PubMed=8335077;
RA Dassarma S.;
RT "Identification and analysis of the gas vesicle gene cluster on an
RT unstable plasmid of Halobacterium halobium.";
RL Experimentia 49:482-486(1993).
RN [8]
RP SEQUENCE FROM N.A.
RC STRAIN=NRC-1;
RX MEDLINE=93328662; PubMed=8335618;
RA Ng W.L., Dassarma S.;
RT "Minimal replication origin of the 200-kilobase Halobacterium plasmid

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RT PNR100.0.
 RL J. Bacteriol. 175:4584-4596(1993).
 RN [9]
 RP SEQUENCE FROM N.A.
 RC STRAIN-NRC-1;
 RX MEDLINE=95095934; PubMed=8002589;
 RA Dassarma S., Arora P., Lin F., Molinari E., Yin L.R.;
 RT "Wild-type gas vesicle formation requires at least ten genes in the
 gp gene cluster of Halobacterium halobium plasmid pNRC100.0";
 RL J. Bacteriol. 176:7646-7652(1994).
 RN [10]
 RP SEQUENCE FROM N.A.
 RC STRAIN-NRC-1;
 RA Ng W.L., Arora P., Dassarma S.;
 RL Syst. Appl. Microbiol. 16:560-568(1994).
 RN [11]
 RP SEQUENCE FROM N.A.
 RC STRAIN-NRC-1;
 RA Dassarma S.;
 RL (In) Robb F.T., Place A.R., Sowers K.R., Schreier H.J., Dassarma S.,
 RL Fleischmann E.M. (eds.);
 RL Archaea:
 RL A laboratory manual - halophiles, pp.253-255,
 RL Cold Spring Harbor Laboratory Press, New York (1995).
 RN [12]
 RP SEQUENCE FROM N.A.
 RC STRAIN-NRC-1;
 RA Dassarma S., Arora P.;
 RL FEMS Microbiol. Lett. 153:1-10(1997).
 RN [13]
 RP SEQUENCE FROM N.A.
 RC STRAIN-NRC-1;
 RA Ng W.L., Ciuffo S.A., Smith T.M., Bumgarner R.E., Loretz C., Baskin D.,
 RA Faust J., Seto J., Slagel J., Hood L., Dassarma S.;
 RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
 RN [14]
 RP SEQUENCE FROM N.A.
 RC STRAIN-NRC-1;
 RA Ng W.L., Ciuffo S.A., Smith T.M., Bumgarner R.E., Loretz C., Baskin D.,
 RA Faust J., Seto J., Slagel J., Hood L., Dassarma S.;
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF016485; AAC82795.1;
 KW Plasmid.
 SQ SEQUENCE 1073 AA; 120578 MW; FBEE9BC662051675 CRC64;

Query Match 54.3%; Score 44; DB 1; Length 1073;
 Best Local Similarity 58.3%; Pred. No. 24;
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 HATGAWFNSAT 12
 | | : ||||| : ||
 Db 722 HLTASWFGSGT 733

RESULT 15
 Q9SU66 PRELIMINARY; PRT; 349 AA.
 AC Q9SU66;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
 DE HYPOTHETICAL 38.7 KDA PROTEIN.
 GN T17F15.100.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
 OC Brassicales; Brassicaceae; Arabidopsi.
 OX NCBI_TaxID=3702;
 [1]
 RN SEQUENCE FROM N.A.
 RA Choisine N., Robert C., Brottier P., Wincker P., Cattolico L.,
 RA Artiguenave F., Saurin W., Weissenbach J., Mewes H.W., Mayer K.F.X.,

RA Lencke K., Schueller C., Quetier F., Salanoubat M.;
 RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA EU Arabidopsis sequencing project;
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL049658; CAB41136.1;
 DR INTERPRO; IPR001841;
 DR PFAM; PF00097; zf-C3HC4; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 349 AA; 38686 MW; A080BD4C1D9DEBBE CRC64;

Query Match 53.1%; Score 43; DB 10; Length 349;
 Best Local Similarity 46.2%; Pred. No. 12;
 Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 HATGAWFNSATC 13
 | | : ||||| : ||
 Db 233 HCIDTWLLSNSTC 245

Search completed: May 23, 2001, 15:35:13
 Job time: 619 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 23, 2001, 15:28:28 ; Search time 184.73 Seconds
(without alignments)
6.808 Million cell updates/sec

Title: US-08-887-977-10_COPY_111_132

Perfect score: 115

Sequence: 1 LLKGIYAINFCGMLLLTCISM 22

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 390729 seqs, 57163235.residues

Total number of hits satisfying chosen parameters: 390729

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_0401:*

- 1: /SID56/gcgdata/geneseq/geneseq/AA1980.DAT:*
- 2: /SID56/gcgdata/geneseq/geneseq/AA1981.DAT:*
- 3: /SID56/gcgdata/geneseq/geneseq/AA1982.DAT:*
- 4: /SID56/gcgdata/geneseq/geneseq/AA1983.DAT:*
- 5: /SID56/gcgdata/geneseq/geneseq/AA1984.DAT:*
- 6: /SID56/gcgdata/geneseq/geneseq/AA1985.DAT:*
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- 8: /SID56/gcgdata/geneseq/geneseq/AA1987.DAT:*
- 9: /SID56/gcgdata/geneseq/geneseq/AA1988.DAT:*
- 10: /SID56/gcgdata/geneseq/geneseq/AA1989.DAT:*
- 11: /SID56/gcgdata/geneseq/geneseq/AA1990.DAT:*
- 12: /SID56/gcgdata/geneseq/geneseq/AA1991.DAT:*
- 13: /SID56/gcgdata/geneseq/geneseq/AA1992.DAT:*
- 14: /SID56/gcgdata/geneseq/geneseq/AA1993.DAT:*
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- 19: /SID56/gcgdata/geneseq/geneseq/AA1998.DAT:*
- 20: /SID56/gcgdata/geneseq/geneseq/AA1999.DAT:*
- 21: /SID56/gcgdata/geneseq/geneseq/AA2000.DAT:*
- 22: /SID56/gcgdata/geneseq/geneseq/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	115	100.0	365	19 W48086	Human dendritic ce
2	115	100.0	365	21 Y97077	Primate (human) ch
3	67	58.3	342	19 W80806	STRL33 protein seq
4	67	58.3	342	19 W54041	Human HBMEU14 prot
5	67	58.3	342	20 Y39366	Platelet factor-4
6	67	58.3	342	20 W97783	Human HIV/SIV rece
7	67	58.3	342	20 W97784	African green monk
8	66	57.4	342	20 W97785	Pig-tailed macaque
9	64	55.7	378	20 Y41682	Murine D6 protein
10	62	53.9	302	19 W70001	Rodent chemokine r
11	62	53.9	351	20 Y23825	A7 times membrane

12	61	53.0	359	15	R53747	Seven transmembran
13	61	53.0	359	19	W48728	Murine V31 seven t
14	61	53.0	359	21	B21691	Murine 7TM recepto
15	61	53.0	378	21	B21699	7TM receptor prote
16	57	49.6	358	15	R53745	Partial sequence o
17	57	49.6	358	21	B21689	Human 7TM receptor
18	57	49.6	378	15	R54079	Epstein Barr virus
19	57	49.6	378	15	R53744	Putative seven tra
20	57	49.6	378	19	W48724	Human V31 seven tr
21	57	49.6	378	19	W56164	G-protein coupled
22	57	49.6	378	19	W53622	Epstein Barr virus
23	57	49.6	378	21	B21688	Human 7TM receptor
24	57	49.6	378	21	Y90629	Human G protein-co
25	57	49.6	378	21	Y90663	Human mutant G pro
26	57	49.6	378	22	B50859	Human CCR7. Homo
27	57	49.6	410	15	R53743	Putative seven tra
28	57	49.6	410	19	W48723	Polypeptide sequen
29	57	49.6	410	21	B21687	Genomic clone of 7
30	56	48.7	362	21	B01448	Primate GPR2 amino
31	56	48.7	362	21	B01449	Rodent GPR2 protei
32	55.5	48.3	154	15	R53749	Seven transmembran
33	55.5	48.3	154	19	W48730	Human V112 seven t
34	55.5	48.3	154	21	B21694	Human 7TM receptor
35	55.5	48.3	360	20	W97786	Human HIV/SIV rece
36	55.5	48.3	360	21	Y90617	Human G protein-co
37	55.5	48.3	360	21	Y90651	Human mutant G pro
38	52	45.2	479	20	W96320	Glutathione reduct
39	52	45.2	537	19	W4943	Avian infectious b
40	51.5	44.8	360	20	W97787	African green monk
41	51.5	44.8	360	20	W97788	Pig-tailed macaque
42	51	44.3	25	19	W40018	Peptide effecting
43	51	44.3	159	21	B41786	Human ORFX ORF150
44	51	44.3	246	20	Y57292	Human BGCKr protei
45	51	44.3	263	20	Y30126	A seven-pass trans

ALIGNMENTS

RESULT 1

W48086 ID W48086 standard; Protein; 365 AA.

XX AC W48086;

XX DT 11-JUN-1998 (first entry)

XX DE Human dendritic cell chemokine receptor.

XX KW Human; thymus expressed chemokine; TECK; MIP-3alpha; MIP-3beta; receptor; dendritic cell; macrophage; inflammation; asthma.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT Misc-difference 193

XX FT /note= "encoded by CAN"

XX PN WO9801557-A2.

XX PD 15-JAN-1998.

XX PF 02-JUL-1997; 97WO-US10819.

XX PR 04-JUN-1997; 97US-0048593.

XX PR 05-JUL-1996; 96US-0675814.

XX PR 11-OCT-1996; 96US-0028329.

XX PA (SCHE) SCHERING CORP.

XX PI Gish KC, Schall TJ, Vicari A, Wang W, Zlotnik A;

XX WPI; 1998-101054/09.

DR N-PSDB; V15418.
 XX Novel chemokines, e.g. thymus expressed chemokine - used for
 PT treating inflammatory conditions including asthma.
 XX
 XX Claim 3; Page 94-95; 202pp; English.
 XX
 XX The present sequence represents human dendritic cell chemokine receptor.
 CC Antibodies which bind to the protein can be used in detecting or
 CC diagnosing various immunological conditions related to expression
 CC of the protein. The nucleic acid can be used for screening and
 CC isolating DNA clones for the chemokines, especially from other
 CC species. The chemokine can be used in the treatment of conditions
 CC associated with abnormal physiology or development, including
 CC inflammatory conditions such as asthma.
 XX
 XX Sequence 365 AA;
 SQ

Query Match 100.0%; Score 115; DB 19; Length 365;
 Best Local Similarity 100.0%; Pred. No. 4e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKGIYAINFCGMLLTCISM 22
 DB 111 llkgiyainfcgmltltcism 132
 |||||

RESULT 2
 Y97077
 ID Y97077 standard; Protein; 365 AA.
 XX AC Y97077;
 XX
 XX 04-DEC-2000 (first entry)
 XX
 XX Primate (human) chemokine receptor CCR6.
 DE
 XX MIP-3-alpha; chemokine; CCR6 receptor; ligand; cytostatic; agonist;
 KW antagonist; anti-psoriatic; dermatological; immunosuppressive;
 KW anti-inflammatory.
 KW
 XX Homo sapiens.
 OS
 XX Key Location/Qualifiers
 FH Misc-difference 193
 FT /note= "Encoded by CAN#"
 FT
 XX WO200046248-A1.
 PN
 XX 10-AUG-2000.
 XX
 XX 02-FEB-2000; 2000WO-US00511.
 XX
 XX 03-FEB-1999; 99US-0244281.
 XX
 XX (SCHE) SCHERING CORP.
 XX
 XX Oldham ER, Honey B, Dieu-Nosjean M, Caux C, Zlotnik A;
 XX WPI; 2000-543477/49.
 DR N-PSDB; A51971.
 XX
 XX Novel methods for modulating the migration of cells within or to the
 PT skin using MIP-3-alpha or CCR6 agonists or antagonists, useful for
 PT treating skin disorders, e.g. cancer
 XX.
 XX Disclosure; Page 53-54; 61pp; English.
 XX
 XX The MIP-3-alpha chemokine is expressed in inflamed skin cells. This
 CC chemokine is the ligand for the CCR6 receptor. MIP-3-alpha or CCR6
 CC agonists or antagonists can be used to modulate the migration of a cell
 CC within or to the skin of a mammal. MIP-3-alpha can be used to purify a

CC population of cells expressing a MIP-3-alpha receptor. The methods are
 CC useful for treating a mammalian subject with a skin disease or condition,
 CC e.g. cancer, metastasis, psoriasis, atopic or contact dermatitis,
 CC systemic lupus erythematosus and lichen ruber planus, or for treating
 CC skin transplants or grafts.
 XX
 XX Sequence 365 AA;
 SQ

Query Match 100.0%; Score 115; DB 21; Length 365;
 Best Local Similarity 100.0%; Pred. No. 4e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKGIYAINFCGMLLTCISM 22
 DB 111 llkgiyainfcgmltltcism 132
 |||||

RESULT 3
 W80806
 ID W80806 standard; Protein; 342 AA.
 XX AC W80806;
 XX
 XX 22-JAN-1999 (first entry)
 XX
 XX STRL33 protein sequence.
 DE
 XX STRL33; human; HIV-1; HIV related disorder; therapy; CD4; diagnosis;
 KW fusion accessory factor.
 KW
 XX Homo sapiens.
 OS
 XX WO9844098-A2.
 PN
 XX 08-OCT-1998.
 XX
 XX 31-MAR-1998; 98WO-US06517.
 XX
 XX 31-MAR-1997; 97US-0042880.
 PR
 XX (USSH) US SEC HEALTH & HUMAN SERVICES.
 PA
 XX Alkhatib G, Berger EA, Farber JM, Liao F;
 PI WPI; 1998-557107/47.
 DR N-PSDB; V68515.
 DR
 XX New isolated fusion accessory factor STRL33 - which mediates HIV
 PT infection of cells, used to develop products for the study,
 PT prevention and therapy of HIV-related disorders
 XX
 XX Claim 65; Fig 4; 74pp; English.
 PS
 XX This sequence is the human STRL33 polypeptide that is expressed by
 CC the recombinant cell line of the invention. The STRL33 polypeptide is a
 CC fusion accessory factor that can function with CD4 to mediate fusion with
 CC cells bearing HIV-1 env from both laboratory-adapted TCL-tropic variants
 CC and from M-tropic variants. Agents that suppress STRL33 can be used in a
 CC method to treat HIV-related disorders. The products and methods can be
 CC used for the study, prevention and therapy of HIV-related disorders.
 XX
 XX Sequence 342 AA;
 SQ

Query Match 58.3%; Score 67; DB 19; Length 342;
 Best Local Similarity 61.9%; Pred. No. 0.0034;
 Matches 13; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 2 LKGIYAINFCGMLLTCISM 22
 DB 105 llgiyinfytsmltltciv 125
 |||||

```

RESULT 4
W54041
ID W54041 standard; Protein: 342 AA.
XX
AC W54041;
XX
DT 07-AUG-1998 (first entry)
XX
DE Human HBMBU14 protein.
XX
XX Human; 7-transmembrane receptor; HBMBU14; infection; HIV; cancer; asthma;
KW anorexia; Parkinson's disease; acute heart failure; atherosclerosis;
KW osteoporosis; angina pectoris; myocardial infarction; psychotic disorder;
KW benign prostatic hypertrophy; neurological disorder; therapy;
KW Huntington's disease; Gilles de la Tourette's syndrome.
XX
XX Homo sapiens.
OS
XX EP834563-A2.
PN
XX
PD 08-APR-1998.
XX
PF 23-SEP-1997; 97EP-0307428.
XX
PR 26-SEP-1996; 96US-0026669.
XX
PA (SMIK ) SMITHKLINE BEECHAM CORP.
XX
PI Bergsma DJ, Ellis CE, Elshourbagy NA;
XX
DR WPI; 1998-208924/19.
DR N-PSDB; V24017.
XX
XX New isolated human 7-trans-membrane receptor, HBMBU14 - useful for
PT developing products for treating, e.g. infections, pain, cancers,
PT anorexia, hypotension, osteoporosis and asthma
XX
XX Claim 12; Fig 1; 36pp; English.
PS
XX This sequence is the human HBMBU14 protein of the invention. HBMBU14
CC is a human 7-transmembrane (TM) receptor. The products can be used for
CC treating or preventing conditions related to abnormal HBMBU14 expression
CC or activity, e.g. infections such as bacterial, fungal, protozoan and
CC viral infections especially infections caused by HIV-1 and HIV-2, pain,
CC cancers, anorexia, bulimia, asthma, Parkinson's disease, acute heart
CC failure, atherosclerosis, hypotension, hypertension, urinary retention,
CC osteoporosis, angina pectoris, myocardial infarction, ulcers, asthma,
CC allergies, benign prostatic hypertrophy and psychotic and neurological
CC disorders, including anxiety, schizophrenia, manic depression, delirium,
CC dementia or severe mental retardation, and dyskinesias, such as
CC Huntington's disease or Gilles de la Tourette's syndrome. The products
CC can also be used for diagnosing a disease or susceptibility to a disease
CC related to the expression of HBMBU14 and for identifying compounds which
CC bind to and activate or inhibit a receptor for the polypeptide.
XX
SQ Sequence 342 AA;

Query Match 58.3%; Score 67; DB 19; Length 342;
Best Local Similarity 61.9%; Pred. No. 0.0034;
Matches 13; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 2 LKGIYAINFCGMLLLTCISM 22
| | | | | | | | | | | | | |
Db 105 llgiytnfytsmliltciv 125

RESULT 5
Y39366
ID Y39366 standard; Protein: 342 AA.
XX
AC Y39366;

```

```

XX 05-JAN-2000 (first entry)
DT
DE Platelet factor-4 (PF-4) receptor amino acid sequence.
XX
KW PF-4; platelet factor-4; alpha granules; collagen; thrombotic stimuli;
KW thrombosis; inflammatory activity; chemokine; PF-4 receptor; HBMBU14;
KW BOMZO; TYNSTR; agonist; antagonist; HIV; AIDS; rheumatoid arthritis;
KW asthma; psoriasis; atherosclerosis; inflammatory disorder.
XX
OS Homo sapiens.
XX
PN WO9950670-A1.
XX
PD 07-OCT-1999.
XX
PF 26-MAR-1999; 99WO-GB00950.
XX
PR 27-MAR-1998; 98GB-0006677.
XX
PA (SMIK ) SMITHKLINE BEECHAM PLC.
XX
PI MacPhee CH, Moores K, Berkhout TA;
XX
DR WPI; 1999-591378/50.
DR N-PSDB; Z28362.
XX
XX Novel PF-4 receptor assays used to identify antagonists and agonists of
PT the receptor for use in therapy
XX
XX Example 1; Page 27-28; 35pp; English.
XX
XX This sequence is the platelet factor-4 (PF-4) receptor amino acid
CC sequence. PF-4 is a 70 residue polypeptide released from alpha-granules
CC when platelets are activated by contacting collagen or other thrombotic
CC stimuli. PF-4 promotes thrombosis at sites of platelet activation, and
CC also exhibits several inflammatory activities. The carboxy terminal
CC tridecapeptide of PF-4 is a potent chemotactic agent for monocytes. PF-4
CC is a CXC chemokine. The PF-4 receptor, also known as HBMBU14, TYNSTR and
CC BOMZO, is used in the methods of the invention. The invention relates to
CC a novel screening method for identifying antagonists and agonists of the
CC PF-4 receptor, involving using PF-4 and the PF-4 receptor together. PF-4
CC and the PF-4 receptor are used to identify further chemokine ligands for
CC the receptor using a competitive binding assay and labelled PF-4. PF-4 is
CC used to identify neutralizing or activating antibodies to the PF-4
CC receptor for use in therapy. PF-4 can be used in a screening method for
CC identifying an antagonist of the receptor. Antagonists and agonists may
CC be used for therapeutic purposes, such as treatment of HIV, AIDS,
CC rheumatoid arthritis, asthma, psoriasis, atherosclerosis, and other
CC inflammatory diseases.
XX
SQ Sequence 342 AA;

Query Match 58.3%; Score 67; DB 20; Length 342;
Best Local Similarity 61.9%; Pred. No. 0.0034;
Matches 13; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 2 LKGIYAINFCGMLLLTCISM 22
| | | | | | | | | | | | | |
Db 105 llgiytnfytsmliltciv 125

RESULT 6
W97783
ID W97783 standard; Protein: 342 AA.
XX
AC W97783;
XX
XX 21-MAY-1999 (first entry)
XX
XX Human HIV/SIV receptor protein Bonzo.
XX

```

KW SIV receptor; HIV receptor; Bonzo; translocation promoting agent;
 KW human; G protein coupled receptor; chemokine receptor; AIDS;
 KW infection; virus transmission.

OS Homo sapiens.

XX Key Location/Qualifiers

FH Misc-difference 53

FT /note= "encoded by TG"

FT Misc-difference 9..71

FT /note= "encoded by TG"

FT Misc-difference 102

FT /note= "encoded by CG"

XX WO9903888-AL.

PN 28-JAN-1999.

PD 17-JUL-1998; 98WO-US14857.

XX 17-JUL-1997; 97US-0896155.

XX (UYNV) UNIV NEW YORK STATE.

XX Deng H, Kewalramani VN, Littman DR, Unutmaz D;

XX WPI; 1999-132164/11.

XX N-PSDB; X07289.

XX New nucleic acid encoding the human translocation promoter Bonzo -

XX used to screen for potential agents for treating acquired immune

XX deficiency syndrome

XX Claim 4; Page 78-79; 97pp; English.

XX This is the amino acid sequence of human Bonzo, a novel HIV/SIV

XX translocation promoting agent that acts in conjunction with CD4 to

XX serve as a receptor for the entry into a cell of a virus having a

XX specific viral envelope glycoprotein. Bonzo is a member of the

XX 7-transmembrane G-protein coupled receptor family, is closely

XX related to the chemokine receptor family, and is expressed in

XX lymphoid tissues. The invention provides the amino acid sequences

XX (see W97783-88) and DNA sequences (see X07289-94) of human,

XX African green monkey and pig-tailed macaque Bonzo and Bob (brother

XX of Bonzo) translocation promoting agents. These novel receptors

XX were identified using an expression cloning strategy. They were

XX found to be used by particular strains of HIV-2 and M-tropic HIV-1.

XX The invention also includes: mammalian cells transfected with Bonzo

XX and/or Bob and human CD4, which can be used to screen potential

XX therapeutic agents and identify ligands; antibodies to Bonzo, which

XX can be used therapeutically, e.g. as antagonists or to target

XX toxins or radioisotopes to HIV-permissive cells; transgenic

XX animals; and antisense and ribozyme molecules, which may also be

XX used therapeutically, particularly expressed from a gene therapy

XX vector.

XX Sequence 342 AA;

XX Query Match 58.3%; Score 67; DB 20; Length 342;

XX Best Local Similarity 61.9%; Pred. No. 0.0034;

XX Matches 13; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

XX QY 2 LKGIYAINFCGMILLTICISM 22

XX Db 105 llgiytnfytsmliltciv 125

XX RESULT 7

XX W97784

XX ID W97784 standard; Protein: 342 AA.

XX AC W97784;

XX

DT 21-MAY-1999 (first entry)

XX African green monkey HIV/SIV receptor protein Bonzo.

DE SIV receptor; HIV receptor; Bonzo; translocation promoting agent;

KW G protein coupled receptor; chemokine receptor; AIDS; infection;

KW virus transmission; African green monkey.

XX Cercopithecus aethiops.

OS WO9903888-AL.

XX 28-JAN-1999.

XX 17-JUL-1998; 98WO-US14857.

XX 17-JUL-1997; 97US-0896155.

XX (UYNV) UNIV NEW YORK STATE.

XX Deng H, Kewalramani VN, Littman DR, Unutmaz D;

XX WPI; 1999-132164/11.

XX N-PSDB; X07290.

XX New nucleic acid encoding the human translocation promoter Bonzo -

XX used to screen for potential agents for treating acquired immune

XX deficiency syndrome

XX Disclosure; Page 80-81; 97pp; English.

XX This is the amino acid sequence of African green monkey Bonzo, a

XX novel HIV/SIV translocation promoting agent that acts in conjunction

XX with CD4 to serve as a receptor for the entry into a cell of a virus

XX having a specific viral envelope glycoprotein. Bonzo is a member of

XX the 7-transmembrane G-protein coupled receptor family, is closely

XX related to the chemokine receptor family, and is expressed in

XX lymphoid tissues. The invention provides the amino acid sequences

XX (see W97783-88) and DNA sequences (see X07289-94) of human,

XX African green monkey and pig-tailed macaque Bonzo and Bob (brother

XX of Bonzo) translocation promoting agents. These novel receptors

XX were identified using an expression cloning strategy. They were

XX found to be used by particular strains of HIV-2 and M-tropic HIV-1.

XX The invention also includes: mammalian cells transfected with Bonzo

XX and/or Bob and human CD4, which can be used to screen potential

XX therapeutic agents and identify ligands; antibodies to Bonzo, which

XX can be used therapeutically, e.g. as antagonists or to target

XX toxins or radioisotopes to HIV-permissive cells; transgenic

XX animals; and antisense and ribozyme molecules, which may also be

XX used therapeutically, particularly expressed from a gene therapy

XX vector.

XX Sequence 342 AA;

XX Query Match 58.3%; Score 67; DB 20; Length 342;

XX Best Local Similarity 61.9%; Pred. No. 0.0034;

XX Matches 13; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

XX QY 2 LKGIYAINFCGMILLTICISM 22

XX Db 105 llgiytnfytsmliltciv 125

XX RESULT 8

XX W97785

XX ID W97785 standard; Protein: 342 AA.

XX AC W97785;

XX 21-MAY-1999 (first entry)

XX

DE Pig-tailed macaque HIV/SIV receptor protein Bonzo.
 XX
 KW SIV receptor; HIV receptor; Bonzo; translocation promoting agent;
 KW G protein coupled receptor; chemokine receptor; AIDS; infection;
 KW virus transmission; pig-tailed macaque.
 XX
 OS Macaca nemestrina.
 XX
 PN WO9903888-A1.
 XX
 PD 28-JAN-1999.
 XX
 PF 17-JUL-1998; 98WO-US14857.
 XX
 PR 17-JUL-1997; 97US-0896155.
 XX
 PA (UYNV) UNIV NEW YORK STATE.
 XX
 PI Deng H, Kewalramani VN, Littman DR, Unutmaz D;
 DR WPI; 1999-132164/11.
 DR N-PSDB; X07291.
 XX
 PT New nucleic acid encoding the human translocation promoter Bonzo -
 PT used to screen for potential agents for treating acquired immune
 PT deficiency syndrome
 XX
 PS Disclosure; Page 82-83; 97pp; English.
 XX
 CC This is the amino acid sequence of pig-tailed macaque Bonzo, a
 CC novel HIV/SIV translocation promoting agent that acts in conjunction
 CC with CD4 to serve as a receptor for the entry into a cell of a virus
 CC having a specific viral envelope glycoprotein. Bonzo is a member of
 CC the 7-transmembrane G-protein coupled receptor family, is closely
 CC related to the chemokine receptor family, and is expressed in
 CC lymphoid tissues. The invention provides the amino acid sequences
 CC (see W97/83-88) and DNA sequences (see X07289-94) of human,
 CC African green monkey and pig-tailed macaque Bonzo and Bob (brother
 CC of Bonzo) translocation promoting agents. These novel receptors
 CC were identified using an expression cloning strategy. They were
 CC found to be used by particular strains of HIV-2 and M-tropic HIV-1.
 CC The invention also includes: mammalian cells transfected with Bonzo
 CC and/or Bob and human CD4, which can be used to screen potential
 CC therapeutic agents and identify ligands; antibodies to Bonzo, which
 CC can be used therapeutically, e.g. as antagonists or to target
 CC toxins or radioisotopes to HIV-permissive cells; transgenic
 CC animals; and antisense and ribozyme molecules, which may also be
 CC used therapeutically, particularly expressed from a gene therapy
 CC vector.
 XX
 SQ Sequence 342 AA;
 Query Match 57.4%; Score 66; DB 20; Length 342;
 Best Local Similarity 57.1%; Pred. No. 0.005;
 Matches 12; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
 OY 2 LKGIYAINFCGMLLTCTISM 22
 Db 105 llgvytnifysmltltctiv 125
 RESULT 9
 Y41682
 ID Y41682 standard; Protein; 378 AA.
 XX
 AC Y41682;
 XX
 DT 06-DEC-1999 (first entry)
 XX
 DE Murine D6 protein.
 XX
 KW D6; G protein-coupled heptahelical receptor; diagnosis; asthma;

KW respiratory inflammatory disorder; identification.
 XX
 OS Mus sp.
 XX
 PN WO9947697-A1.
 XX
 PD 23-SEP-1999.
 XX
 PF 19-MAR-1999; 99WO-US06075.
 XX
 PR 20-MAR-1998; 98US-0045583.
 XX
 PA (MILL-) MILLENNIUM PHARM INC.
 PA (CRCT-) CRC TECHNOLOGY LTD.
 XX
 PI Graham GJ, Benjamin Nibbs RJ, Gonzalo J, Gutierrez-Ramos J;
 DR WPI; 1999-562123/47.
 DR N-PSDB; Z25023, Z25024.
 XX
 PT Identification of D6 G-protein coupled receptor binding compounds and
 PT modulators, useful in treatment of asthma
 XX
 PS Claim 1; Fig 2; 152pp; English.
 XX
 CC Methods have been developed for identifying a compound, which binds to a
 CC human or murine D6 protein, an allelic variant or a fragment comprises
 CC detecting binding of the test compound to the protein. Also described in
 CC the present invention are: (1) a method for identifying a compound
 CC capable of treating a disorder characterized by aberrant D6 nucleic acid
 CC expression of D6 protein activity; (2) a method for treating a subject
 CC having a disorder characterized by aberrant D6 protein activity or
 CC nucleic acid expression comprising administering to the subject a D6
 CC modulator such that treatment of the subject occurs; and (3) methods for
 CC identifying a compound that modulates the activity of a human or murine
 CC D6 protein, an allelic variant or a fragment. The methods are useful for
 CC identifying compounds capable of treating disorders, especially a
 CC respiratory inflammatory disorder, characterized by aberrant D6 nucleic
 CC acid expression or D6 protein activity. In particular, the disorder is
 CC asthma. D6 modulators are used to treat asthma. The present sequence
 CC represents the murine D6 protein.
 XX
 SQ Sequence 378 AA;
 Query Match 55.7%; Score 64; DB 20; Length 378;
 Best Local Similarity 40.9%; Pred. No. 0.012;
 Matches 9; Conservative 8; Mismatches 5; Indels 0; Gaps 0;
 OY 1 LLKGIYAINFCGMLLTCTISM 22
 Db 118 vistlysinfcyqffitcmsl 139
 RESULT 10
 W70001
 ID W70001 standard; Protein; 302 AA.
 XX
 AC W70001;
 XX
 DT 20-OCT-1998 (first entry)
 XX
 DE Rodent chemokine receptor 941D12 amino acid sequence.
 XX
 KW Chemokine; primate; human; rodent; chemokine receptor; asthma;
 KW inflammatory response; immune response; leukocyte migration; GPCR;
 KW leukocyte adhesion; chemoattractant; modulation; antiviral response;
 KW cellular morphology modification response; G-protein coupled receptor;
 KW phosphoinositide lipid turnover; abnormal proliferation; regeneration;
 KW atrophy; 941D12.
 XX
 OS Mus sp.

PN W09832858-A2.

XX 30-JUL-1998.

XX 22-JAN-1998; 98WO-US00902.

XX 23-JAN-1997; 97US-0036715.

XX (SCHE) SCHERING CORP.

XX Gorman DM, Hedrick JA, Mattson JD, Soto-trejo H;

XX Zlotnik A;

XX WPI; 1998-427954/36.

XX N-PSDB; V43795.

XX Rodent and primate chemokines and chemokine receptors - useful

XX diagnostically and therapeutically to treat conditions associated

XX with abnormal physiology or development e.g. inflammatory conditions

XX Claim 5; Pages 97-99; 105pp; English.

XX This represents a rodent chemokine receptor 941D12 amino acid sequence.

XX The invention provides novel primate and rodent chemokines and chemokine

XX receptors. The chemokines, receptors and binding compounds (optionally

XX antibodies/fragments specifically binding the chemokines) are useful

XX therapeutically to treat conditions associated with abnormal physiology

XX or development e.g. inflammatory conditions such as asthma. Chemokines

XX are important in immune and inflammatory responses in that they induce

XX leukocyte migration and adhesion. They are also chemoattractants for

XX several cells involved in inflammation and can induce other biological

XX responses e.g. modulation of second messenger levels (e.g. Ca⁺⁺),

XX cellular morphology modification responses, phosphoinositide lipid

XX turnover, possible antiviral responses etc. The chemokine receptors of

XX the invention exhibit structural properties of G-protein coupled

XX receptors (GPCR), although their ligands have not yet been identified.

XX The chemokine and chemokine receptor polypeptides are useful to produce

XX ligand:receptor complexes in vivo or in assay techniques. Assays may

XX also involve chemical antagonists which block complex production or

XX utilise competitive binding. Binding compounds identified (agonists or

XX antagonists) can be used to modulate the physiological responses in cells

XX (especially neurons, macrophages or lymphocytes) to treat e.g. abnormal

XX proliferation, regeneration, generation and atrophy. The polypeptides

XX are also used to produce antibodies useful diagnostically, for drug

XX screening or for polypeptide purification. The polynucleotides are useful

XX to produce probes for detecting the polypeptides, and to isolate the

XX polypeptides or related sequences, especially from other species. They

XX also allow transformation of cells for polypeptide production.

XX Sequence 302 AA;

SQ

Query Match

Best Local Similarity 53.9%; Score 62; DB 19; Length 302;

Matches 11; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 2 LKGIYAINFCGMILLTCISM 22

Db 114 lrgmytmfymvsmittctiv 134

RESULT 11

ID Y23825 standard; Protein; 351 AA.

XX Y23825;

XX 15-SEP-1999 (first entry)

XX A7 times membrane penetrating type receptor protein ET60.

XX 7 times membrane-penetrating type receptor protein; ET60;

XX leukocyte function; control; drug.

KW

SQ

XX Unidentified.

XX JP11155573-A.

XX 15-JUN-1999.

XX 27-NOV-1997; 97JP-0325823.

XX 27-NOV-1997; 97JP-0325823.

XX (ASAH) ASahi KASEI KOGYO KK.

XX WPI; 1999-398070/34.

XX N-PSDB; X86032.

XX New 7 times membrane-penetrating type receptor protein ET60 - useful

XX for detecting drug controlling function of leukocyte

XX Claim 1; Page 17-18; 20pp; Japanese.

XX The present sequence represents a 7 times membrane-penetrating type

XX receptor protein ET60. The 7 times membrane-penetrating type

XX receptor protein ET60 can be used for detecting a drug controlling

XX the function of leukocyte.

XX Sequence 351 AA;

SQ

Query Match

Best Local Similarity 53.9%; Score 62; DB 20; Length 351;

Matches 11; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 2 LKGIYAINFCGMILLTCISM 22

Db 114 lrgmytmfymvsmittctiv 134

RESULT 12

ID R53747 standard; Protein; 359 AA.

XX R53747;

XX 03-FEB-1995 (first entry)

XX Seven transmembrane receptor (V31) partial sequence of mouse.

XX Primer; seven transmembrane receptor; receptor; amplification; PCR;

XX polymerase chain reaction.

XX Mus musculus.

XX W09412635-A.

XX 09-JUN-1994.

XX 17-NOV-1993; 93WO-US11153.

XX 17-NOV-1992; 92US-0977452.

XX (ICOS-) ICOS CORP.

XX Godiska R, Gray PW, Schweickart VL;

XX WPI; 1994-200264/24.

XX N-PSDB; Q66164.

XX DNA encoding seven transmembrane receptors - used to develop

XX prods. for use as therapeutic or diagnostic agents for conditions

XX involving the receptors.

XX Example 5; Page 61-62; 100pp; English.

PS

XX Two primers (Q66148, Q66149) were used to amplify human genomic DNA
 CC purified from leukocytes. Approximately 1000 clones were isolated
 CC after the initial amplification reaction and probed with sequences
 CC specific for seven transmembrane receptors IL8R1, AT2R and R20.
 CC Clones which did not hybridise were then chosen for sequence
 CC analysis. Three new clones were identified that appeared to encode
 CC seven transmembrane receptor segments. Two more primers (Q66151,
 CC Q66152) were used to isolate a full length version of one of the
 CC human V31 clone (See Q66153). A fragment of the human clone was used
 CC to isolate a V31 genomic clone of the mouse from a library.
 XX
 SQ Sequence 359 AA;

Query Match 53.0%; Score 61; DB 15; Length 359;
 Best Local Similarity 63.2%; Pred. No. 0.036; Length 359;
 Matches 12; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 4 GIYAINFNCGMLLLTCISM 22
 III :I IIIII III:
 Db 114 giyklisffsgmlllclisi 132

RESULT 13

W48728
 ID W48728 standard; Protein; 359 AA.

XX
 AC W48728;

XX
 DT 25-SEP-1998 (first entry)

XX Murine V31 seven transmembrane (7TM) receptor.

XX V28; placenta; seven transmembrane receptor; 7TM; signal transduction;
 KW immunology; inflammation; V31; ss.

XX
 OS Mus sp.

XX US5759804-A.

XX
 PD 02-JUN-1998.

XX
 PF 17-NOV-1993; 93US-0153848.

XX
 PR 17-NOV-1992; 92US-0977452.

XX (ICOS-) ICOS CORP.

XX Godiska R, Gray PW, Schweickart VL;

XX WPI; 1998-332132/29.

XX N-PSDB; V18351.

XX DNA encoding V28 seven transmembrane receptor polypeptide - useful
 PT for producing recombinant polypeptide and anti-V28 antibodies, and
 PT in screening assays for V28 agonists and antagonists

XX Example 5; Columns 55-58; 56pp; English.

XX The present sequence represents the murine V31 seven transmembrane
 CC (7TM) receptor which is encoded by the murine V31 genomic DNA (V18351)
 CC isolated from a mouse genomic library. The invention claims for the
 CC full length V28 genomic DNA sequence isolated from a human placenta
 CC genomic library. V28 (W48722) and V31 proteins are seven transmembrane
 CC (7TM) receptors which are probably involved in signal transduction.
 CC The invention also claims that cells transformed with V28 DNA can be
 CC used to produce the recombinant polypeptide, to produce anti-V28
 CC antibodies or in screening assays for V28 agonists or antagonists. The
 CC antibodies, agonists and antagonists could then be used to modulate
 CC V28 receptor-ligand binding, for e.g. in immunological and/or
 CC inflammatory events in vivo.

XX

SQ Sequence 359 AA;

Query Match 53.0%; Score 61; DB 19; Length 359;
 Best Local Similarity 63.2%; Pred. No. 0.036; Length 359;
 Matches 12; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 4 GIYAINFNCGMLLLTCISM 22
 III :I IIIII III:
 Db 114 giyklisffsgmlllclisi 132

RESULT 14

B21691

ID B21691 standard; Protein; 359 AA.

XX
 AC B21691;

XX
 DT 26-JAN-2001 (first entry)

XX Murine 7TM receptor V31cDNA clone protein.

XX Seven transmembrane receptor; 7TM; heptahelical; serpentine;

KW G-protein-coupled; V28; V31; V112; R20; R2; R12; RM3; gene therapy;
 cancer.

XX
 OS Mus sp.

XX US6107475-A.

XX
 PD 22-AUG-2000.

XX
 PF 26-APR-1999; 99US-0299843.

XX
 PR 17-MAY-1994; 94US-0245242.

XX
 PR 01-JUN-1998; 98US-0088337.

XX
 PR 17-NOV-1992; 92US-0977452.

XX
 PR 17-NOV-1993; 93US-0153848.

XX (ICOS-) ICOS CORP.

XX Schweickart VL, Gray PW, Godiska R;

XX WPI; 2000-571335/53.

XX N-PSDB; A91711.

XX Polynucleotide encoding seven transmembrane receptors, antibody
 PT specific to the receptor, agonist and antagonist of the receptor useful
 PT for treating inflammation in a mammal

XX Example 4; Columns 57-60; 61pp; English.

XX The present sequence is a novel seven transmembrane (7TM) receptors
 CC (also known as heptahelical, serpentine or G-protein-coupled receptors).

CC The coding sequence for the present sequence may be used for gene
 CC therapy for diseases such as cancer.

XX
 SQ Sequence 359 AA;

Query Match 53.0%; Score 61; DB 21; Length 359;
 Best Local Similarity 63.2%; Pred. No. 0.036; Length 359;
 Matches 12; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 4 GIYAINFNCGMLLLTCISM 22
 III :I IIIII III:
 Db 114 giyklisffsgmlllclisi 132

RESULT 15

B21699

ID B21699 standard; Protein; 378 AA.

XX

AC B21699;
 XX 26-JAN-2001 (first entry)
 XX 7TM receptor protein.
 XX Seven transmembrane receptor; 7TM; heptahelical; serpentine;
 KW G-protein-coupled; V28; V31; V112; R20; R2; R12; RM3; gene therapy;
 KW cancer.
 XX Unidentified.
 XX US6107475-A.
 XX 22-AUG-2000.
 XX 26-APR-1999; 99US-0299843.
 XX 17-MAY-1994; 94US-0245242.
 PR 01-JUN-1998; 98US-0088337.
 PR 17-NOV-1992; 92US-0977452.
 PR 17-NOV-1993; 93US-0153848.
 XX (ICOS-) ICOS CORP.
 PA
 XX
 PI Schweickart VL, Gray PW, Godiska R;
 XX
 DR WPI; 2000-571335/53.
 DR N-PSDB; A91745.
 XX
 PT Polynucleotide encoding seven transmembrane receptors, antibody
 specific to the receptor, agonist and antagonist of the receptor useful
 for treating inflammation in a mammal -
 XX
 PS Disclosure; Columns 111-112; 61pp; English.
 XX
 CC The present sequence is a novel seven transmembrane (7TM) receptors
 (also known as heptahelical, serpentine or G-protein-coupled receptors).
 CC The coding sequence for the present sequence may be used for gene
 CC therapy for diseases such as cancer.
 XX
 SQ Sequence 378 AA;
 Query Match 53.0%; Score 61; DB 21; Length 378;
 Best Local Similarity 63.2%; Pred. No. 0.038;
 Matches 12; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 QY 4 GIYAINFCGMLLTCISM 22
 Db 134 giykisffsgmlllcisi 152

Search completed: May 23, 2001, 15:28:28
 Job time: 405 sec

RESULT 2
US-08-153-848-24
; Sequence 24, Application US/08153848
; Patent No. 5759804
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schweikart, Vicki L.
; TITLE OF INVENTION: No. 5759804el Seven Transmembrane Receptors
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/153,848
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/977,452
; FILING DATE: 17-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5759804and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31794
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 359 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-153-848-24

Query Match 53.0%; Score 61; DB 1; Length 359;
Best Local Similarity 63.2%; Pred. No. 0.012;
Matches 12; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 4 GIYAINFCGMLLLTCISM 22
||| :| ||||| |||
Db 114 GIYKLSFFSGMLLLCISI 132

RESULT 3
US-09-299-843A-24
; Sequence 24, Application US/09299843A
; Patent No. 6107475
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schweikart, Vicki L.
; TITLE OF INVENTION: No. 6107475el Seven Transmembrane Receptors
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois

COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/299,843A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/088,337
FILING DATE: 01-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/153,848
FILING DATE: 17-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Jill E. Uhl
REGISTRATION NUMBER: 43,213
REFERENCE/DOCKET NUMBER: 27866/32059B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX:
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 359 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-299-843A-24

Query Match 53.0%; Score 61; DB 3; Length 359;
Best Local Similarity 63.2%; Pred. No. 0.012;
Matches 12; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 4 GIYAINFCGMLLLTCISM 22
||| :| ||||| |||
Db 114 GIYKLSFFSGMLLLCISI 132

RESULT 4
PCT-US93-11153-24
; Sequence 24, Application PC/TUS9311153
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schweikart, Vicki L.
; TITLE OF INVENTION: Novel Seven Transmembrane Receptors
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/11153
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/977,452
; FILING DATE: 17-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Noland, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31794
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 359 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US93-11153-24

Query Match 53.0%; Score 61; DB 5; Length 359;
Best Local Similarity 63.2%; Pred. No. 0.012;
Matches 12; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 4 GIYAINFCGMLLLTCISM 22
||| :| |||| |||
Db 114 GIYKLSFFSGMLLLCISI 132

RESULT 5
US-09-299-843A-66
; Sequence 66, Application US/09299843A
; Patent No. 6107475
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schweikart, Vicki L.
; TITLE OF INVENTION: No. 6107475e1 Seven Transmembrane Receptors
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/299,843A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/088,337
; FILING DATE: 01-JUN-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/153,848
; FILING DATE: 17-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/977,452
; FILING DATE: 17-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Jill E. Uhl
; REGISTRATION NUMBER: 43,213
; REFERENCE/DOCKET NUMBER: 27866/32059B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX:
; INFORMATION FOR SEQ ID NO: 66:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 378 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-299-843A-66

Query Match 53.0%; Score 61; DB 3; Length 378;
Best Local Similarity 63.2%; Pred. No. 0.012;
Matches 12; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 4 GIYAINFCGMLLLTCISM 22
||| :| |||| |||
Db 134 GIYKLSFFSGMLLLCISI 152

RESULT 6
US-08-153-848-19
; Sequence 19, Application US/08153848
; Patent No. 5759804
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schweikart, Vicki L.
; TITLE OF INVENTION: No. 5759804e1 Seven Transmembrane Receptors
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/153,848
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/977,452
; FILING DATE: 17-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5759804and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31794
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 358 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-153-848-19

Query Match 49.6%; Score 57; DB 1; Length 358;
Best Local Similarity 54.5%; Pred. No. 0.055;
Matches 12; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 LLKGIYAINFCGMLLLTCISM 22
|: || :| |||| |||
Db 111 LIFAIYKMSFFSGMLLLCISI 132

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7
US-09-299-843A-19
; Sequence 19, Application US/09299843A
; Patent No. 6107475
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schweikart, Vicki L.
; TITLE OF INVENTION: NO. 6107475el Seven Transmembrane Receptors
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/299.843A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/088.337
; FILING DATE: 01-JUN-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/153.848
; FILING DATE: 17-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/977.452
; FILING DATE: 17-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Jill E. Uhl
; REGISTRATION NUMBER: 43,213
; REFERENCE/DOCKET NUMBER: 27866/32059B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX:
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 358 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-299-843A-19

Query Match 49.6%; Score 57; DB 3; Length 358;
Best Local Similarity 54.5%; Pred. No. 0.055;
Matches 12; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

OY 1 LLKGIYAINFCGMILLTCISM 22
Db 111 LFAIYKMSFFSGMILLLCISI 132

RESULT 8
PCT-US93-11153-19
; Sequence 19, Application PC/TUS9311153
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schweikart, Vicki L.
; TITLE OF INVENTION: Novel Seven Transmembrane Receptors
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &

```

```

; ADDRESSEE: Bicknell
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/11153
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/977.452
; FILING DATE: 17-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Noland, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31794
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 358 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US93-11153-19

Query Match 49.6%; Score 57; DB 5; Length 358;
Best Local Similarity 54.5%; Pred. No. 0.055;
Matches 12; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

OY 1 LLKGIYAINFCGMILLTCISM 22
Db 111 LFAIYKMSFFSGMILLLCISI 132

RESULT 9
US-08-383-750-2
; Sequence 2, Application US/08383750
; Patent No. 5744301
; GENERAL INFORMATION:
; APPLICANT: Birkenbach, Mark
; APPLICANT: Kieff, Elliot
; TITLE OF INVENTION: Epstein Barr Virus Induced Genes
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, N.W.,
; STREET: Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/383.750
; FILING DATE: Herewith
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Fox, Samuel, L.
; REGISTRATION NUMBER: 30,353

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REFERENCE/DOCKET NUMBER: 0627.3300001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 378 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-383-750-2

Query Match 49.6%; Score 57; DB 1; Length 378;
Best Local Similarity 54.5%; Pred. No. 0.059;
Matches 12; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 LLKGIYAINFCGMLLLTCISM 22
| : || :||| |||
DB 131 LIFAIYKMSFFSGMLLLCISI 152

RESULT 10
US-08-383-751A-2
Sequence 2, Application US/08383751A
Patent No. 5753516
GENERAL INFORMATION:
APPLICANT: Heagy, Wyrtta E.
APPLICANT: Finberg, Robert W.
TITLE OF INVENTION: Identification and Uses of Opioid
RECEPTORS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: US
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/383.751A
FILING DATE: 03-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: Wilson, Mark B.
REGISTRATION NUMBER: 37,259
REFERENCE/DOCKET NUMBER: DFCI:001/WIM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
TOPOLOGY: linear
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 378 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-383-751A-2

Query Match 49.6%; Score 57; DB 1; Length 378;
Best Local Similarity 54.5%; Pred. No. 0.059;
Matches 12; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 LLKGIYAINFCGMLLLTCISM 22
| : || :||| |||
DB 131 LIFAIYKMSFFSGMLLLCISI 152

RESULT 11

US-08-153-848-15
Sequence 15, Application US/08153848
Patent No. 5759804
GENERAL INFORMATION:
APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schwellart, Vicki L.
TITLE OF INVENTION: No. 5759804el Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Bicknell
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/153.848
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 5759804and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31794
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 378 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-153-848-15

Query Match 49.6%; Score 57; DB 1; Length 378;
Best Local Similarity 54.5%; Pred. No. 0.059;
Matches 12; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 LLKGIYAINFCGMLLLTCISM 22
| : || :||| |||
DB 131 LIFAIYKMSFFSGMLLLCISI 152

RESULT 12
US-08-352-678-2
Sequence 2, Application US/08352678
Patent No. 6043351
GENERAL INFORMATION:
APPLICANT: Birkenbach, Mark
APPLICANT: Kieff, Elliott
TITLE OF INVENTION: EPSTEIN BARR VIRUS INDUCED GENES
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
STREET: 600 Atlantic Avenue
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/352,678
FILING DATE: 30-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/980,518
FILING DATE: 25-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Gates, Edward R.
REGISTRATION NUMBER: 31,616
REFERENCE/DOCKET NUMBER: B0801/7044
TELEPHONE: 617-720-3500
TELEFAX: 617-720-2441
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 378 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-352-678-2

Query Match 49.6%; Score 57; DB 3; Length 378;
Best Local Similarity 54.5%; Pred. No. 0.059;
Matches 12; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 LLKGIYAINFCGMLLLTCISM 22
I: | | : | | | | | | | | | |
Db 131 LFAIYKMSFFSGMLLLCISI 152

RESULT 13

US-09-299-843A-15
Sequence 15, Application US/09299843A
Patent No. 6107475
GENERAL INFORMATION:
APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schweikart, Vicki L.
TITLE OF INVENTION: No. 6107475el Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/299,843A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/088,337
FILING DATE: 01-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/153,848
FILING DATE: 17-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Jill E. Uhl

REGISTRATION NUMBER: 43,213
REFERENCE/DOCKET NUMBER: 27866/32059B
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX:
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 378 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-299-843A-15

Query Match 49.6%; Score 57; DB 3; Length 378;
Best Local Similarity 54.5%; Pred. No. 0.059;
Matches 12; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 LLKGIYAINFCGMLLLTCISM 22
I: | | : | | | | | | | | | |
Db 131 LFAIYKMSFFSGMLLLCISI 152

RESULT 14

US-09-251-545-1
Sequence 1, Application US/09251545
Patent No. 6153441
GENERAL INFORMATION:
APPLICANT: Edward R. Appelbaum
APPLICANT: Henry M. Sarau
APPLICANT: John R. White
TITLE OF INVENTION: METHODS OF SCREENING FOR AGONISTS AND
TITLE OF INVENTION: ANTAGONISTS OF THE INTERACTION BETWEEN HUMAN CCR7 RECEPTOR
TITLE OF INVENTION: AND CK(-9 LIGAND AND INTERACTION THEREOF
FILE REFERENCE: P50753
CURRENT APPLICATION NUMBER: US/09/251,545
CURRENT FILING DATE: 1999-02-17
EARLIER APPLICATION NUMBER: 60/074,883
EARLIER FILING DATE: 1998-02-17
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1
LENGTH: 378
TYPE: PRT
ORGANISM: Human
US-09-251-545-1

Query Match 49.6%; Score 57; DB 4; Length 378;
Best Local Similarity 54.5%; Pred. No. 0.059;
Matches 12; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 LLKGIYAINFCGMLLLTCISM 22
I: | | : | | | | | | | | | |
Db 131 LFAIYKMSFFSGMLLLCISI 152

RESULT 15

PCT-US93-09636-2
Sequence 2, Application PC/TUS9309636
GENERAL INFORMATION:
APPLICANT: Birkenbach, Mark
APPLICANT: Kieff, Elliot
TITLE OF INVENTION: Epstein Barr Virus Induced Genes
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue N.W., Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-3934

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/09636
FILING DATE: herewith
CLASSIFICATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 378 amino acids
TYPE: amino acid
TOPOLOGY: linear
PCT-US93-09636-2

Query Match 49.6%; Score 57; DB 5; Length 378;
Best Local Similarity 54.5%; Pred. No. 0.059;
Matches 12; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 LKGIYAINFCGMMLLTCTISM 22
| : || : || || || || :
Db 131 LIFAIYKMSFFSGMMLLLCISI 152

Search completed: May 23, 2001, 15:30:06
Job time: 413 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 23, 2001, 15:32:00 ; Search time 110.15 Seconds
(without alignments)
13,726 Million cell updates/sec

Title: US-08-887-977-10_COPY_111_132

Perfect score: 115

Sequence: 1 LLKGIYAINFNCGMLLTTCISM 22

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 198801 seqs, 68722935 residues

Total number of hits satisfying chosen parameters: 198801

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR-67.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	115	100.0	369	2 JC5068	G protein-coupled
2	61	53.0	378	2 A55735	G protein-coupled
3	57	49.6	378	2 A55680	G protein-coupled
4	57	49.6	378	2 B55735	lymphocyte-specific
5	56	48.7	354	2 B55733	G protein-coupled
6	55.5	48.3	360	2 G02064	G protein-coupled
7	53	46.1	87	2 B41869	pro-sigma K proces
8	52	45.2	374	2 S32785	G protein-coupled
9	52	45.2	479	1 RDHUU	glutathione reduct
10	51	44.3	327	2 S56162	MDCK15 protein - h
11	51	44.3	372	2 S26667	G protein-coupled
12	51	44.3	373	2 A47556	ATP receptor P2u -
13	51	44.3	375	2 A54946	P-2U nucleotide re
14	51	44.3	466	2 S39494	glutathione reduct
15	50	43.5	350	2 JN0621	G protein-coupled
16	49.5	43.0	350	2 A39445	interleukin-8 rece
17	49.5	43.0	360	2 A53611	interleukin-8 rece
18	49	42.6	318	2 T11857	NADH dehydrogenase
19	49	42.6	318	2 T11363	NADH dehydrogenase
20	49	42.6	354	2 A23669	interleukin-8 rece
21	49	42.6	355	2 J01231	interleukin-8 rece
22	49	42.6	358	2 A53752	interleukin-8 rece
23	49	42.6	374	2 S42628	G protein-coupled
24	49	42.6	1162	2 S07421	E2 glycoprotein pr
25	48	41.7	316	1 VNWRTS	nucleocapsid prote
26	48	41.7	480	2 A82033	TLDP protein homol
27	48	41.7	480	2 F81010	TLDP protein NMB20
28	47	40.9	367	2 J50349	interferon-inducib
29	46.5	40.4	613	2 T27077	hypothetical prote

30	46	40.0	341	2 I57997	hypothetical calci
31	46	40.0	397	2 S66518	proteinase-activat
32	46	40.0	399	2 I48705	proteinase activat
33	46	40.0	485	2 F82718	Tidd protein XF112
34	45	39.1	261	2 F84924	probable thiosulfa
35	45	39.1	300	2 JC5714	G protein-coupled
36	45	39.1	362	2 A39714	G protein-coupled
37	45	39.1	365	2 S68679	G protein-coupled
38	44	38.3	265	2 C72012	CpDiacylglycerol-
39	44	38.3	511	2 T37681	kinesin-like prote
40	44	38.3	533	2 C84706	phosphate permease
41	44	38.3	690	2 T08604	hypothetical prote
42	44	38.3	1162	1 VGIHAK	E2 glycoprotein pr
43	44	38.3	1162	2 S14939	E2 glycoprotein pr
44	44	38.3	1162	2 S14940	E2 glycoprotein pr
45	44	38.3	2052	2 T37711	probable n-end-rec

ALIGNMENTS

RESULT 1

JC5068

G protein-coupled receptor CKR-L3 - human

C:Species: Homo sapiens (man)

C:Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 21-Jul-2000

C:Accession: JC5068

R:Zaballos, A.; Varona, R.; Gutierrez, J.; Lind, P.; Marquez, G.

Biochem. Biophys. Res. Commun. 227, 846-853, 1996

A:Title: Molecular cloning and RNA expression of two new human chemokine receptor-lik

A:Reference number: JC5067; MUID:97040707

A:Accession: JC5068

A:Molecule type: DNA

A:Residues: 1-369 <ZAB>

A:Cross-references: EMBL:Z79784; NID:gl668737; PIDN:CA802144.1; PID:gl668738

C:Comment: This protein belongs to the family of alpha chemokine receptors.

C:Genetics:

A:Gene: GDB:CMKBR6; STRL22; GPR29; CCR6; CKR-L3; GPR-CY4

A:Cross-references: GDB:5370639; OMIM:601835

A:Map position: 6q27-6q27

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor; transmembrane protein

F;42-68/Domain: transmembrane #status predicted <TM1>

F;79-99/Domain: transmembrane #status predicted <TM2>

F;115-136/Domain: transmembrane #status predicted <TM3>

F;160-180/Domain: transmembrane #status predicted <TM4>

F;212-233/Domain: transmembrane #status predicted <TM5>

F;250-271/Domain: transmembrane #status predicted <TM6>

F;292-315/Domain: transmembrane #status predicted <TM7>

Query Match 100.0%; Score 115; DB 2: Length 369;

Best Local Similarity 100.0%; Pred. No. 1e-10;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLKGIYAINFNCGMLLTTCISM 22

Db 115 LLKGIYAINFNCGMLLTTCISM 136

RESULT 2

A55735

G protein-coupled receptor EB11 - mouse

C:Species: Mus musculus (house mouse)

C:Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 24-Nov-1999

C:Accession: A55735

R:Schweickart, V.L.; Raport, C.J.; Godiska, R.; Byers, M.G.; Eddy Jr., R.L.; Shows, T

Genomics 23, 643-650, 1994

A:Title: Cloning of human and mouse EB11, a lymphoid-specific G-protein-coupled recep

A:Reference number: A55735; MUID:95154835

A:Accession: A55735

A>Status: preliminary

A:Molecule type: mRNA

A;Residues: 1-378 <SCH>

A;Cross-references: GB:L31580; NID:g468340; PIDN:AAA74232.1; PID:g468341

C;Superfamily: vertebrate rhodopsin

C;Keywords: G protein-coupled receptor

Query Match 53.0%; Score 61; DB 2; Length 378;
Best Local Similarity 63.2%; Pred. No. 0.04;
Matches 12; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 4 GYAINFNCMLLLTCISM 22

I : : : : :
Db 134 GYKLSFFSGMLLLJCISI 152

RESULT 3

A45680

G protein-coupled peptide receptor EBI 1 - human

C;Species: Homo sapiens (man)

C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 24-Nov-1999

C;Accession: A45680

R;Birkenbach, M.; Josefsen, K.; Yalamanchilli, R.; Lenoir, G.; Kieff, E.

J. Virol. 67, 2209-2220, 1993

A;Title: Epstein-Barr virus-induced genes: first lymphocyte-specific G protein-coupled R

A;Reference number: A45680; MUID:93188173

A;Accession: A45680

A;Status: preliminary

A;Molecule type: nucleic acid

A;Residues: 1-378 <BIK>

A;Cross-references: GB:L08176; NID:g183484; PID:g183485

A;Experimental source: B-lymphocytes

A;Note: sequence extracted from NCBI backbone (NCBIN:127094, NCBI:127095)

C;Superfamily: vertebrate rhodopsin

C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 49.6%; Score 57; DB 2; Length 378;
Best Local Similarity 54.5%; Pred. No. 0.17;
Matches 12; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 1 LLKGIYAINFNCMLLLTCISM 22

I : : : : :
Db 131 LFAYIKMSFFSGMLLLJCISI 152

RESULT 4

B55735

Lymphocyte-specific G protein-coupled receptor EB11 - human

N;Alternate names: Burkitt's lymphoma receptor 2; Epstein-Barr virus induced protein 1

C;Species: Homo sapiens (man)

C;Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 19-May-2000

C;Accession: B55735; S52443

R;Schweickart, V.L.; Raport, C.J.; Godiska, R.; Byers, M.G.; Eddy Jr., R.L.; Shows, T.B.

Genomics 23, 643-650, 1994

A;Title: Cloning of human and mouse EB11, a lymphoid-specific G-protein-coupled receptor

A;Reference number: A55735; MUID:95154835

A;Accession: B55735

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-378 <SCH>

A;Cross-references: GB:L31581; NID:g468319; PIDN:AAA74231.1; PID:g468320

R;Burgstahler, R.; Kempkes, B.; Staube, K.; Lipp, M.

submitted to the EMBL Data Library, February 1995

A;Description: The expression of the chemokine receptor BLR2/EB11 is specifically trans

A;Reference number: S52443

A;Accession: S52443

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 21-378 <BUR>

A;Cross-references: EMBL:X84702

C;Genetics:

A;Gene: GDB:CMKBR7; EB11; BLR2; CCR7

A;Cross-references: GDB:342065; OMIM:600242

A;Map position: 17q12-17q21.2

C;Superfamily: vertebrate rhodopsin

C;Keywords: G protein-coupled receptor

Query Match 49.6%; Score 57; DB 2; Length 378;
Best Local Similarity 54.5%; Pred. No. 0.17;
Matches 12; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 1 LLKGIYAINFNCMLLLTCISM 22

I : : : : :
Db 131 LFAYIKMSFFSGMLLLJCISI 152

RESULT 5

B55733

G protein-coupled receptor GPR2 - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 26-Aug-1999

C;Accession: B55733

R;Marchese, A.; Docherty, J.M.; Nguyen, T.; Heiber, M.; Cheng, R.; Heng, H.H.Q.; Tsui

Genomics 23, 609-618, 1994

A;Title: Cloning of human genes encoding novel G protein-coupled receptors.

A;Reference number: A55733; MUID:95154831

A;Accession: B55733

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-354 <MAR>

A;Cross-references: GB:U13667

C;Genetics:

A;Gene: GDB:GPR2

A;Cross-references: GDB:371708; OMIM:600240

A;Map position: 17q21.1-17q21.3

C;Superfamily: vertebrate rhodopsin

C;Keywords: G protein-coupled receptor

Query Match 48.7%; Score 56; DB 2; Length 354;
Best Local Similarity 45.0%; Pred. No. 0.23;
Matches 9; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

Qy 2 LKGIYAINFNCMLLLTCIS 21

I : : : : :
Db 108 ISGLYSASFHAGFLACIS 127

RESULT 6

G02064

G protein-coupled receptor 15 - human

C;Species: Homo sapiens (man)

C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 24-Nov-1999

C;Accession: G02064

R;O'Dowd, B.F.

submitted to the EMBL Data Library, August 1995

A;Reference number: H00762

A;Accession: G02064

A;Status: preliminary; translated from GB/EMBL/DBDJ

A;Molecule type: DNA

A;Residues: 1-360 <OXD>

A;Cross-references: EMBL:U34806; NID:g1171145; PID:g1171146

C;Genetics:

A;Gene: GDB:GPR15

A;Cross-references: GDB:624476

A;Map position: 3q11.2-3q13.1

C;Superfamily: vertebrate rhodopsin

Query Match 48.3%; Score 55.5; DB 2; Length 360;
Best Local Similarity 44.0%; Pred. No. 0.28;
Matches 11; Conservative 7; Mismatches 4; Indels 3; Gaps 1;

Qy 1 LLKG---IYAINFNCMLLLTCISM 22

I : : : : :
: : : : :
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Db 105 LCKGSSYMISSVNMHCSVLLTCSMV 129

RESULT

B41869
 pro-sigma K processing regulatory protein bofa - *Bacillus subtilis*
 N:Alternate names: bypass-of-forespore A; pro-sigma-K processing machinery inhibitor bofa
 C:Species: *Bacillus subtilis*
 C:Date: 03-May-1994 #sequence-revision 27-Jan-1995 #text_change 15-Oct-1999
 C:Accession: B41869; S13789; S66053; H65955
 J. Bacteriol. 174, 3177-3184, 1992
 A:Title: Characterization of bofa, a gene involved in intercompartmental regulation of P
 A:Reference number: A41869; MUID:92250411
 A:Accession: B41869
 A:Molecule type: DNA
 A:Residues: 1-54, 'G', 56-87 <RIC>
 R:Alonso, J.C.; Shirahige, K.; Ogasawara, N.
 Nucleic Acids Res. 18, 6771-6777, 1990
 A:Title: Molecular cloning, genetic characterization and DNA sequence analysis of the re
 A:Reference number: S13786; MUID:91088245
 A:Accession: S13789
 A:Molecule type: DNA
 A:Residues: 1-87 <ALO>
 A:Cross-references: EMBL:X17014; NID:g453236; PIDN:CAA34880.1; PID:g40075
 R:Ogasawara, N.; Nakai, S.; Yoshikawa, H.
 DNA Res. 1, 1-14, 1994
 A:Title: Systematic sequencing of the 180 kilobase region of the *Bacillus subtilis* chrom
 A:Reference number: S65967; MUID:96051385
 A:Accession: S66053
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-87 <OGA>
 A:Cross-references: EMBL:D26185; NID:g467326; PIDN:BAA05259.1; PID:dl1005801; PID:g467413
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1993
 R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte
 C.: Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch
 A.: Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
 Nature 390, 249-256, 1997
 A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fuma, S.; Galizzi, A.; Gallen
 lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
 Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
 Y, M.; Ogawa, K.; Ogihara, A.; Oudega, B.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maue
 Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon
 A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seron
 akeuchi M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama
 T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.
 A:Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
 A:Title: The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*.
 A:Reference number: A69580; MUID:98044033

A:Accession: H69595
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-87 <KUN>
A:Cross-references: GB:Z99104; GB:AL009126; NID:g2532267; PIDN:CAB11799.1; PID:ell181956;
A:Experimental source: strain 168
C:Comment: By controlling the proteolytic activation of the precursor of sigma factor X, factor G in the forespore.
C:Genetics:
A:Gene: bofA
C:Keywords: sporulation; transmembrane protein

Query Match 46.1%; Score 53; DB 2; Length 87;
Best Local Similarity 52.6%; Pred. No. 0.19;
Matches 10; Conservative 3; Mismatches 6; Indels

QY 4 GIYAINFNCGMLLLTCISM 22

db 31 GITAVKEFVAGALLVCVNM 49

31 GITAVKEVAGALLVCVNM 49

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RESULT

S32785
G protein-coupled receptor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 24-Nov-1999
C:Accession: S32785
E:Kouba, M.; Vanetti, M.; Wang, X.; Schaefer, M.; Hoellt, V.
FEBS Lett. 321, 173-178, 1993
A:Title: Cloning of a novel putative G-protein-coupled receptor (NLR) which
A:Reference number: S32785; MUID:93238948
A:Accession: S32785
A:Molecule type: mRNA
A:Residues: 1-374 <KOD>
A:Cross-references: GB: X71463; GB: S59748; NID: g599926; PIDN: CAA50582.1; PID
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 45.2%; Score 52; DB 2; Length 374;
Best Local Similarity 50.0%; Pred. NO. 1.1;
Matches 9; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 5 IYAINFCGMLLLTCISM 22

21 3 TRAIN NEGATIVE CISH 22
:: ||| | ||| { | ::
Db 130 LHKINFCSSLLDACIAV 147

RESULT

glutathione reductase (NADPH) (EC 1.6.4.2) - human
 C:Species: Homo sapiens (man)
 C:Date: 02-Apr-1982 #sequence_revision 22-Apr-1995 #text_change 11-Jun-1999
 C:Accession: S08979; A00404; S10730
 E:Tutic, M.; Lu, Y.; Schirmer, R.H.; Werner, D.
 Eur. J. Biochem. 188, 523-526, 1990
 A:Title: Cloning and sequencing of mammalian glutathione reductase cDNA.
 A:Reference number: S08979; MUID:90235822
 A:Accession: S08979
 A:Molecule type: mRNA
 A:Residues: 1-479, <num>

R; Krauth-S.

Eur. J. Biochem. 121, 259-267, 1982

A:Title: Glutathione reductase from human erythrocytes. The sequences of the NADPH do

A:Reference number: A91112; MUID:82138780

A:Accession: A00404

A:Molecule type: protein

A:Residues: 2-479 <KRA>

A:Note: this is the final paper in a series

R:Thieme, R.; Pai, E.F.; Schirmer, R.H.; Schulz, G.E.

J. Mol. Biol. 152, 763-782, 1981

A:Title: Three-dimensional structure of glutathione reductase at 2 angstrom resolution

A:Reference number: A92874; MUID:82145544

A:Contents: annotation; X-ray crystallography, 2 angstroms

R:Arnold, H.H.; Heinze, H.

FEBS Lett. 267, 189-192, 1990

A:Title: Treatment of human peripheral lymphocytes with concanavalin A activates expr

A:Reference number: S10730; MUID:90336771

A:Accession: S10730

A:Molecule type: mRNA

A:Residues: 78-96;98-116;118-136;138-156;158-176;178-196;198-216;218-236;238-256;258-

A:Cross-references: GB:X54507; NID:g31828; PIDN:CAA38367.1; PID:g31829

A:Note: in the displayed figure the last codon of the sequence plus amino acid are sk

C:Genetics:

F:23-51/Region: beta-alpha-beta FAD nucleotide-binding fold
 F:25-475/Domain: dihydrolipoamide dehydrogenase homology <DLD>
 F:190-221/Region: beta-alpha-beta NADP nucleotide-binding fold
 F:2/Modified site: acetylated amino end (Ala) (in mature form) #status experimental
 F:59-64/Disulfide bonds: redox-active #status experimental
 F:91/Disulfide bonds: interchain #status experimental
 F:468/Active site: His #status experimental

Query Match 45.2%; Score 52; DB 1; Length 479;
 Best Local Similarity 47.6%; Pred. No. 1.3;
 Matches 10; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 2 LKGIYAINFCGMLLLTCISM 22
 :||||: ||| ||| :||
 Db 324 VKGIYAVGDCGKALLTPVAI 344

RESULT 10

S56162
 MDCR15 protein - human
 C:Species: Homo sapiens (man)
 C:Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 08-Oct-1999
 C:Accession: S56162
 R:Barella, L.; Loetscher, M.; Tobler, A.; Baggiolini, M.; Moser, B.
 Biochem. J. 309, 773-779, 1995
 A:Title: Sequence variation of a novel heptahelical leucocyte receptor through alternati
 A:Reference number: S56162; MUID:93366951
 A:Accession: S56162
 A:Status: preliminary; nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-327 <BAR>
 A:Cross-references: EMBL:X68829; NID:g840783; PIDN:CAA48723.1; PID:g840784
 C:Superfamily: vertebrate rhodopsin

Query Match 44.3%; Score 51; DB 2; Length 327;
 Best Local Similarity 44.4%; Pred. No. 1.4;
 Matches 8; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 5 IYAINFCGMLLLTCISM 22
 :::||| ||| ||| :||
 Db 83 LHKVNFYCSSLLACIAV 100

RESULT 11

S26667
 G protein-coupled receptor BLR1 - human
 C:Species: Homo sapiens (man)
 C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jul-2000
 C:Accession: S26667
 R:Dobner, T.; Wolf, I.; Emrich, T.; Lipp, M.
 Eur. J. Immunol. 22, 2795-2799, 1992
 A:Title: Differentiation-specific expression of a novel G protein-coupled receptor from
 A:Reference number: S26667; MUID:93049615
 A:Accession: S26667
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-372 <DOB>
 A:Cross-references: EMBL:X68149; NID:g29459; PIDN:CAA48252.1; PID:g29460
 C:Genetics:
 A:Gene: GDB:BLR1
 A:Cross-references: GDB:136235; OMIM:601613
 A:Map position: 15q26.1-15q26.1
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 44.3%; Score 51; DB 2; Length 372;
 Best Local Similarity 44.4%; Pred. No. 1.5;
 Matches 8; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 5 IYAINFCGMLLLTCISM 22

Db 128 LHKVNFYCSSLLACIAV 145
 :::||| ||| ||| :||

RESULT 12

A47556
 ATP receptor p2u - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-Sep-1999
 C:Accession: A47556
 R:Lustig, K.D.; Shiau, A.K.; Brake, A.J.; Julius, D.
 Proc. Natl. Acad. Sci. U.S.A. 90, 5113-5117, 1993
 A:Title: Expression cloning of an ATP receptor from mouse neuroblastoma cells.
 A:Reference number: A47556; MUID:93281707
 A:Accession: A47556
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-373 <LUS>
 A:Cross-references: GB:L14751; NID:g309457; PIDN:AAA39871.1; PID:g309458
 C:Superfamily: ATP receptor P2u
 C:Keywords: transmembrane protein

Query Match 44.3%; Score 51; DB 2; Length 373;
 Best Local Similarity 40.9%; Pred. No. 1.5;
 Matches 9; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 LKGIYAINFCGMLLLTCISM 22
 :::||| ||| ||| :||
 Db 108 LVRFLFYTNLYCSILFLTCISV 129

RESULT 13

A54946
 P-2U nucleotide receptor - human
 C:Species: Homo sapiens (man)
 C:Date: 11-Nov-1994 #sequence_revision 11-Nov-1994 #text_change 17-Mar-1999
 C:Accession: A54946
 R:Paar, C.E.; Sullivan, D.M.; Paradiso, A.M.; Lazarowski, E.R.; Burch, L.H.; Olsen, J.
 Proc. Natl. Acad. Sci. U.S.A. 91, 3275-3279, 1994
 A:Title: Cloning and expression of a human P-2U nucleotide receptor, a target for cys
 A:Reference number: A54946; MUID:94211846
 A:Accession: A54946
 A:Status: preliminary
 A:Molecule type: mRNA; protein
 A:Residues: 1-375 <PAR>
 A:Cross-references: GB:U07225
 A:Note: parts of this sequence were confirmed by protein sequencing
 C:Genetics:
 A:Gene: GDB:P2RY2; HP20; P2U
 A:Cross-references: GDB:362713; OMIM:600041
 A:Map position: 11q13.5-11q14.1
 C:Superfamily: ATP receptor P2u
 C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 44.3%; Score 51; DB 2; Length 375;
 Best Local Similarity 40.9%; Pred. No. 1.5;
 Matches 9; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 LKGIYAINFCGMLLLTCISM 22
 :::||| ||| ||| :||
 Db 108 LVRFLFYTNLYCSILFLTCISV 129

RESULT 14

S39494
 glutathione reductase (NADPH) (EC 1.6.4.2) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 22-Jan-1994 #sequence_revision 12-Apr-1996 #text_change 20-Jun-2000
 C:Accession: S39494; S39493
 R:Tutic, M.; Lu, X.; Schirmer, R.H.; Werner, D.
 submitted to the EMBL Data Library, November 1993

Job time: 507 sec

A;Description: Cloning and sequencing of mammalian glutathione reductase cDNA.

A;Reference number: S39494

A;Accession: S39494

A;Molecule type: mRNA

A;Residues: 1-466 <TU1>

A;Cross-references: EMBL:X76341; NID:9433595; PIDN:CAA53959.1; PID:g1334126

R;Tutic, M.; Lu, X.; Schirmer, R.H.; Werner, D.

Eur. J. Biochem. 188, 523-528, 1990

A;Title: Cloning and sequencing of mammalian glutathione reductase cDNA.

A;Reference number: S08979; MUID:90235822

A;Accession: S39493

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 65-306 <TU2>

A;Cross-references: EMBL:X76341

C;Superfamily: dihydrolipoamide dehydrogenase; dihydrolipoamide dehydrogenase homology

C;Keywords: FAD; flavoprotein; NADP; oxidoreductase; redox-active disulfide

F;10-38/Region: beta-alpha-beta FAD nucleotide-binding fold

F;12-462/Domain: dihydrolipoamide dehydrogenase homology <BLD>

F;177-208/Region: beta-alpha-beta NADP nucleotide-binding fold

F;46-51/Disulfide bonds: redox-active #status predicted

F;78/Disulfide bonds: interchain #status predicted

F;455/Active site: His #status predicted

Query Match 44.3%; Score 51; DB 2; Length 466;

Best Local Similarity 42.9%; Pred. No. 1.9;

Matches 9; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

Qy 2 LKGIYAINFNCGMLLLTCTISM 22

Db 311 VKGVYAVGVGCGKALLTPVAI 331

RESULT 15

JN0621

G protein-coupled receptor type B - bovine

C;Species: Bos primigenius taurus (cattle)

C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 19-May-2000

C;Accession: JN0621

R;Matsuoka, I.; Mori, T.; Aoki, J.; Sato, T.; Kurihara, K.

Biochem. Biophys. Res. Commun. 194, 504-511, 1993

A;Title: Identification of novel members of G-protein coupled receptor superfamily expressed

A;Reference number: JN0621; MUID:93326166

A;Accession: JN0621

A;Molecule type: mRNA

A;Residues: 1-350 <MAT>

A;Cross-references: GB:S63848; NID:9399710; PIDN:AAB27547.1; PID:g399711

A;Experimental source: tongue taste papillae

C;Comment: This protein is involved in modulating taste sensitivity or regeneration of taste

C;Superfamily: vertebrate rhodopsin

C;Keywords: G protein-coupled receptor; glycoprotein; receptor; transmembrane protein

F;42-66/Domain: transmembrane #status predicted <TM1>

F;80-99/Domain: transmembrane #status predicted <TM2>

F;114-135/Domain: transmembrane #status predicted <TM3>

F;154-175/Domain: transmembrane #status predicted <TM4>

F;200-222/Domain: transmembrane #status predicted <TM5>

F;242-265/Domain: transmembrane #status predicted <TM6>

F;284-306/Domain: transmembrane #status predicted <TM7>

F;6,19/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 43.5%;

Best Local Similarity 52.9%; Score 50; DB 2; Length 350;

Matches 9; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 5 IYAINFNCGMLLLTCTIS 21

Db 118 LYTQNFVSGMQFLACIS 134

Search completed: May 23, 2001, 15:32:00

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 23, 2001, 15:36:18 ; Search time 62.39 Seconds
(without alignments)

12.079 Million cell updates/sec

Title: US-08-887-977-10_COPY_111_132
Perfect score: 115
Sequence: 1 LKGIYAINFCGMLLITCISM 22

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	115	100.0	374	1 CRR6_HUMAN	P51684 homo sapien
2	102	88.7	367	1 CRR6_MOUSE	O54689 mus musculus
3	67	58.3	342	1 BONZ_CERAE	O18983 cercopithec
4	67	58.3	342	1 BONZ_HUMAN	O00574 homo sapien
5	66	57.4	342	1 BONZ_MACNE	O19024 macaca neme
6	66	57.4	343	1 BONZ_MACMU	O9xt45 macaca mula
7	61	53.0	378	1 CRR7_MOUSE	P47774 mus musculus
8	57	49.6	378	1 CRR7_HUMAN	P32248 homo sapien
9	56	48.7	362	1 CKRA_HUMAN	P46092 homo sapien
10	55.5	48.3	360	1 GPRF_HUMAN	P49685 homo sapien
11	53.5	46.5	360	1 IL8B_BOVIN	O28003 bos taurus
12	53	46.1	87	1 BOFA_BACSU	P24282 bacillus su
13	53	46.1	362	1 CKRA_MOUSE	O9j121 mus musculus
14	52	45.2	374	1 CCR5_RAT	P34997 rattus norv
15	52	45.2	478	1 GSHR_HUMAN	P00390 homo sapien
16	51.5	44.8	360	1 GPRF_CERAE	O18982 cercopithec
17	51.5	44.8	360	1 GPRF_MACMU	O97663 macaca mula
18	51.5	44.8	360	1 GPRF_MACNE	P56412 macaca neme
19	51	44.3	368	1 CCR3_HUMAN	P49682 homo sapien
20	51	44.3	372	1 CCR5_HUMAN	P32302 homo sapien
21	51	44.3	373	1 P2UR_MOUSE	P35383 mus musculus
22	51	44.3	374	1 P2UR_RAT	P41232 rattus norv
23	51	44.3	377	1 P2UR_HUMAN	P41231 homo sapien
24	51	44.3	466	1 GSHR_MOUSE	P47791 mus musculus
25	50	43.5	350	1 GUSB_BOVIN	P33350 bos taurus
26	50	43.5	358	1 GPRK_HUMAN	O99678 homo sapien
27	49.5	43.0	350	1 IL8A_GORGO	P55919 gorilla gor
28	49.5	43.0	350	1 IL8A_HUMAN	P25024 homo sapien
29	49.5	43.0	350	1 IL8A_PANTR	P55920 pan troglod
30	49.5	43.0	353	1 IL8B_GORGO	O28422 gorilla gor
31	49.5	43.0	353	1 IL8B_MACMU	O28519 macaca mula
32	49.5	43.0	353	1 IL8B_PANTR	O28807 pan troglod
33	49.5	43.0	360	1 IL8B_HUMAN	P25025 homo sapien

RESULT 1

ID	CKR6_HUMAN	STANDARD;	PRT;	374 AA.
AC	P51684: Q92846: P78553:			
DT	01-OCT-1996 (Rel. 34, Created)			
DT	15-JUL-1998 (Rel. 36, Last sequence update)			
DT	01-OCT-2000 (Rel. 40, Last annotation update)			
DE	C-C CHEMOKINE RECEPTOR TYPE 6 (C-C CKR-6) (CC-CKR-6) (CCR-6) (LARC RECEPTOR) (GPR-CY4) (GPCY4) (CHEMOKINE RECEPTOR-LIKE 3) (CKR-L3) (DRY6).			
GN	CKR6 OR CMKBR6 OR STRL22 OR GPR29 OR CRL3.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A., AND FUNCTION.			
RX	MEDLINE-97313465; PubMed-9169459;			
RA	Baba M., Inai T., Nishimura M., Kakizaki M., Takagi S., Hieshima K.,			
RA	Nomiyama H., Yoshie O.;			
RT	"Identification of CKR6, the specific receptor for a novel lymphocyte-directed CC chemokine LARC."			
RL	J. Biol. Chem. 272:14893-14898(1997).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	Lautens L.L., Modi W., Bonner T.I.;			
RL	Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE-97040707; PubMed-8886020;			
RA	Zaballos A., Varona R., Gutierrez J., Lind P., Marquez G.;			
RT	"Molecular cloning and RNA expression of two new human chemokine receptor-like genes."			
RL	Biochem. Biophys. Res. Commun. 227:846-853(1996).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RA	McCoy R., Perlmuter D.H.;			
RL	Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE-97224503; PubMed-9070937;			
RA	Liao F., Lee H.-H., Farber J.M.;			
RT	"Cloning of STRL22, a new human gene encoding a G-protein-coupled receptor related to chemokine receptors and located on chromosome 6q27."			
RL	Genomics 40:175-180(1997).			
CC	-!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-3-ALPHA/LARC AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.			
CC	-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.			
CC	-!- TISSUE SPECIFICITY: SPLEEN, LYMPH NODES, APPENDIX, AND FETAL LIVER. EXPRESSED IN LYMPHOCYTES, T CELLS AND B CELLS BUT NOT IN NATURAL KILLER CELLS, MONOCYTES, OR GRANULOCYTES.			
CC	-!- INDUCTION: INTERLEUKIN-2.			
CC	-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.			
CC	-!- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-6 IS THE INITIATOR.			

p92475 equus asinu
p48652 equus cabal
p21109 oryctolagus
p35344 oryctolagus
q04683 mus musculus
p12651 avian infec
p70612 rattus norv
p27207 maize strip
o88410 mus musculus
o81305 drosophila
q06138 mus musculus
p55085 homo sapien

1 NULM_EQUAS
1 NULM_HORSE
1 IL8A_RABIT
1 IL8B_RABIT
1 CCR3_MOUSE
1 VGL2_IBVM
1 IL8A_RAT
1 COAT_MSTV
1 CCR3_MOUSE
1 DB80_DROME
1 MO25_MOUSE
1 PAR2_HUMAN

ALIGNMENTS

34 49 42.6 318 1
35 49 42.6 318 1
36 49 42.6 355 1
37 49 42.6 358 1
38 49 42.6 374 1
39 49 42.6 1162 1
40 48.5 42.2 349 1
41 48 41.7 316 1
42 47 40.5 367 1
43 47 40.5 460 1
44 46 40.0 341 1
45 46 40.0 397 1


```

RESULT 3
BONZ_CERA 3
ID BONZ_CERA STANDARD; PRT; 342 AA.
AC O18983;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE G PROTEIN-COUPLED RECEPTOR BONZO
GN BONZO.
OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9534;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97373958; PubMed=9230441;
RA Deng H.K., Unutmaz D., Kewalramani V.N., Littman D.R.;
RT "Expression cloning of new receptors used by simian and human
RT immunodeficiency viruses.";
RL Nature 388:296-300(1997).
CC -1- FUNCTION: ORPHAN RECEPTOR. COULD BE A CHEMOKINE RECEPTOR. USED AS
CC A CORECEPTOR BY SIVS AND BY STRAINS OF HIV-2 AND M-TROPIC HIV-1.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CC -----
DR EMBL; AF007859; AAB64225.1; -
DR GCRDB; GCR_2411; -
DR InterPro; IPR000276; -
DR InterPro; IPR002235; -
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOOPS.
DR PRINTS; PR01105; BONZOORPHANR.
DR PROSITE; PS00237; G-PROTEIN_RECP_FL_1; 1.
DR PROSITE; PS02362; G-PROTEIN_RECP_FL_2; 1.
DR G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 32
FT EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 33 59
FT DOMAIN 60 68
FT CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 69 89
FT DOMAIN 90 103
FT EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 104 125
FT CYTOPLASMIC (POTENTIAL).
FT DOMAIN 126 143
FT TRANSMEM 144 164
FT DOMAIN 165 187
FT EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 188 215
FT CYTOPLASMIC (POTENTIAL).
FT DOMAIN 216 231
FT CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 232 259
FT DOMAIN 260 275
FT EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 276 293
FT DOMAIN 294 342
FT CYTOPLASMIC (POTENTIAL).
FT DISULFID 102 180
FT BY SIMILARITY.
FT CARBOHYD 16 16
FT N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 342 AA; 39226 MW; 6CBFE389C6E5919E CRC64;

Query Match 58.3%; Score 67; DB 1; Length 342;
Best Local Similarity 61.9%; Pred. No. 0.003;
Matches 13; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Oy 2 LKGIYAINFCGMLLLTCISM 22
| ||| ||| ||| ||| |||
Db 105 LIGIVTINFTSMILITCIV 125

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RESULT 4
BONZ_HUMAN 4
ID BONZ_HUMAN STANDARD; PRT; 342 AA.
AC O00574; O00575;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE G PROTEIN-COUPLED RECEPTOR BONZO (G PROTEIN-COUPLED RECEPTOR STRL33).
GN BONZO OR STRL33 OR TYMSTR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97373958; PubMed=9230441;
RA Deng H.K., Unutmaz D., Kewalramani V.N., Littman D.R.;
RT "Expression cloning of new receptors used by simian and human
RT immunodeficiency viruses.";
RL Nature 388:296-300(1997).
CC [2]
CC SEQUENCE FROM N.A.
RX MEDLINE=97311099; PubMed=9166430;
RA Liao F., Alkhatib G., Peden K.W.C., Sharma G., Berger E.A.,
RA Farber J.M.;
RT "STRL33, A novel chemokine receptor-like protein, functions as a
RT fusion cofactor for both macrophage-tropic and T cell line-tropic
RT HIV-1.";
RL J. Exp. Med. 185:2015-2023(1997).
CC [3]
CC SEQUENCE FROM N.A.
RX MEDLINE=97431687; PubMed=9285716;
RA Loetscher M., Amara A., Oberlin E., Brass N., Legler D.F.,
RA Loetscher P., D'Apuzzo M., Meese E.U., Rousset D., Virelizier J.L.,
RA Baggiolini M., Arenzana-Seisdedos F., Moser B.;
RT "TYMSTR, a putative chemokine receptor selectively expressed in
RT activated T cells, exhibits HIV-1 coreceptor function.";
RL Curr. Biol. 7:652-660(1997).
CC -1- FUNCTION: ORPHAN RECEPTOR. COULD BE A CHEMOKINE RECEPTOR. USED AS
CC A CORECEPTOR BY SIVS AND BY STRAINS OF HIV-2 AND M-TROPIC HIV-1.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN LYMPHOID TISSUES AND ACTIVATED T
CC CELLS.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CC -----
DR EMBL; AF007545; AAB64221.1; -
DR EMBL; U73529; AAB61456.1; -
DR EMBL; U73531; AAB61457.1; -
DR EMBL; Y13248; CAA73698.1; -
DR MIM; 605163; -
DR GCRDB; GCR_1328; -
DR GCRDB; GCR_1330; -
DR GCRDB; GCR_2393; -
DR InterPro; IPR000276; -
DR InterPro; IPR002235; -
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOOPS.
DR PRINTS; PR01105; BONZOORPHANR.
DR PROSITE; PS00237; G-PROTEIN_RECP_FL_1; 1.
DR PROSITE; PS02362; G-PROTEIN_RECP_FL_2; 1.
DR G-protein coupled receptor; Transmembrane; Glycoprotein; Polymorphism.
FT DOMAIN 1 32
FT EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 33 59

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-----CC
EMBL; AF007858; AAB64224.1; -.
GCRdb; GCR_2409; -.
InterPro; IPR000276; -.
InterPro; IPR002235; -.
Pfam; PF00001; 7tm_1; 1.
PRINTS; P00237; GPCRHHODOPSN.
PRINTS; PR01105; BONZOORPHANK.
PROSITE; PS00237; G_PROTEIN_REC_F1_1; 1.
PROSITE; PS00362; G_PROTEIN_REC_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein.
KW

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 CC -----
 CC EMBL; AF124380; AAD31419.1; -
 CC InterPro; IPR000276; -
 CC InterPro; IPR002235; -
 CC Pfam; PF00001; 7tm.1. 1
 CC PRINTS; PR00237; GCR8RHODOPSIN.
 CC PRINTS; PR01105; BONZOORPHAN.
 CC PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 CC PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
 CC G-protein coupled receptor; Transmembrane; Glycoprotein.
 CC DOMAIN 1 33 EXTRACELLULAR (POTENTIAL).
 CC TRANSMEM 34 60 1 (POTENTIAL).
 CC FT
 CC FT

G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
 POTENTIAL.
 CHAIN 1 24
 FT SIGNAL 25 378
 FT DOMAIN 25 59
 FT TRANSMEM 60 86
 FT DOMAIN 87 95
 FT TRANSMEM 96 116
 FT DOMAIN 117 130
 FT TRANSMEM 131 152
 FT DOMAIN 153 170
 FT TRANSMEM 171 191
 FT DOMAIN 192 219
 FT TRANSMEM 220 247
 FT DOMAIN 248 263
 FT TRANSMEM 264 289
 FT DOMAIN 290 313
 FT TRANSMEM 314 331
 FT DOMAIN 332 378
 FT CARBOHYD 36 36
 FT DISULFID 129 210
 SQ SEQUENCE 378 AA; 42941 MW; ACBIA422CF54AA54 CRC64;

Query Match 53.0%; Score 61; DB 1; Length 378;
 Best Local Similarity 63.2%; Pred. No. 0.028;
 Matches 12; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 4 GIYAINFCGMLLLTCISM 22
 III : : I I I I I I I I
 Db 134 GIYKLSFFSGMLLLCISI 152

RESULT 8
 CKR7_HUMAN
 ID CKR7_HUMAN STANDARD; PRT; 378 AA.
 AC P32248;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE C-C CHEMOKINE RECEPTOR TYPE 7 PRECURSOR (C-C CKR-7) (CCR-7)
 DE (MIP-3 BETA RECEPTOR) (EBV-INDUCED G PROTEIN-COUPLED RECEPTOR 1)
 DE (EB1) (BLR2).
 DE CKR7 OR CMKBR7 OR EB1L OR EVIL.
 OS Homo sapiens (Human).
 OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RP MEDLINE=93188173; PubMed=8383238;
 RA Birkenbach M.P., Josefsen K., Yalamanchili R.R., Lenoir G.M.,
 RA Elliott K.;
 RA "Epstein-Barr virus-induced genes: first lymphocyte-specific G
 RT protein-coupled peptide receptors.";
 RL J. Virol. 67:2209-2220(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RP TISSUE=Placenta;
 RX MEDLINE=95154835; PubMed=7851893;
 RA Schweickart V.L., Raport C.J., Godiska R., Byers M.G., Eddy R.L. Jr.,
 RA Shows T.B., Gray P.W.;
 RT "Cloning of human and mouse EB1, a lymphoid-specific
 RT G-protein-coupled receptor encoded on human chromosome 17q12-q21.2.";
 RL Genomics 23:643-650(1994).
 CC -1- FUNCTION: RECEPTOR FOR THE MIP-3-BETA CHEMOKINE. PROBABLE MEDIATOR
 CC OF EBV EFFECTS ON B LYMPHOCYTES OR OF NORMAL LYMPHOCYTE FUNCTIONS.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN VARIOUS LYMPHOID TISSUES AND
 CC ACTIVATED B AND T LYMPHOCYTES, STRONGLY UPREGULATED IN B CELLS
 CC INFECTED WITH EPSTEIN-BARR VIRUS AND T CELLS INFECTED WITH
 CC HERPESVIRUS 6 OR 7.
 CC -1- INDUCTION: BY EBV.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

CC	EMBL; U34806; AAC50826.1; -
DR	GCRDB; GCR_1962; -
DR	MIM; 601166; -
DR	Interpro: IPR000276; -
DR	Pfam: PF00001; 7tm.1; 1.
DR	PRINTS; PR00237; GCRRHADOPSN.
DR	PROSITE; PS00237; G PROTEIN RECEPTOR.
DR	PROSITE; PS00237; G PROTEIN RECEPTOR.

DR PRINTS; PR00427; INTRLEUKIN8R.

DR PROSITE; PS50262; G_PROTEIN_RECEPTOR_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 Chemotaxis.
 FT DOMAIN 1 48 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 49 75 1 (POTENTIAL).
 FT DOMAIN 76 84 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 85 105 2 (POTENTIAL).
 FT DOMAIN 106 120 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 121 142 3 (POTENTIAL).
 FT DOMAIN 143 163 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 164 183 4 (POTENTIAL).
 FT DOMAIN 184 208 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 209 231 5 (POTENTIAL).
 FT DOMAIN 232 251 6 (POTENTIAL).
 FT TRANSMEM 252 273 6 (POTENTIAL).
 FT DOMAIN 274 294 7 (POTENTIAL).
 FT TRANSMEM 295 316 7 (POTENTIAL).
 FT DOMAIN 316 360 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 119 196 BY SIMILARITY.
 FT CARBOHYD 10 10 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 24 24 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 360 AA; 40625 MW; 9A7F70C982A632D1 CRC64;

Query Match 46.5%; Score 53.5; DB 1; Length 360;
 Best Local Similarity 59.1%; Pred. No. 0.39;
 Matches 13; Conservative 2; Mismatches 4; Indels 3; Gaps 1;

OY 1 LKGIYAINFCGMLLLTICISM 22
 ||| :|| :||| ||||
 Db 124 LK---EVNFYSGILLACISM 142

RESULT 12
 BOFA_BACSU STANDARD; PRT; 87 AA.
 ID BOFA_BACSU STANDARD; PRT; 87 AA.
 AC P24282;
 DT 01-MAR-1992 (Rel. 21, Created)
 DT 01-MAR-1992 (Rel. 21, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE SIGMA-K FACTOR PROCESSING REGULATORY PROTEIN BOFA (BYPASS-OF-FORESPORE
 DE PROTEIN A).
 GN BOFA.
 OS Bacillus subtilis.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;
 OC Bacillus/Staphylococcus group; Bacillus.
 OX NCBI_TaxID=1423;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91088245; PubMed=2124672;
 RA Alonso C., Shirahige K., Ogasawara N.;
 RT "Molecular cloning, genetic characterization and DNA sequence
 RL analysis of the recM region of Bacillus subtilis.";
 RL Nucleic Acids Res. 18:6771-6777(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX STRAIN=168;
 RC MEDLINE=96051385; PubMed=7584024;
 RA Ogasawara N., Nakai S., Yoshikawa H.;
 RT "Systematic sequencing of the 180 kilobase region of the Bacillus
 RL subtilis chromosome containing the replication origin.";
 RL DNA Res. 1:1-14(1994).
 RN [3]
 RP CHARACTERIZATION.
 RX MEDLINE=92250411; PubMed=1577688;
 RA Ricca E., Cutting S.M., Losick R.;
 RT "Characterization of bofa, a gene involved in intercompartmental
 RL regulation of pro-sigma K processing during sporulation in Bacillus
 RL subtilis.";
 RL J. Bacteriol. 174:3177-3184(1992).
 RN [4]
 RP TOPOLOGY.
 RX MEDLINE=97286525; PubMed=9141672;

RA Varcamonti M., Marasco R., de Felice M., Sacco M.;
 RT "Membrane topology analysis of the Bacillus subtilis BofA protein
 RL involved in pro-sigma K processing.";
 RL Microbiology 143:1053-1058(1997).
 CC -!- FUNCTION: INVOLVED IN THE MEDIATION OF THE INTERCOMPARTMENTAL
 CC COUPLING OF PRO-SIGMA K PROCESSING TO EVENTS IN THE FORESPORE.
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -----
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 CC -----
 CC EMBL; X17014; CAA34880.1; -
 DR EMBL; D26185; BAA05259.1; -
 DR EMBL; Z99104; CAB11799.1; -
 DR PIR; S13789; S13789.
 DR PIR; B41869; B41869.
 DR Subtilist; BGI0087; bofa.
 KW Sporulation; Transmembrane.
 FT DOMAIN 1 2 EXTRACELLULAR (PROBABLE).
 FT TRANSMEM 3 23 PROBABLE.
 FT DOMAIN 24 36 CYTOPLASMIC (PROBABLE).
 FT TRANSMEM 37 57 PROBABLE.
 FT DOMAIN 58 87 EXTRACELLULAR (PROBABLE).
 FT SEQUENCE 87 AA; 9010 MW; FF1DA14E6826B70E CRC64;

Query Match 46.1%; Score 53; DB 1; Length 87;
 Best Local Similarity 52.6%; Pred. No. 0.13;
 Matches 10; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

OY 4 GIYAINFCGMLLLTICISM 22
 ||| :|| :||| ||||
 Db 31 GITAVKEVAGALLVCVNM 49

RESULT 13

CKRA_MOUSE STANDARD; PRT; 362 AA.
 ID CKRA_MOUSE STANDARD; PRT; 362 AA.
 AC Q9JL21; Q9JL20; Q9JIP1;
 DT 01-OCT-2000 (Rel. 40, Created)
 DT 01-OCT-2000 (Rel. 40, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE C-C CHEMOKINE RECEPTOR TYPE 10 (C-C CKR-10) (CC-CCR-10) (CCR-10)
 DE (CHEMOKINE C-C RECEPTOR 9) (G-PROTEIN COUPLED RECEPTOR 2).
 GN CCR10 OR CMKBR9 OR GPR2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.; AND CHARACTERIZATION.
 RX STRAIN=BALB/C; TISSUE=Peyer's patch;
 RX MEDLINE=20191997; PubMed=10725696;
 RA Jarmin D.I., Rits M., Bota D., Gerard N.P., Graham G.J.,
 RA Clark-Lewis I., Gerard C.;
 RT "Cutting edge: Identification of the orphan receptor G-protein-coupled
 RL receptor 2 as CCR10, a specific receptor for the chemokine ESKine.";
 RL J. Immunol. 164:3460-3464(2000).
 RN [2]
 RP SEQUENCE FROM N.A.; TISSUE SPECIFICITY, AND LIGAND BINDING.
 RX TISSUE=Thymocytes;
 RX MEDLINE=20357357; PubMed=10781587;
 RA Wang W., Soto H., Oldham E.R., Buchanan M.E., Homey B., Catron D.,
 RA Jenkins N., Copeland N.G., Gilbert D.J., Nguyen N., Abrams J.,
 RA Kershenovich D., Smith K., McClanahan T., Vicari A.P., Zlotnik A.;
 RT "Identification of a novel chemokine (CCL28), which binds CCR10
 RL (GPR2).";
 RL J. Biol. Chem. 275:22313-22323(2000).

```

CC -1- FUNCTION: RECEPTOR FOR CHEMOKINES SCYA27 AND SCYA28. SUBSEQUENTLY
CC TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS
CC LEVEL.
CC
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC
CC -1- TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVELS IN SMALL INTESTINE,
CC COLON, LYMPH NODES, PEYER'S PATCHES AND AT LOWER LEVELS IN THYMUS,
CC LUNG, AND SPLEEN.
CC
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AF215982; AAF63710.1; -
CC DR EMBL: AF215983; AAF63711.1; -
CC DR EMBL: AF208238; AAF72872.1; -
CC DR MGD: MGI:1096320; Cmkbr9.
CC DR PROSITE: PS00237; G.PROTEIN.RECEP_FL1; 1.
CC DR PROSITE: PS50262; G.PROTEIN.RECEP_FL2; 1.
CC KW G-protein coupled receptor; Transmembrane; Glycoprotein.
CC FT DOMAIN 1 48
CC FT TRANSMEM 49 69
CC FT DOMAIN 70 80
CC FT TRANSMEM 81 101
CC FT DOMAIN 102 115
CC FT TRANSMEM 116 136
CC FT DOMAIN 137 159
CC FT TRANSMEM 160 180
CC FT DOMAIN 181 208
CC FT TRANSMEM 209 229
CC FT DOMAIN 230 247
CC FT TRANSMEM 248 268
CC FT DOMAIN 269 291
CC FT TRANSMEM 292 312
CC FT DOMAIN 313 362
CC FT DISULFID 113 191
CC FT CONFLICT 135 135
CC SQ SEQUENCE 362 AA; 38926 MW; 0FF4EA2005B94E99 CRC64;
CC
CC Query Match 46.1%; Score 53; DB 1; Length 362;
CC Best Local Similarity 40.0%; Pred. No. 0.47;
CC Matches 8; Conservative 6; Mismatches 6; Indels 0; Gaps 0;
CC
CC QY 2 LKGIYAINFNGCMLLLRCS 21
CC : 1:1: :: 1:1: ||:
CC
CC Db 116 ISGLYSASFHAGFLFLACIN 135
CC
CC RESULT 14
CC CCR5_RAT
CC ID CCR5_RAT STANDARD; PRT; 374 AA.
CC AC P34997;
CC DT 01-FEB-1994 (Rel. 28, Created)
CC DT 01-FEB-1994 (Rel. 28, Last sequence update)
CC DT 30-MAY-2000 (Rel. 39, Last annotation update)
CC DE C-X-C CHEMOKINE RECEPTOR TYPE 5 (CXCR-5) (CXCR-5) (BURKITT'S LYMPHOMA
CC DE RECEPTOR 1 HOMOLOG) (NEUROLYMPHATIC RECEPTOR) (NLR).
CC GN BLR1 OR CXCR5.
CC OS Rattus norvegicus (Rat).
CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
CC ON NCBI_TaxID=10116;
CC RX [1]
CC SEQUENCE FROM N.A.
CC PC TISSUE=Spleen;
CC RX MEDLINE=33238948; PubMed=83866678;
CC RA Kouba M., Vanetti M., Wang X., Schaefer M., Hoeltt V.;
CC RT "Cloning of a novel putative G-protein-coupled receptor (NLR) which

```

RX MEDLINE=90235822; PubMed=2185014;
 RA Tutic M., Lu X.A., Schirmer R.H., Werner D.;
 RT "Cloning and sequencing of mammalian glutathione reductase cDNA.";
 RL Eur. J. Biochem. 188:523-528(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=20175207; PubMed=10708558;
 RX Kelnner M.J., Montoya M.A.;
 RT "Structural organization of the human glutathione reductase (GSR)
 gene: determination of correct cDNA sequence and identification of a
 mitochondrial leader sequence.";
 RL Biochem. Biophys. Res. Commun. 269:366-368(2000).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Reichwald K., Blechschmidt K., Schilhabel M., Baumgart C., Menzel U.,
 RA Dette M., Jahn N., Korenberg J.R., Schlegelberger B., Rosenthal A.;
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE.
 RA MEDLINE=82138780; PubMed=7060551;
 RX Krauth-Siegel R.L., Blatterspiel R., Saleh M., Schiltz E.,
 RA Schirmer R.H., Untucht-Grau R.;
 RT "Glutathione reductase from human erythrocytes. The sequences of the
 NADPH domain and of the interface domain.";
 RL Eur. J. Biochem. 121:259-267(1982).
 RN [5]
 RP SEQUENCE OF 54-66.
 RC TISSUE=Erythrocyte;
 RX MEDLINE=78043204; PubMed=923580;
 RA Krohne-Ehrich G., Schirmer R.H., Untucht-Grau R.;
 RT "Glutathione reductase from human erythrocytes. Isolation of the
 enzyme and sequence analysis of the redox-active peptide.";
 RL Eur. J. Biochem. 80:65-71(1977).
 RN [6]
 RP X-RAY CRYSTALLOGRAPHY (2 ANGSTROMS).
 RX MEDLINE=82145544; PubMed=7334521;
 RA Thieme R., Pai E.F., Schirmer R.H., Schulz G.E.;
 RT "Three-dimensional structure of glutathione reductase at 2-A
 resolution.";
 RL J. Mol. Biol. 152:763-782(1981).
 RN [7]
 RP X-RAY CRYSTALLOGRAPHY (1.57 ANGSTROMS).
 RX MEDLINE=88011277; PubMed=3656429;
 RA Karplus P.A., Schulz G.E.;
 RT "Refined structure of glutathione reductase at 1.54-A resolution.";
 RL J. Mol. Biol. 195:701-729(1987).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS) OF 18-478.
 RX MEDLINE=98206290; PubMed=9546215;
 RA Becker K., Savvides S.N., Keese M., Schirmer R.H., Karplus P.A.;
 RT "Enzyme inactivation through sulphydryl oxidation by physiologic NO-
 carriers.";
 RL Nat. Struct. Biol. 5:267-271(1998).
 CC -!- FUNCTION: MAINTAIN HIGH LEVELS OF REDUCED GLUTATHIONE IN THE
 CYTOSOL.
 CC -!- CATALYTIC ACTIVITY: NADPH + OXIDIZED GLUTATHIONE = NADP(+) +
 2 GLUTATHIONE.
 CC -!- COFACTOR: FAD.
 CC -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED.
 CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -!- DOMAIN: EACH SUBUNIT CAN BE DIVIDED INTO 4 DOMAINS THAT ARE
 CONSECUTIVE ALONG THE POLYPEPTIDE CHAIN. DOMAINS 1 & 2 BIND FAD
 AND NADPH, RESPECTIVELY. DOMAIN 4 FORMS THE INTERFACE.
 CC -!- MISCELLANEOUS: THE ACTIVE SITE IS A REDOX-ACTIVE DISULFIDE BOND.
 CC -!- SIMILARITY: BELONGS TO THE PYRIDINE NUCLEOTIDE-DISULFIDE
 OXIDOREDUCTASES CLASS-I.
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 DR EMBL; X15722; CAA33744.1; -
 DR EMBL; AF228703; AAF37573.1; -
 DR EMBL; AF215848; AAF20007.1; -
 DR PIR; A00404; RDHUU.
 DR PIR; S08979; S08979.
 DR PDB; 4GR1; 31-JUL-94.
 DR PDB; 1GRA; 31-JAN-94.
 DR PDB; 1GRE; 31-JAN-94.
 DR PDB; 1GRE; 31-JAN-94.
 DR PDB; 1GRF; 31-JAN-94.
 DR PDB; 1GRG; 31-JAN-94.
 DR PDB; 1GRH; 31-JAN-94.
 DR PDB; 3GRS; 16-APR-88.
 DR PDB; 1GRT; 16-JUN-97.
 DR PDB; 2GRT; 12-AUG-97.
 DR PDB; 3GRT; 12-AUG-97.
 DR PDB; 4GRT; 12-AUG-97.
 DR PDB; 5GRT; 12-AUG-97.
 DR PDB; 1ALG; 15-OCT-97.
 DR PDB; 1XAN; 11-JUL-96.
 DR PDB; 1DNC; 27-MAY-98.
 DR PDB; 1GSN; 27-MAY-98.
 DR MIM; 138300; -
 DR InterPro; IPR001100; -
 DR InterPro; IPR001327; -
 DR Pfam; PF00070; PYR_redox; 1.
 DR PRINTS; PR00368; FADPNR.
 DR PRINTS; PR00411; PNDROTASEI.
 DR PROSITE; PS00076; PYRIDINE_REDOX_1; 1.
 KW Redox-active center; Oxidoreductase; Flavoprotein; FAD; NADP;
 KW Acetylation; 3D-structure.
 FT INIT_MET 0 0
 FT MOD_RES 1 1 ACETYLATION.
 FT NP_BIND 22 52 FAD (ADP PART) (PROBABLE).
 FT DISULFID 58 63 REDOX-ACTIVE.
 FT DISULFID 90 90 INTERCHAIN (WITH DIMER).
 FT NP_BIND 321 331 FAD (FLAVIN PART) (BY SIMILARITY).
 FT ACT_SITE 467 467
 FT STRAND 19 20
 FT STRAND 23 26
 FT HELIX 30 41
 FT TURN 42 43
 FT TURN 46 50
 FT TURN 54 55
 FT HELIX 56 61
 FT HELIX 63 80
 FT TURN 81 82
 FT HELIX 83 85
 FT TURN 86 86
 FT HELIX 96 120
 FT TURN 121 122
 FT STRAND 124 127
 FT STRAND 131 132
 FT STRAND 139 142
 FT TURN 143 144
 FT STRAND 145 148
 FT STRAND 152 154
 FT STRAND 158 160
 FT TURN 165 167
 FT TURN 169 170
 FT HELIX 171 173
 FT STRAND 175 175
 FT HELIX 177 180
 FT TURN 181 182
 FT STRAND 189 193
 FT HELIX 197 208
 FT TURN 209 210
 FT STRAND 212 216
 FT TURN 224 225
 FT HELIX 228 240
 FT TURN 241 242

FT	STRAND	244	246
FT	TURN	247	248
FT	STRAND	249	257
FT	TURN	258	259
FT	STRAND	260	267
FT	TURN	270	271
FT	STRAND	275	282
FT	STRAND	284	287
FT	STRAND	291	293
FT	TURN	296	299
FT	TURN	300	302
FT	TURN	303	304
FT	STRAND	307	307
FT	TURN	309	310
FT	STRAND	313	313
FT	TURN	317	318
FT	STRAND	320	320
FT	TURN	324	325
FT	STRAND	326	328
FT	TURN	330	333
FT	TURN	334	334
FT	TURN	339	354
FT	TURN	358	359
FT	TURN	365	366
FT	STRAND	369	371
FT	STRAND	377	381
FT	TURN	384	391
FT	TURN	393	395
FT	STRAND	396	403
FT	TURN	406	410
FT	STRAND	417	424
FT	TURN	425	428
FT	STRAND	429	436
FT	TURN	438	439
FT	TURN	440	452
FT	TURN	453	454
FT	STRAND	456	456
FT	TURN	457	461
FT	TURN	462	462
FT	TURN	471	475

Query Match 45.2%; Score 52; DB 1; Length 478;
Best Local Similarity 47.6%; Pred. No. 0.86;
Matches 10; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

Qy 2 LKGIYAINFCGMLLTICISM 22
Db 323 VKGIYAVGDCGKALLTPVAI 343

Search completed: May 23, 2001, 15:36:18
Job time: 649 sec

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OM protein - protein search, using sw model

Run on: May 23, 2001, 15:35:13 ; Search time 189.03 Seconds
(without alignments)
13.641 Million cell updates/sec

Title: US-08-887-977-10_COPY_111_132
Perfect score: 115
Sequence: 1 LLKGIYAINFCGMLLTICISM 22

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: SPTEMBL_15:*
- 2: sp_archaea:*
- 3: sp_bacteria:*
- 4: sp_fungi:*
- 5: sp_human:*
- 6: sp_invertebrate:*
- 7: sp_mammal:*
- 8: sp_mhc:*
- 9: sp_organelle:*
- 10: sp_phase:*
- 11: sp_plant:*
- 12: sp_rodent:*
- 13: sp_unclassified:*
- 14: sp_vertebrate:*
- 15: sp_virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	102	88.7	367	11	Q9R1V0
2	67	58.3	342	6	Q9TV16
3	66	57.4	343	6	Q9XT45
4	66	57.4	343	6	Q9N020
5	64	55.7	378	11	Q08707
6	63	54.8	382	11	Q09027
7	58	50.4	368	13	Q42444
8	56	48.7	361	4	Q9N2G2
9	56	48.7	362	11	Q9J1P1
10	53	46.1	360	11	Q9J1L2
11	53	46.1	362	11	Q9J1L2
12	52	45.2	522	4	Q9NP63
13	51.5	44.8	360	6	Q97663
14	51.5	44.8	360	6	Q9TV17
15	51	44.3	350	4	Q9NPB9
16	51	44.3	415	4	O15185
17	51	44.3	420	11	P70619
18	50	43.5	353	11	O35797
19	49.5	43.0	111	4	Q9P2T7

20	49	42.6	384	4	O00537	000537 homo sapien
21	49	42.6	384	4	O00590	000590 homo sapien
22	49	42.6	553	14	Q9Q3F4	Q9Q3F4 avian infec
23	49	42.6	553	14	Q9IWU9	Q9IWU9 avian infec
24	49	42.6	1153	14	O66178	Q66178 avian infec
25	48	41.7	342	13	O93239	Q93239 cyprinus ca
26	48	41.7	480	2	Q9JXG0	Q9JXG0 neisseria m
27	48	41.7	480	2	Q9JWH8	Q9JWH8 neisseria m
28	47	40.9	367	11	O88410	O88410 mus musculu
29	47	40.9	367	11	Q9QWN6	Q9QWN6 mus musculu
30	47	40.9	367	11	Q9J1I9	Q9J1I9 rattus norv
31	46.5	40.4	613	5	Q9XXQ9	Q9XXQ9 caenorhabdi
32	46	40.0	216	10	Q9LUB4	Q9LUB4 arabidopsis
33	46	40.0	337	11	Q9QX13	Q9QX13 rattus norv
34	46	40.0	341	4	Q9Y376	Q9Y376 homo sapien
35	46	40.0	485	2	Q9PEA1	Q9PEA1 xylella fas
36	46	40.0	1061	5	O96998	O96998 leishmania
37	46	40.0	1090	10	Q9LQK8	Q9LQK8 arabidopsis
38	45	39.1	361	11	O35811	O35811 rattus norv
39	45	39.1	361	11	Q9JJS7	Q9JJS7 mus musculu
40	45	39.1	452	5	O25631	O25631 onchocerca
41	45	39.1	462	5	O01412	O01412 onchocerca
42	45	39.1	552	14	Q9Q6Q7	Q9Q6Q7 avian infec
43	44.5	38.7	115	8	Q9MJJ4	Q9MJJ4 carabus gen
44	44.5	38.7	246	10	Q9ZQP8	Q9ZQP8 arabidopsis
45	44	38.3	265	2	Q9Z6S6	Q9Z6S6 chlamydia p

ALIGNMENTS

RESULT	1				
Q9R1V0					
ID	Q9R1V0	PRELIMINARY;	PRT;	367	AA.
AC	Q9R1V0;				
DT	01-MAY-2000 (TREMBLrel. 13, Created)				
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)				
DT	01-JUN-2000 (TREMBLrel. 14, Last annotation update)				
DE	CC CHEMOKINE LARC SPECIFIC RECEPTOR.				
GN	MCCR6.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX	NCBI_TaxID=10090;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	Tanaka Y.;				
RT	"Molecular Cloning of Murine Homologue of CCR6, the Specific Receptor for CC Chemokine LARC."				
RL	Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; AB016031; BAA82443.1; -				
DR	INTERPRO: IPR000190; -				
DR	INTERPRO: IPR000276; -				
DR	INTERPRO: IPR000355; -				
DR	PFAM: PF00001; 7tm.1; 1.				
DR	PRINTS: PR00237; GPCRHHODPSN.				
DR	PRINTS: PR00635; ANGIOTENSINR.				
DR	PRINTS: PR00637; CCHEMOKINER.				
DR	PROSITE: PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.				
KW	Receptor.				
SQ	SEQUENCE 367 AA; 42082 MW; 207FD98B2F7A6DD3 CRC64;				

Query Match	88.7%;	Score 102;	DB 11;	Length 367;
Best Local Similarity	81.8%;	Pred. No. 1.9e-08;		
Matches	18;	Conservative	2;	Mismatches 2; Indels 0; Gaps 0;
QY	1	LLKGIYAINFCGMLLTICISM 22		
		1:11 11:111111111111		
DB	112	LMKGTAYVNFNCGMLLTICISM 133		
RESULT	2			

RESULT	3		
Q9XT45			
ID	Q9XT45	PRELIMINARY;	PRT; 343 AA.
AC	Q9XT45;		
DT	01-NOV-1999	(TrEMBLrel. 12, Created)	
DT	01-NOV-1999	(TrEMBLrel. 12, Last sequence update)	
DT	01-JUN-2000	(TrEMBLrel. 14, Last annotation update)	
DE	CEMOKINE RECEPTOR BONZO.		
GN	STRL33.		
OS	Macaca mulatta (Rhesus macaque).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;		
OC	Cercopithecinae; Macaca.		
OX	NCBI_TaxID=9544;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Margulies B.J., Hauer D.A., Clements J.F.;		
RT	"Identification of Thirteen Rhesus Macaque Chemokine Receptors.";		
RL	Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AF124380; AAD31419.1; -		
DR	INTERPRO; IPR000248; -		
DR	INTERPRO; IPR000276; -		
DR	INTERPRO; IPR000355; -		
DR	INTERPRO; IPR001277; -		
DR	INTERPRO; IPR002235; -		
DR	PFAM; PF00001; 7tm1.1;		
DR	PRINTS; PR00237; GPCRHHODPSN.		
DR	PRINTS; PR00241; ANGIOTENSINR.		
DR	PRINTS; PR00645; LCR1ORPHANR.		

DR EMBL; Y12879; CAA73379.1; -
DR MGD; MGI:1096320; Cmkbr9.
DR INTERPRO; IPR000276; -
DR PFAM; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
SQ SEQUENCE 378 AA; 43255 MW; 7A125FF3C7B2F5E0 CRC64;

Query Match 55.7%; Score 64; DB 11; Length 378;
Best Local Similarity 40.9%; Pred. No. 0.022;
Matches 9; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

OY 1 LLKGIYAINFCGMLLLTCISM 22
:: :||| ||: :||:|
Db 118 VISTLYSINFCGIFITCMLS 139

RESULT 6
O09027 ID O09027 PRELIMINARY; PRT; 382 AA.

AC O09027; 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE CCR10-RELATED RECEPTOR.
GN RCCR10RR.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN-SPRAGUE-DAWLEY;
RA Bonini J.A., Steiner D.F.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U92803; AAB61572.1; -
DR INTERPRO; IPR000276; -
DR PFAM; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
SQ SEQUENCE 382 AA; 43293 MW; E8714CE23DB96772 CRC64;

Query Match 54.8%; Score 63; DB 11; Length 382;
Best Local Similarity 50.0%; Pred. No. 0.033;
Matches 9; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

OY 5 IYAINFCGMLLLTCISM 22
:|:|:| ||: :||:|
Db 123 IYSINFCGIFITCMLS 140

RESULT 7
O42444 ID O42444 PRELIMINARY; PRT; 368 AA.

AC O42444; 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE INTERLEUKIN-8-LIKE RECEPTOR.
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
[1]
RP SEQUENCE FROM N.A.
RA Zou J., Daniels G.D., Cunningham C., Secombes C.J.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ003159; CAA05917.1; -
DR INTERPRO; IPR000276; -
DR PFAM; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.

SQ SEQUENCE 368 AA; 41523 MW; BE28E2D4C47E821A CRC64;

Query Match 50.4%; Score 58; DB 13; Length 368;
Best Local Similarity 70.6%; Pred. No. 0.2;
Matches 12; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 6 YAINFCGMLLLTCISM 22
| ||| ||| ||| |||
Db 126 YKINFFSMLLLTCISV 142

RESULT 8

O9NZG2 ID O9NZG2 PRELIMINARY; PRT; 361 AA.
AC O9NZG2; 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE 7-TRANSMEMBRANE G-PROTEIN COUPLED RECEPTOR 2.
GN GPR2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20191998; PubMed=10725697;
RA Honey B., Wang W., Buchanan M., Wisenborn A., Soto H., Catron D.,
RA Orozco R., Ruzicka T., Lehmann P., Oldham E., Zlotnik A.;
RT "Cutting edge: the orphan chemokine receptor G protein-coupled
RT receptor-2 (GPR-2, CCR10) binds the skin-associated chemokine CCL27
RT (CTACK/ALP/ILC).";
RL J. Immunol. 164:3465-3470(2000).
DR EMBL; AF208237; AAF72871.1; -
RW Receptor; Transmembrane.
SQ SEQUENCE 361 AA; 38302 MW; F8AA749118E3926F CRC64;

Query Match 48.7%; Score 56; DB 4; Length 361;
Best Local Similarity 45.0%; Pred. No. 0.41;
Matches 9; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

OY 2 LKGIYAINFCGMLLLTCIS 21
:|:|:| :|:| :|:| |||
Db 116 ISGLYSASFHAGFLFLACIS 135

RESULT 9

O9JIP1 ID O9JIP1 PRELIMINARY; PRT; 362 AA.
AC O9JIP1; 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE 7-TRANSMEMBRANE G-PROTEIN COUPLED RECEPTOR 2.
GN GPR2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RP SEQUENCE FROM N.A.
RA Wang W., Soto H., Oldham E.R., Buchanan M.E., Honey B., Catron D.,
RA Jenkins N., Copeland N.G., Gilbert D.J., Nguyen N., Abrams J.,
RA Kershenovich D., Smith K., Mcclanahan T., Vicari A.P., Zlotnik A.;
RT "Identification of a novel chemokine (CCL28), which binds CCR10
RT (GPR2).";
RL J. Biol. Chem. 275:22313-22323(2000).
DR EMBL; AF208238; AAF72872.1; -
RW Receptor; Transmembrane.
SQ SEQUENCE 362 AA; 38899 MW; 13C4292859C376CE CRC64;

SQ SEQUENCE 362 AA; 38926 MW; 0FF4EA2005B94E99 CRC64;

RT "Two alleles for rhesus macaque GPR15.";
RT
BY NIDS Rec Hum Pat rnr1 rnrscs 15-045-047/1999\

CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 DR EMBL; AF10203; AAC72401.1; -
 DR EMBL; AF084226; AAD52038.1; -
 DR INTERPRO; IPR000248; -
 DR INTERPRO; IPR000276; -
 DR PFAM; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRHHODOPSN.
 DR PRINTS; PR00241; ANGIOTENSINR.
 DR PROSITE; PS00237; G-PROTEIN_RECEPTOR; 1.
 KW Receptor; G-protein coupled receptor; Transmembrane; Glycoprotein.
 SQ SEQUENCE 360 AA; 40787 MW; ECCEDID0BC34E959 CRC64;

Query Match 44.8%; Score 51.5; DB 6; Length 360;
 Best Local Similarity 40.0%; Pred. No. 2.1;
 Matches 10; Conservative 7; Mismatches 5; Indels 3; Gaps 1;

QY 1 LLKG---IYAINFCGMLLLTCISM 22
 | | | : : | : | | | : |
 Db 105 LCKGSSYMSVNMHCVFLLTCMSV 129

RESULT 14

Q9TV17 PRELIMINARY; PRT; 360 AA.
 AC Q9TV17;
 DT 01-MAY-2000 (TRENBLrel. 13, Created)
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TRENBLrel. 14, Last annotation update)
 DE G PROTEIN-COUPLED RECEPTOR GPR15.
 GN GPR15.
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecoidea; Macaca.
 OX NCBI_TaxID=9544;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99335217; PubMed=10408732;
 RA Pretet J.L., Brussel A., Guillet J.G., Butor C.;
 RT "two alleles for rhesus macaque GPR15 (BOB).";
 RL AIDS Res. Hum. Retroviruses 15:945-947(1999).
 DR EMBL; AF084227; AAD52039.1; -
 DR INTERPRO; IPR000248; -
 DR INTERPRO; IPR000276; -
 DR PFAM; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRHHODOPSN.
 DR PRINTS; PR00241; ANGIOTENSINR.
 DR PROSITE; PS00237; G-PROTEIN_RECEPTOR; 1.
 KW Receptor.
 SQ SEQUENCE 360 AA; 40806 MW; 96F0BBE1CBIDA4 CRC64;

Query Match 44.8%; Score 51.5; DB 6; Length 360;
 Best Local Similarity 40.0%; Pred. No. 2.1;
 Matches 10; Conservative 7; Mismatches 5; Indels 3; Gaps 1;

QY 1 LLKG---IYAINFCGMLLLTCISM 22
 | | | : : | : | | | : |
 Db 105 LCKGSSYMSVNMHCVFLLTCMSV 129

RESULT 15

Q9NPB9 PRELIMINARY; PRT; 350 AA.
 AC Q9NPB9;
 DT 01-OCT-2000 (TRENBLrel. 15, Created)
 DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TRENBLrel. 15, Last annotation update)
 DE CHEMOKINE RECEPTOR (CC CHEMOKINE RECEPTOR) (ORPHAN SEVEN-TRANSMEMBRANE RECEPTOR).
 GN CCR11 OR CCR2 OR VSHK1.

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea;
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Schweickart V.L., Epp A., Raport C.J., Gray P.W.;
 RT "CCR11 is a Functional Receptor for the Monocyte Chemoattractant Protein Family of Chemokines";
 RL J. Biol. Chem. 275:9550-9556(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20171478; PubMed=10706668;
 RA Gosling J., Dairaghi D.J., Wang Y., Hanley M., Talbot D., Miao Z., Schall T.J.;
 RT "Cutting edge: identification of a novel chemokine receptor that binds dendritic cell- and T cell-active chemokines including ELC, SLC, and TECK";
 RL J. Immunol. 164:2851-2856(2000).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Khoja H., Wang G., Lee Ng C.-T., Tucker J., Brown T., Shymala V.;
 RT "Cloning of CCR11, an orphan seven transmembrane receptor related to chemokine receptors, expressed abundantly in heart";
 RL Gene 246:229-238(2000).
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Shymala V., Khoja H.;
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF193507; AAF61299.1; -
 DR EMBL; AF233281; AAF44751.1; -
 DR EMBL; AF110640; AAF59827.1; -
 KW Receptor; Transmembrane.
 SQ SEQUENCE 350 AA; 39913 MW; 8E26049D2D5757C8 CRC64;

Query Match 44.3%; Score 51; DB 4; Length 350;
 Best Local Similarity 40.9%; Pred. No. 2.5;
 Matches 9; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

QY 1 LLKGIIYAINFCGMLLLTCISM 22
 : : | | | | | | | | | |
 Db 114 ITSALYTLNFVSGMQLACISI 135

Search completed: May 23, 2001, 15:35:14
 Job time: 620 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 23, 2001, 15:28:28 ; Search time 184.73 seconds
(without alignments)
5.570 Million cell updates/sec

Title: US-08-887-977-10_COPY_133_150

Perfect score: 86
Sequence: 1 DRYIAIVQATKSFRLRSR 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 390729 seqs, 57163235 residues

Total number of hits satisfying chosen parameters: 390729

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- A_Geneseq_0401.*
- 1: /SID56/gcgdata/geneseq/geneseq/AA1980.DAT.*
 - 2: /SID56/gcgdata/geneseq/geneseq/AA1981.DAT.*
 - 3: /SID56/gcgdata/geneseq/geneseq/AA1982.DAT.*
 - 4: /SID56/gcgdata/geneseq/geneseq/AA1983.DAT.*
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 - 20: /SID56/gcgdata/geneseq/geneseq/AA1999.DAT.*
 - 21: /SID56/gcgdata/geneseq/geneseq/AA2000.DAT.*
 - 22: /SID56/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	86	100.0	365	19 W48086	Human dendritic ce
2	86	100.0	365	21 Y97077	Primate (human) ch
3	55	64.0	358	15 R53745	Partial sequence o
4	55	64.0	358	21 B21689	Human 7TM receptor
5	55	64.0	361	20 W97348	An Epstein-barr vi
6	55	64.0	378	15 R54079	Epstein Barr virus
7	55	64.0	378	15 R53744	Putative seven tra
8	55	64.0	378	19 W48724	Human V31 seven tr
9	55	64.0	378	19 W56164	G-protein coupled
10	55	64.0	378	19 W53622	Epstein Barr virus
11	55	64.0	378	21 B21688	Human 7TM receptor

12	55	64.0	378	21 Y90629	Human G protein-co
13	55	64.0	378	21 Y90663	Human mutant G pro
14	55	64.0	378	22 B50859	Human CCR7. Homo
15	55	64.0	410	15 R53743	Putative seven tra
16	55	64.0	410	19 W48723	Polyptide sequen
17	55	64.0	410	21 B21687	Genomic clone of 7
18	53	61.6	302	19 W70001	Rodent chemokine r
19	53	61.6	351	20 Y23825	A7-times membrane
20	53	61.6	359	15 R53747	Seven transmembran
21	53	61.6	359	19 W48728	Murine 7TM recepto
22	53	61.6	359	21 B21691	Murine 7TM recepto
23	53	61.6	378	21 B21699	7TM receptor prote
24	49	57.0	337	15 R53753	Seven transmembran
25	49	57.0	337	18 W08141	G-protein receptor
26	49	57.0	337	19 W69997	Primate chemokine
27	49	57.0	337	19 W48734	Human RM3 seven tr
28	49	57.0	337	21 B21698	Human 7TM receptor
29	49	57.0	337	21 B02847	Human G protein co
30	49	57.0	337	21 B02856	Human G protein co
31	49	57.0	352	13 R27792	New platelet facto
32	49	57.0	352	16 R68812	Human monocyte PF4
33	49	57.0	352	16 R80757	Chemokine superfam
34	49	57.0	352	20 Y39993	Human CXCR4 protei
35	49	57.0	352	21 Y52507	Human CXCR4 chemok
36	49	57.0	356	20 W97362	G-protein coupled
37	49	57.0	359	19 W64778	A murine CXCR4 chemo
38	49	57.0	359	20 Y39994	Mouse CXCR4 protei
39	48	55.8	73	19 W69998	Rodent chemokine r
40	48	55.8	418	14 R39263	Human somatostatin
41	48	55.8	428	14 R39264	Murine somatostati
42	47	54.7	244	19 W69996	Primate chemokine
43	47	54.7	339	15 R53752	Seven transmembran
44	47	54.7	339	18 W07617	Human G-protein th
45	47	54.7	339	19 W48733	Human R12 seven tr

ALIGNMENTS

RESULT	1
W48086	W48086 standard; Protein; 365 AA.
ID	W48086 standard; Protein; 365 AA.
XX	XX
AC	W48086;
XX	XX
DT	11-JUN-1998 (first entry)
XX	XX
DE	Human dendritic cell chemokine receptor.
XX	XX
DE	Human; thymus expressed chemokine; TECK; MIP-3alpha; MIP-3beta; receptor; dendritic cell; macrophage; inflammation; asthma.
KW	Human dendritic cell chemokine receptor.
XX	XX
OS	Homo sapiens.
XX	XX
XX	XX
PH	Key Location/Qualifiers
FT	Misc-difference 193
FT	/note= "encoded by CAN"
XX	XX
PN	W09801557-A2.
XX	XX
PD	15-JAN-1998.
XX	XX
PF	02-JUL-1997; 97WO-US10819.
XX	XX
PR	04-JUN-1997; 97US-0048593.
PR	05-JUL-1996; 96US-0675814.
PR	11-OCT-1996; 96US-0028329.
XX	XX
PA	(SCHE) SCHERING CORP.
XX	XX
PI	Gish KC, Schall TJ, Vicari A, Wang W, Zlotnik A;
XX	XX
DR	WPI; 1998-101054/09.

DR N-PSDB; V15418.

XX Novel chemokines, e.g. thymus expressed chemokine - used for
 PT treating inflammatory conditions including asthma.

XX Claim 3; Page 94-95; 202pp; English.

XX The present sequence represents human dendritic cell chemokine receptor.
 CC Antibodies which bind to the protein can be used in detecting or
 CC diagnosing various immunological conditions related to expression
 CC of the protein. The nucleic acid can be used for screening and
 CC isolating DNA clones for the chemokines, especially from other
 CC species. The chemokine can be used in the treatment of conditions
 CC associated with abnormal physiology or development, including
 CC inflammatory conditions such as asthma.

XX Sequence 365 AA;

Query Match 100.0%; Score 86; DB 19; Length 365;
 Best Local Similarity 100.0%; Pred. No. 1.1e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRYIAIVQATKSFRLRSR 18

|||||
 133 dryiaivqatksfrlrsr 150

RESULT 2

Y97077
 ID Y97077 standard; Protein; 365 AA.

AC Y97077;

DT 04-DEC-2000 (first entry)

DE Primate (human) chemokine receptor CCR6.

KW MIP-3-alpha; chemokine; CCR6 receptor; ligand; cytostatic; agonist;
 KW antagonist; anti-psoriatic; dermatological; immunosuppressive;
 KW anti-inflammatory.

XX Homo sapiens.

XX Key Location/Qualifiers

FH Misc-difference 193
 FT /note= "Encoded by CAN#"

XX WO2000046248-A1.

XX 10-AUG-2000.

XX 02-FEB-2000; 2000WO-US00511.

XX 03-FEB-1999; 99US-0244281.

XX (SCHE) SCHERING CORP.

XX Oldham ER, Homey B, Dieu-Nosjean M, Caux C, Zlotnik A;
 XX WPI; 2000-543477/49.

XX N-PSDB; A51971.

XX Novel methods for modulating the migration of cells within or to the
 PT skin using MIP-3-alpha or CCR6 agonists or antagonists, useful for
 PT treating skin disorders, e.g. cancer

XX Disclosure; Page 53-54; 61pp; English.

XX The MIP-3-alpha chemokine is expressed in inflamed skin cells. This
 CC chemokine is the ligand for the CCR6 receptor. MIP-3-alpha or CCR6
 CC agonists or antagonists can be used to modulate the migration of a cell
 CC within or to the skin of a mammal. MIP-3-alpha can be used to purify a

CC population of cells expressing a MIP-3-alpha receptor. The methods are
 CC useful for treating a mammalian subject with a skin disease or condition,
 CC e.g. cancer, metastasis, psoriasis, atopic or contact dermatitis,
 CC systemic lupus erythematosus and lichen ruber planus, or for treating
 CC skin transplants or grafts.

XX Sequence 365 AA;

Query Match 100.0%; Score 86; DB 21; Length 365;
 Best Local Similarity 100.0%; Pred. No. 1.1e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRYIAIVQATKSFRLRSR 18

|||||
 133 dryiaivqatksfrlrsr 150

RESULT 3

R53745
 ID R53745 standard; Protein; 358 AA.

XX R53745;

XX 02-FEB-1995 (first entry)

XX Partial sequence of seven transmembrane receptor (V31).

XX Primer; seven transmembrane receptor; receptor; amplification; PCR;
 KW polymerase chain reaction.

XX Homo sapiens.

XX WO9412635-A.

XX 09-JUN-1994.

XX 17-NOV-1993; 93WO-US111153.

XX 17-NOV-1992; 92US-0977452.

XX (ICOS-) ICOS CORP.

XX Godiska R, Gray PW, Schweickart VL;

XX WPI; 1994-200264/24.

XX N-PSDB; Q66162.

XX DNA encoding seven transmembrane receptors - used to develop
 PT prods. for use as therapeutic or diagnostic agents for conditions
 PT involving the receptors.

XX Example 3; Page 56-57; 100pp; English.

XX Two primers (Q66148, Q66149) were used to amplify human genomic DNA
 CC purified from leukocytes. Approximately 1000 clones were isolated
 CC after the initial amplification reaction and probed with sequences
 CC specific for seven transmembrane receptors IL8R1, AT2R and R20.

CC Clones which did not hybridise were then chosen for sequence
 CC analysis. Three new clones were identified that appeared to encode
 CC seven transmembrane receptor segments. Two more primers (Q66151,
 CC Q66152) were used to isolate a full length version of one of these
 CC clones designated V31 (See Q66153). This is the sequence encoded
 CC by exon 3 of the V31 genomic clone

XX Sequence 358 AA;

Query Match 64.0%; Score 55; DB 15; Length 358;

Best Local Similarity 61.1%; Pred. No. 0.047;
 Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 DRYIAIVQATKSFRLRSR 18

```

Db      133 dryvaivqavsahrhr 150
      |||:||||| : | :|
RESULT  4
B21689
ID      B21689 standard; Protein; 358 AA.
XX
AC      B21689;
XX
DT      26-JAN-2001 (first entry)
XX
DE      Human 7TM receptor V31-B cDNA clone exon 1 protein.
XX
KW      Seven transmembrane receptor; 7TM; heptahelical; serpentine;
KW      G-protein-coupled; V28; V31; V112; R20; R2; R12; RM3; gene therapy;
KW      cancer.
XX
OS      Homo sapiens.
XX
PN      US6107475-A.
XX
PD      22-AUG-2000.
XX
PF      26-APR-1999; 99US-0299843.
XX
PR      17-MAY-1994; 94US-0245242.
PR      01-JUN-1998; 98US-0088337.
PR      17-NOV-1992; 92US-0977452.
PR      17-NOV-1993; 93US-0153848.
XX
PA      (ICOS-) ICOS CORP.
XX
PI      Schweickart VL, Gray PW, Godiska R;
XX
DR      WPI; 2000-571335/53.
XX
DR      N-PSDB; A91709.
XX
PT      Polynucleotide encoding seven transmembrane receptors, antibody
PT      specific to the receptor, agonist and antagonist of the receptor useful
PT      for treating inflammation in a mammal -
XX
PS      Example 3; Columns 49-52; 61pp; English.
XX
CC      The present sequence is a novel seven transmembrane (7TM) receptors
CC      (also known as heptahelical, serpentine or G-protein-coupled receptors).
CC      The coding sequence for the present sequence may be used for gene
CC      therapy for diseases such as cancer.
XX
SQ      Sequence 358 AA;

Query Match      64.0%; Score 55; DB 21; Length 358;
Best Local Similarity 51.1%; Pred. NO. 0.047;
Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY      1 DRYIAIVQATKSFRLRSR 18
      |||:||||| : | :|
DB      133 dryvaivqavsahrhr 150

RESULT  5
W97348
ID      W97348 standard; Protein; 361 AA.
XX
AC      W97348;
XX
DT      12-MAY-1999 (first entry)
XX
DE      An Epstein-barr virus-induced G-protein coupled receptor.
XX
KW      Epstein-barr virus-induced G-protein coupled receptor; EBI 3;
KW      splicing variant; EBI 1; vaccine; infection; HIV-1; HIV-2; pain;
KW

cancer; anorexia; bulimia; asthma; Parkinson's disease;
acute heart failure; hypotension; hypertension; urinary retention;
osteoporosis; angina pectoris; myocardial infarction; ulcer; allergy;
benign prostatic hypertrophy; psychotic disorder; neurological disorder;
anxiety; schizophrenia; manic depression; delirium; dementia;
severe mental retardation; dyskinesias; Huntington's disease;
Gilles de la Tourette's syndrome.
Homo sapiens.
EP894854-A2.
03-FEB-1999.
04-DEC-1997; 97EP-0309791.
29-JUL-1997; 97US-0902294.
(SMIK ) SMITHKLINE BEECHAM CORP.
Zhu Y;
WPI; 1999-108346/10.
N-PSDB; X15857.
New Epstein-barr virus-induced G-protein coupled receptor (EBI 3)
gene and protein - useful as diagnostic reagents and for prevention
and treatment of HIV infections and cancer
Claim 2; Page 7; 20pp; English.

The present sequence represents a Epstein-barr virus-induced G-protein
coupled receptor (EBI 3), which is a splicing variant of EBI 1. EBI 3
antibodies are useful for inducing an immune response to immunize and
prevent disease, and for isolating EBI 3 clones or purifying the
polypeptides by affinity chromatography. EBI 3 polypeptides can be
administered directly or as a vaccine to inoculate against disease.
Diseases diagnosed, prevented and treated include: bacterial, fungal,
viral and protozoan infections, particularly infections caused by HIV-1
or HIV-2; pain; cancers; anorexia; bulimia; asthma; Parkinson's disease;
acute heart failure; hypotension; hypertension; urinary retention;
osteoporosis; angina pectoris; myocardial infarction; ulcers; allergies;
benign prostatic hypertrophy; and psychotic and neurological disorders,
including anxiety, schizophrenia, manic depression, delirium, dementia,
severe mental retardation and dyskinesias, such as Huntington's disease
or Gilles de la Tourette's syndrome.
Sequence 361 AA;

Query Match      64.0%; Score 55; DB 20; Length 361;
Best Local Similarity 51.1%; Pred. NO. 0.048;
Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY      1 DRYIAIVQATKSFRLRSR 18
      |||:||||| : | :|
DB      136 dryvaivqavsahrhr 153

RESULT  6
R54079
ID      R54079 standard; Protein; 378 AA.
XX
AC      R54079;
XX
DT      03-FEB-1995 (first entry)
XX
DE      Epstein Barr virus induced (EBI-1) polypeptide.
XX
KW      Epstein Barr virus; EBV; induction; detection; diagnosis;
KW      lymphocytes; antigen; growth; differentiation; mediator;
KW      infectious mononucleosis.
KW

```

OS Homo sapiens.
 XX Key
 FH Region
 FT 1..24 Location/Qualifiers
 FT /label= Hydrophobic region.
 FT /note= "Predicted to be a signal peptide for
 FT membrane translocation."
 FT Modified-site 36
 FT /note= "Potential N-linked glycosylation site."
 FT Region 60..86
 FT /label= Hydrophobic region.
 FT Region 96..116
 FT /label= Hydrophobic region.
 FT Region 131..152
 FT /label= Hydrophobic region.
 FT Region 151..159
 FT /note= "This sequences motif
 FT (S-[I/V]-D-R-[Y/F]-X-X-X) is highly
 FT conserved among a large number of G-protein
 FT coupled receptors."
 FT Region 171..191
 FT /label= Hydrophobic region.
 FT Region 220..247
 FT /label= Hydrophobic region.
 FT Region 264..289
 FT /label= Hydrophobic region.
 FT Modified-site 292
 FT /note= "Potential N-linked glycosylation site."
 FT Region 314..331
 FT /label= Hydrophobic region.
 XX
 PN W09412519-A.
 XX
 PD 09-JUN-1994.
 XX
 PF 08-OCT-1993; 93WO-US09636.
 XX
 PR 25-NOV-1992; 92US-0980518.
 XX
 PA (BGHM) BRIGHAM & WOMENS HOSPITAL.
 XX
 PI Birkenbach M, Kieff E;
 XX
 DR WPI; 1994-200183/24.
 XX
 DR N-PSDB; Q64125.
 XX
 PT DNA coding for Epstein Barr Virus induced (EBI) polypeptide(s)
 PT and antibodies to EB1, 2 and 3 - useful for detecting EBV by
 PT hybridisation or by immunoassay
 XX
 PS Claim 8; Page 54-56; 84pp; English.
 XX
 CC EBV infected B lymphocytes recapitulate features of antigen
 CC stimulation in enlarging, increasing RNA synthesis, expressing
 CC activation antigens and adhesion molecules, secreting Ig and
 CC proliferating. Unlike antigen stimulated B lymphocytes, EBV
 CC infected B lymphocytes continue to proliferate (in vitro) as
 CC immortalised lymphoblastoid cell lines. Because of the similar
 CC effects of EBV and antigen, EBV induced genes are likely to include
 CC mediators of antigen induced B lymphocyte growth or differentiation.
 XX
 SQ Sequence 378 AA;

Query Match 64.0%; Score 55; DB 15; Length 378;
 Best Local Similarity 61.1%; Pred. NO. 0.05;
 Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 QY 1 DRYIAIVQATKSFRLRSR 18
 |||:||||| : | : |
 Db 153 dryvaivqavsahrhr 170

RESULT 7
 R53744
 ID R53744 standard; Protein; 378 AA.
 XX
 AC R53744;
 XX
 DT 02-FEB-1995 (first entry)
 XX
 DE Putative seven transmembrane receptor (V31).
 XX
 KW Primer; seven transmembrane receptor; receptor; amplification; PCR;
 KW polymerase chain reaction.
 XX
 OS Homo sapiens.
 XX
 PN W09412635-A.
 XX
 PD 09-JUN-1994.
 XX
 PF 17-NOV-1993; 93WO-US11153.
 XX
 PR 17-NOV-1992; 92US-0977452.
 XX
 PA (ICOS-) ICOS CORP.
 XX
 PI Godiska R, Gray PW, Schweickart VL;
 XX
 DR WPI; 1994-200264/24.
 DR N-PSDB; Q66160.
 XX
 PT DNA encoding seven transmembrane receptors - used to develop
 PT prods. for use as therapeutic or diagnostic agents for conditions
 PT involving the receptors.
 XX
 PS Claim 1; Page 52-53; 100pp; English.
 XX
 CC A human cDNA encoding the seven transmembrane receptor V31 was
 CC isolated by first amplifying a partial cDNA clone from a human
 CC tonsil cDNA library using two primers (Q66154, Q66155). The resulting
 CC amplified products were probed using two radioactively labelled
 CC sequences (Q66156, Q66157). A hybridising band was isolated from the
 CC gel and cloned. The resulting clone was named pv31-5'end (Q66158). A
 CC full length cDNA clone was isolated from a peripheral blood
 CC mononuclear cell library using V31 specific primers (Q66159, Q66152).
 CC Clone PBMC75 was isolated and the V31 cDNA insert in the clone was
 CC designated cDNA V31-B (Q66160).
 XX
 SQ Sequence 378 AA;
 Query Match 64.0%; Score 55; DB 15; Length 378;
 Best Local Similarity 61.1%; Pred. NO. 0.05;
 Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 QY 1 DRYIAIVQATKSFRLRSR 18
 |||:||||| : | : |
 Db 153 dryvaivqavsahrhr 170
 RESULT 8
 W48724
 ID W48724 standard; Protein; 378 AA.
 XX
 AC W48724;
 XX
 DT 25-SEP-1998 (first entry)
 XX
 DE Human V31 seven transmembrane receptor.
 XX
 KW V28; placenta; seven transmembrane receptor; 7TM; signal transduction;
 KW immunology; inflammation; V31.
 XX
 OS Homo sapiens.

```

XX FH Key Location/Qualifiers
XX FT Domain 58..86
XX FT Domain /note= "Transmembrane domain 1"
XX FT Domain 96..119
XX FT Domain /note= "Transmembrane domain 2"
XX FT Domain 131..152
XX FT Domain /note= "Transmembrane domain 3"
XX FT Domain 171..196
XX FT Domain /note= "Transmembrane domain 4"
XX FT Domain 219..247
XX FT Domain /note= "Transmembrane domain 5"
XX FT Domain 264..285
XX FT Domain /note= "Transmembrane domain 6"
XX FT Domain 306..331
XX FT Domain /note= "Transmembrane domain 7"
XX FN US5759804-A.
XX XX
XX PD 02-JUN-1998.
XX XX
XX PF 17-NOV-1993; 93US-0153848.
XX XX
XX PR 17-NOV-1992; 92US-0977452.
XX XX
XX PA (ICOS-) ICOS CORP.
XX XX
XX PI Godiska R, Gray PW, Schweickart VL;
XX XX
XX DR WPI; 1998-332132/29;
XX DR N-PSDB; V18347.
XX XX
XX PT DNA encoding V28 seven transmembrane receptor polypeptide - useful
XX PT for producing recombinant polypeptide and anti-V28 antibodies, and
XX PT in screening assays for V28 agonists and antagonists
XX PS
XX XX
XX CC Example 3; Columns 39-42; 56pp; English.
XX CC
XX CC The present sequence represents the V31 seven transmembrane (7TM)
XX CC receptor encoded by the V31 cDNA (V18347). The invention claims for
XX CC a full length V28 genomic DNA (V18343) and the V28 protein it
XX CC encodes (W48722). V28 and V31 proteins are 7TM receptors which
XX CC are probably involved in signal transduction. The invention also
XX CC claims that cells transformed with V28 DNA can be used to produce the
XX CC recombinant polypeptide, to produce anti-V28 antibodies or in screening
XX CC assays for V28 agonists or antagonists. The antibodies, agonists and
XX CC antagonists could then be used to modulate V28 receptor-ligand binding,
XX CC for e.g. in immunological and/or inflammatory events in vivo.
XX SQ Sequence 378 AA;

Query Match 64.0%; Score 55; DB 19; Length 378;
Best Local Similarity 61.1%; Pred. No. 0.05;
Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DRYIAIVQATKSFRLRSR 18
Db 153 dryvaivqavsahrhrar 170
||||| : |||

RESULT 9
W56164
ID W56164 standard; Protein; 378 AA.
XX AC W56164;
XX DT 20-JUL-1998 (first entry)
XX DE G-protein coupled receptor (R7G) designated EB11.
XX KW Lymphocyte R7G; EB11; G-protein coupled receptor;
XX opiate/opioid recognition site; opiate; opioid; opiod binding protein;

KW screening; lymphocyte receptor; compound; agonist; antagonist;
KW lymphocyte receptor protein; immune-cell specific lymphocyte receptor;
KW neuronal type opiod receptor.
XX Homo sapiens.
XX OS US5753516-A.
XX PN 19-MAY-1998.
XX PD
XX PF 03-FEB-1995; 95US-0383751.
XX PR 03-FEB-1995; 95US-0383751.
XX XX
XX PA (FINB/) FINBERG R W.
XX PA (HEAG/) HEAGY W E.
XX XX
XX PI Finberg RW, Heagy WE;
XX XX
XX DR WPI; 1998-311410/27.
XX DR N-PSDB; V22684.
XX XX
XX PT Screening assay for lymphocyte opiod receptor ligands - using
XX PT recombinant receptor protein
XX XX
XX PS Claim 1; Columns 87-88; 70pp; English.
XX CC
XX CC The present sequence represents a novel lymphocyte R7G, termed EB11. R7G
XX CC proteins are part of the G-protein coupled receptor superfamily. EB11 is
XX CC a functional opiate/opioid recognition site that probably plays a major
XX CC role in mediating the effects that opiate/opioids have on lymphocytes.
XX CC The EB11 protein is an opiod binding protein that is displayed on the
XX CC surface of lymphocytes. A process for screening a candidate substance for
XX CC ability to interact with a lymphocyte receptor comprises selecting a
XX CC candidate substance having a chemical structure or biological activity
XX CC suggestive of an ability to mimic the biological activity of an
XX CC opiate, opiod drug or opiod peptide having known binding affinity for
XX CC EB11. The ability of the candidate substance is tested to interact with
XX CC the lymphocyte receptor protein. This method can be used to screen for
XX CC agonists or antagonists to the lymphocyte receptor protein. The method
XX CC can be modified and used to screen for agonists or antagonists to the
XX CC immune-cell specific lymphocyte receptor polypeptide or the neuronal type
XX CC opiod receptor polypeptide.
XX SQ Sequence 378 AA;

Query Match 64.0%; Score 55; DB 19; Length 378;
Best Local Similarity 61.1%; Pred. No. 0.05;
Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DRYIAIVQATKSFRLRSR 18
Db 153 dryvaivqavsahrhrar 170
||||| : |||

RESULT 10
W53622
ID W53622 standard; Protein; 378 AA.
XX AC W53622;
XX XX
XX DT 09-JUL-1998 (first entry)
XX DE Epstein Barr virus induced protein 1 (EBI-1).
XX XX
XX KW Assessing; monitoring; foetal development; placental development;
XX KW Epstein Barr virus; EBV; induced gene 1; EBI-1.
XX OS Homo sapiens.
XX XX
XX PN US5744301-A.

```


CC endogenous, non-endogenous, or a mixture of endogenous and non-endogenous
 CC residues. The constitutively active GPCRs are useful for identifying
 CC antagonists, agonists and partial agonists for use as pharmaceutical
 CC agents. The mutant proteins are also useful in research settings for
 CC elucidating the roles of the receptors in normal and diseased conditions.
 CC Antagonists for a particular GPCR are useful for treating diseases and
 CC disorders associated with that receptor. Because the novel mutant GPCRs
 CC are constitutively active, they can be used directly for screening of
 CC compounds without the need for endogenous ligands. The present
 CC sequence represents a human wild-type GPCR referred to in an
 CC exemplification of the invention.

XX SQ Sequence 378 AA;

Query Match 64.0%; Score 55; DB 21; Length 378;
 Best Local Similarity 61.1%; Pred. No. 0.05;
 Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DRYIAIVQATKSFRLRSR 18
 |||:||||| : | : |
 Db 153 dryvaivqavsahrhrar 170

RESULT 13
 Y90663
 ID Y90663 standard; Protein; 378 AA.

XX AC Y90663;
 XX DT 21-AUG-2000 (first entry)
 XX DE Human mutant G protein-coupled receptor EB11 (I262K).

XX KW G protein-coupled receptor; GPCR; constitutively active;
 KW intracellular loop 3; transmembrane domain 6; drug screening;
 KW agonist; antagonist; mutant; mutein.

XX OS Homo sapiens.
 OS Synthetic.

XX FN WO2000022129-A1.

XX PD 20-APR-2000.

XX PF 12-OCT-1999; 99WO-US23938.

XX PR 13-OCT-1998; 98US-0170496.

XX PA (AREN-) ARENA PHARM INC.

XX PI Behan DP, Chalmers DT, Liaw CW;

XX DR WPI; 2000-329165/28.

XX DR N-PSDB; A30729.

XX PT Non-endogenous constitutively activated human G protein-coupled
 PT receptors, useful for identifying agonists for use as pharmaceutical
 PT agents

XX PS Example 2; Page 259-260; 341pp; English.

XX CC The invention relates to constitutively active, non-endogenous versions
 CC of endogenous human orphan G protein-coupled receptors (GPCRs, Y90643-
 CC Y90677 and Y90683-Y90687), and to DNA encoding them (A30709-A30743 and
 CC A30775-A30779). The mutant proteins of the invention contain a
 CC mutation in a portion of the protein comprising intracellular loop 3
 CC (IC3) and transmembrane domain 6 (TM6). A non-endogenous amino acid, X,
 CC is substituted for an endogenous residue in IC3 at a position 16 amino
 CC acids N-terminal of an endogenous proline in TM6 to form a sequence
 CC X-(AA)15-Pro. The endogenous amino acid is selected from Lys, His, Arg or
 CC Ala, and is preferably Lys. When the endogenous residue at this position
 CC is Lys, this residue is replaced by His, Arg or preferably Ala. The 15

CC amino acid stretch between the substituted amino acid and the Pro may be
 CC endogenous, non-endogenous, or a mixture of endogenous and non-endogenous
 CC residues. The constitutively active GPCRs are useful for identifying
 CC antagonists, agonists and partial agonists for use as pharmaceutical
 CC agents. The mutant proteins are also useful in research settings for
 CC elucidating the roles of the receptors in normal and diseased conditions.
 CC Antagonists for a particular GPCR are useful for treating diseases and
 CC disorders associated with that receptor. Because the novel mutant GPCRs
 CC are constitutively active, they can be used directly for screening of
 CC compounds without the need for endogenous ligands. Sequences Y90643-
 CC Y90677 and Y90683-Y90687 the mutant human GPCRs of the invention.

XX SQ Sequence 378 AA;

Query Match 64.0%; Score 55; DB 21; Length 378;
 Best Local Similarity 61.1%; Pred. No. 0.05;
 Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DRYIAIVQATKSFRLRSR 18
 |||:||||| : | : |
 Db 153 dryvaivqavsahrhrar 170

RESULT 14
 B50859
 ID B50859 standard; protein; 378 AA.

XX AC B50859;

XX DT 16-MAR-2001 (first entry)
 XX DE Human CCR7.

XX KW Human; chemokine receptor 7; CCR7; chemokine beta-9; CKbeta-9;
 KW allergy; autoimmune disease; ischaemia; atherosclerosis; cancer;
 KW chronic inflammatory disorder; organ transplant; tissue graft;
 KW chronic myelogenous leukaemia; Infection.

XX OS Homo sapiens.

XX PN US6153441-A.

XX PD 28-NOV-2000.

XX PF 17-FEB-1999; 99US-0251545.

XX PR 17-FEB-1998; 98US-0074883.

XX PA (SMIK) SMITHKLINE BEECHAM CORP.

XX PI Appelbaum ER, White JR, Sarau HM;

XX DR WPI; 2001-049151/06.

XX PT Identifying agonists or antagonists of interaction between human
 PT protein, chemokine beta-9 and human CC chemokine receptor 7, by
 PT contacting cell expressing receptor with test compound

XX PS Claim 1; Fig 1; 20pp; English.

XX CC The present sequence is human chemokine receptor 7 (CCR7), a cellular
 CC receptor for chemokine beta-9 (Ckbeta-9). The sequence may be
 CC used in a method for discovering agonists and antagonists of the
 CC interaction between Ckbeta-9 and CCR7. A cell expressing CCR7
 CC polypeptide on its surface, associated with a component capable of
 CC providing a detectable signal in response to binding of Ckbeta-9, is
 CC contacted with a compound in the presence of labelled or unlabelled
 CC Ckbeta-9. The compound is identified as an agonist/antagonist by
 CC determining whether it activates or inhibits the detectable signal.
 CC The method is useful for identifying agonists and antagonists of the
 CC interaction between Ckbeta-9 and CCR7 which are useful for treating
 CC diseases including allergic disorders, autoimmune diseases,

CC ischaemia/reperfusion injury, development of atherosclerotic plaques,
CC cancer, chronic inflammatory disorders, chronic rejection of
CC transplanted organs or tissue grafts, chronic myelogenous leukaemia, and
CC infection by HIV and other pathogens.
XX
SQ Sequence 378 AA;

Query Match 64.0%; Score 55; DB 22; Length 378;
Best Local Similarity 61.1%; Pred. No. 0.05;
Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 DRYIAIVQATKSFRLRSR 18
 | | | : | | | | : | | : |
Db 153 dryvaivqavsahrhrar 170

RESULT 15

R53743
ID R53743 standard; Protein; 410 AA.

XX AC R53743;

XX DT 02-FEB-1995 (first entry)

XX DE Putative seven transmembrane receptor (V31).

XX KW Primer; seven transmembrane receptor; receptor; amplification; PCR;
XX KW polymerase chain reaction.

XX OS Homo sapiens.

XX PN W09412635-A.

XX PD 09-JUN-1994.

XX PF 17-NOV-1993; 93WO-US11153.

XX PR 17-NOV-1992; 92US-0977452.

XX PA (ICOS-) ICOS CORP.

XX PI Godiska R, Gray PW, Schweickart VL;

XX DR WPI; 1994-200264/24.

XX DR N-PSDB; Q66153.

XX PT DNA encoding seven transmembrane receptors - used to develop
XX PT prods. for use as therapeutic or diagnostic agents for conditions
XX PT involving the receptors.

XX PS Example 2; Page 46-48; 100pp; English.

XX CC Two primers (Q66148, Q66149) were used to amplify human genomic DNA
XX CC purified from leukocytes. Approximately 1000 clones were isolated
XX CC after the initial amplification reaction and probed with sequences
XX CC specific for seven transmembrane receptors IL8R1, AT2R and R20.
XX CC Clones which did not hybridise were then chosen for sequence
XX CC analysis. Three new clones were identified that appeared to encode
XX CC seven transmembrane receptor segments. Two more primers (Q66151,
XX CC Q66152) were used to isolate a full length version of one of these
XX CC clones, one of which was designated V31 and encoded this
XX CC polypeptide.

XX SQ Sequence 410 AA;

Query Match 64.0%; Score 55; DB 15; Length 410;
Best Local Similarity 61.1%; Pred. No. 0.055;
Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 DRYIAIVQATKSFRLRSR 18
 | | | : | | | | : | | : |

Db 185 dryvaivqavsahrhrar 202

Search completed: May 23, 2001, 15:28:29
Job time: 406 sec

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OM protein - protein search, using sw model

Run on: May 23, 2001, 15:30:06 ; Search time 95.91 Seconds
(without alignments)
3.605 Million cell updates/sec

Title: US-08-887-977-10_COPY_133_150

Perfect score: 86
Sequence: 1 DRYTAIVQATKSFRLRSR 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 185757 seqs, 19210857 residues

Total number of hits satisfying chosen parameters: 185757

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PCBUS_COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	55	64.0	358	1	US-08-153-848-19
2	55	64.0	358	3	US-09-299-843A-19
3	55	64.0	358	5	PCT-US93-11153-19
4	55	64.0	361	2	US-08-902-294-2
5	55	64.0	361	3	US-09-178-637-2
6	55	64.0	378	1	US-08-383-750-2
7	55	64.0	378	1	US-08-383-751A-2
8	55	64.0	378	1	US-08-153-848-15
9	55	64.0	378	3	US-08-352-678-2
10	55	64.0	378	3	US-09-299-843A-15
11	55	64.0	378	4	US-09-251-545-1
12	55	64.0	378	5	PCT-US93-09636-2
13	55	64.0	378	5	PCT-US93-11153-15
14	55	64.0	410	1	US-08-153-848-7
15	55	64.0	410	3	US-09-299-843A-7
16	55	64.0	410	5	PCT-US93-11153-7
17	53	61.6	359	1	US-08-153-848-24
18	53	61.6	359	3	US-09-299-843A-24
19	53	61.6	359	5	PCT-US93-11153-24
20	53	61.6	378	3	US-09-299-843A-66
21	49	57.0	337	1	US-08-153-848-46
22	49	57.0	337	3	US-09-299-843A-46
23	49	57.0	337	5	PCT-US93-11153-46
24	49	57.0	352	1	US-08-202-056-3
25	49	57.0	352	1	US-08-076-093A-4
26	49	57.0	352	1	US-08-450-393A-6
27	49	57.0	352	1	US-08-701-265-4

28	49	57.0	352	2	US-08-284-586-4	Sequence 4, Appli
29	49	57.0	352	2	US-08-805-478-4	Sequence 4, Appli
30	49	57.0	352	2	US-08-802-627A-4	Sequence 4, Appli
31	49	57.0	352	2	US-08-801-238-4	Sequence 4, Appli
32	49	57.0	352	2	US-08-801-228-4	Sequence 4, Appli
33	49	57.0	352	3	US-09-104-296-4	Sequence 4, Appli
34	49	57.0	352	4	US-08-446-669-6	Sequence 6, Appli
35	49	57.0	352	5	PCT-US95-00476-6	Sequence 6, Appli
36	48	55.8	418	1	US-07-816-283-10	Sequence 10, Appl
37	48	55.8	418	1	US-08-417-103-10	Sequence 10, Appl
38	48	55.8	428	1	US-07-816-283-12	Sequence 12, Appl
39	48	55.8	428	1	US-08-417-103-12	Sequence 12, Appl
40	47	54.7	339	1	US-08-153-848-44	Sequence 14, Appl
41	47	54.7	339	2	US-08-813-871-3	Sequence 3, Appli
42	47	54.7	339	3	US-09-299-843A-44	Sequence 44, Appl
43	47	54.7	339	5	PCT-US93-11153-44	Sequence 44, Appl
44	47	54.7	339	5	PCT-US95-07180-2	Sequence 2, Appli
45	47	54.7	360	4	US-08-875-573-20	Sequence 20, Appl

ALIGNMENTS

RESULT 1
US-08-153-848-19
; Sequence 19, Application US/08153848
; Patent No. 5759804
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schweikart, Vicki L.
; TITLE OF INVENTION: No. 5759804el Seven Transmembrane Receptors
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/153,848
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/977,452
; FILING DATE: 17-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5759804and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31794
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 358 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-153-848-19

Query Match 64.0%; Score 55; DB 1; Length 358;
Best Local Similarity 61.1%; Pred No. 0.041;
Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

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Qy 1 DRYAIVQATKSFRLRSR 18
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Db 133 DRYAIVQAVSAHRHRAR 150

RESULT 2
US-09-299-843A-19
; Sequence 19, Application US/09299843A
; Patent No. 6107475
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; APPLICANT: Gray, Patrick W.
; TITLE OF INVENTION: Novel Seven Transmembrane Receptors
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/299,843A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/977,452
; FILING DATE: 17-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Jill E. Uhl
; REGISTRATION NUMBER: 43,213
; REFERENCE/DOCKET NUMBER: 27866/32059B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX:
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 358 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-299-843A-19

Query Match 64.0%; Score 55; DB 3; Length 358;
Best Local Similarity 61.1%; Pred. No. 0.041;
Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DRYAIVQATKSFRLRSR 18
   |||:||||| : |||
Db 133 DRYAIVQAVSAHRHRAR 150

RESULT 4
US-08-902-294-2
; Sequence 2, Application US/08902294
; Patent No. 5874252
; GENERAL INFORMATION:
; APPLICANT: ZHU, YUAN
; TITLE OF INVENTION: A NOVEL SPLICING VARIANT OF
; TITLE OF INVENTION: THE EPSTEIN-BARR VIRUS-INDUCED G-PROTEIN COUPLED
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RATNER & PRESTIA
; STREET: P.O. BOX 980
; CITY: VALLEY FORGE
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:

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APPLICATION NUMBER: US/08/902,294
FILING DATE: 29-JUL-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: PRESTIA, PAUL F
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GP-70177
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
TELEFAX: 610-407-0701
TELEX: 846169
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 361 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-902-294-2

Query Match 64.0%; Score 55; DB 2; Length 361;
Best Local Similarity 61.1%; Pred. No. 0.042;
Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 DRYAIVQATKSPRLRSR 18
Db 136 DRYAIVQAVSAHRHRAR 153

RESULT 5
US-09-178-637-2
Sequence 2, Application US/09178637
Patent No. 6001972
GENERAL INFORMATION:
APPLICANT: ZHU, YUAN
TITLE OF INVENTION: A No. 6001972el Splicing Variant of
the Epstein-Barr Virus-Induced G-Protein Coupled Receptor
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: RATNER & PRESTIA
STREET: P.O. BOX 980
CITY: VALLEY FORGE
STATE: PA
COUNTRY: USA
ZIP: 19482
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/178,637
FILING DATE: 26-OCT-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/902,294
FILING DATE: 29-JUL-1998
ATTORNEY/AGENT INFORMATION:
NAME: PRESTIA, PAUL F
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GP-70177-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
TELEFAX: 610-407-0701
TELEX: 846169
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 361 amino acids
TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-178-637-2

Query Match 64.0%; Score 55; DB 3; Length 361;
Best Local Similarity 61.1%; Pred. No. 0.042;
Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 DRYAIVQATKSPRLRSR 18
Db 136 DRYAIVQAVSAHRHRAR 153

RESULT 6
US-08-383-750-2
Sequence 2, Application US/08383750
Patent No. 5744301
GENERAL INFORMATION:
APPLICANT: Birkenbach, Mark
APPLICANT: Kieff, Elliot
TITLE OF INVENTION: Epstein Barr Virus Induced Genes
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, N.W.,
SUITE: Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/383,750
FILING DATE: Herewith
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Fox, Samuel, L.
REGISTRATION NUMBER: 30,353
REFERENCE/DOCKET NUMBER: 0627.3300001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 378 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-383-750-2

Query Match 64.0%; Score 55; DB 1; Length 378;
Best Local Similarity 61.1%; Pred. No. 0.044;
Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 DRYAIVQATKSPRLRSR 18
Db 153 DRYAIVQAVSAHRHRAR 170

RESULT 7
US-08-383-751A-2
Sequence 2, Application US/08383751A
Patent No. 5753516
GENERAL INFORMATION:
APPLICANT: Heagy, Wyrta E.
APPLICANT: Finberg, Robert W.
TITLE OF INVENTION: Identification and Uses of Opioid

;; TITLE OF INVENTION: Receptors
;; NUMBER OF SEQUENCES: 8
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Arnold, White & Durkee
;; STREET: P.O. Box 4433
;; CITY: Houston
;; STATE: Texas
;; COUNTRY: US
;; ZIP: 77210
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/383,751A
;; FILING DATE: 03-FEB-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Willson, Mark B.
;; REGISTRATION NUMBER: 37,259
;; REFERENCE/DOCKET NUMBER: DFCI:001/WIM
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (512) 418-3000
;; TELEFAX: (512) 474-7577
;; TELEX: 79-0924
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 378 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-383-751A-2

Query Match 64.0%; Score 55; DB 1; Length 378;
Best Local Similarity 61.1%; Pred. No. 0.044;
Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 DRYAIVQATKSPRLRSR 18
| | | | | : | : |
Db 153 DRYAIVQAVSAHRHRAR 170

RESULT 8
US-08-153-848-15
; Sequence 15, Application US/08153848
; Patent No. 5759804
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schweikart, Vicki L.
; TITLE OF INVENTION: No. 5759804el Seven Transmembrane Receptors
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/153,848
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/977,452
; FILING DATE: 17-NOV-1992

;; ATTORNEY/AGENT INFORMATION:
;; NAME: No. 5759804and, Greta E.
;; REGISTRATION NUMBER: 35,302
;; REFERENCE/DOCKET NUMBER: 31794
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (312) 474-6300
;; TELEFAX: (312) 474-0448
;; TELEX: 25-3856
;; INFORMATION FOR SEQ ID NO: 15:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 378 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-153-848-15

Query Match 64.0%; Score 55; DB 1; Length 378;
Best Local Similarity 61.1%; Pred. No. 0.044;
Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 DRYAIVQATKSPRLRSR 18
| | | | | : | : |
Db 153 DRYAIVQAVSAHRHRAR 170

RESULT 9
US-08-352-678-2
; Sequence 2, Application US/08352678
; Patent No. 6043351
; GENERAL INFORMATION:
; APPLICANT: Birkenbach, Mark
; APPLICANT: Kieff, Elliott
; TITLE OF INVENTION: EPSTEIN BARR VIRUS INDUCED GENES
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/352,678
; FILING DATE: 30-NOV-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/980,518
; FILING DATE: 25-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Gates, Edward R.
; REGISTRATION NUMBER: 31,616
; REFERENCE/DOCKET NUMBER: B0801/7044
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 378 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-352-678-2

Query Match 64.0%; Score 55; DB 3; Length 378;
Best Local Similarity 61.1%; Pred. No. 0.044;
Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

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Qy 1 DRYIAIVQATKSFRLRSR 18
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Db 153 DRYVAIVQAVSAHRHRAR 170

RESULT 10
US-09-299-843A-15
; Sequence 15, Application US/09299843A
; Patent No. 6107475
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schwellkart, Vicki L.
; TITLE OF INVENTION: No. 6107475el Seven Transmembrane Receptors
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/299,843A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/088,337
; FILING DATE: 01-JUN-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/153,848
; FILING DATE: 17-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/977,452
; FILING DATE: 17-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Jill E. Uhl
; REGISTRATION NUMBER: 43,213
; REFERENCE/DOCKET NUMBER: 27866/32059B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX:
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 378 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-299-843A-15

Query Match 64.0%; Score 55; DB 3; Length 378;
Best Local Similarity 61.1%; Pred. No. 0.044;
Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DRYIAIVQATKSFRLRSR 18
    |||:||||| : |||
Db 153 DRYVAIVQAVSAHRHRAR 170

RESULT 11
US-09-251-545-1
; Sequence 1, Application US/09251545
; Patent No. 6153441
; GENERAL INFORMATION:
; APPLICANT: Edward R. Appelbaum
; APPLICANT: Henry M. Sarau
; APPLICANT: John R. White
; TITLE OF INVENTION: METHODS OF SCREENING FOR AGONISTS AND
; TITLE OF INVENTION: ANTAGONISTS OF THE INTERACTION BETWEEN HUMAN CCR7 RECEPTOR
; TITLE OF INVENTION: AND CR(-9 LIGAND AND INTERACTION THEREOF
; FILE REFERENCE: P50753
; CURRENT APPLICATION NUMBER: US/09/251,545
; CURRENT FILING DATE: 1999-02-17
; EARLIER APPLICATION NUMBER: 60/074,883
; EARLIER FILING DATE: 1998-02-17
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 378
; TYPE: PRT
; ORGANISM: Human
US-09-251-545-1

Query Match 64.0%; Score 55; DB 4; Length 378;
Best Local Similarity 61.1%; Pred. No. 0.044;
Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DRYIAIVQATKSFRLRSR 18
    |||:||||| : |||
Db 153 DRYVAIVQAVSAHRHRAR 170

RESULT 12
PCT-US93-09636-2
; Sequence 2, Application PC/TUS9309636
; GENERAL INFORMATION:
; APPLICANT: Birkenbach, Mark
; APPLICANT: Kieff, Elliot
; TITLE OF INVENTION: Epstein Barr Virus Induced Genes
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue N.W., Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/09636
; FILING DATE: herewith
; CLASSIFICATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 378 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
PCT-US93-09636-2

Query Match 64.0%; Score 55; DB 5; Length 378;
Best Local Similarity 61.1%; Pred. No. 0.044;
Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DRYIAIVQATKSFRLRSR 18
    |||:||||| : |||
Db 153 DRYVAIVQAVSAHRHRAR 170
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RESULT 13
PCT-US93-11153-15
; Sequence 15, Application PC/TUS9311153
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schweikart, Vicki L.
; TITLE OF INVENTION: Novel Seven Transmembrane Receptors
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/11153
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/977,452
; FILING DATE: 17-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Noland, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31794
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 378 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US93-11153-15

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Query Match 64.0%; Score 55; DB 5; Length 378;
Best Local Similarity 61.1%; Pred. No. 0.044;
Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

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```

QY 1 DRYIAIVQATKSPRLRSR 18
|||:||||:|:|:|
Db 153 DRYAIVQAVSAHRHRAR 170

```

```

RESULT 14
US-08-153-848-7
; Sequence 7, Application US/08153848
; Patent No. 5759804
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schweikart, Vicki L.
; TITLE OF INVENTION: No. 5759804el Seven Transmembrane Receptors
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606

```

```

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/153,848
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/977,452
; FILING DATE: 17-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5759804and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31794
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 410 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-153-848-7

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Query Match 64.0%; Score 55; DB 1; Length 410;
Best Local Similarity 61.1%; Pred. No. 0.048;
Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

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QY 1 DRYIAIVQATKSPRLRSR 18
|||:||||:|:|:|
Db 185 DRYAIVQAVSAHRHRAR 202

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RESULT 15
US-09-299-843A-7
; Sequence 7, Application US/09299843A
; Patent No. 6107475
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schweikart, Vicki L.
; TITLE OF INVENTION: No. 6107475el Seven Transmembrane Receptors
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/299,843A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/088,337
; FILING DATE: 01-JUN-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/153,848
; FILING DATE: 17-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/977,452

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; FILING DATE: 17-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Jill E. Uhl
; REGISTRATION NUMBER: 43,213
; REFERENCE/DOCKET NUMBER: 27866/32059B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX:
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 410 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-299-843A-7

Query Match 64.0%; Score 55; DB 3; Length 410;
Best Local Similarity 61.1%; Pred. No. 0.048;
Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 1 DRYAIVQATKSFRLRSR 18
| | | | | : | | |
Db 185 DRYAIVQAVSAHRHR 202

Search completed: May 23, 2001, 15:30:06
Job time: 413 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 23, 2001, 15:32:00 ; Search time 110.15 Seconds
(without alignments)
11.230 Million cell updates/sec

Title: US-08-887-977-10_COPY_133_150

Perfect score: 86
Sequence: 1 DRYAIVQATKSPRLRSR 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 198801 seqs, 68722935 residues

Total number of hits satisfying chosen parameters: 198801

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR-67: *
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	86	100.0	369	2 JC5068	G protein-coupled
2	55	64.0	378	2 A45680	G protein-coupled
3	55	64.0	378	2 B35735	lymphocyte-specifi
4	53	61.6	378	2 A55735	G protein-coupled
5	49	57.0	352	2 G00048	fusin (LESTRA) - c
6	49	57.0	352	2 A45747	neurotrophin Y/pep
7	48	55.8	418	2 A46226	somatostatin recep
8	48	55.8	428	2 A44021	somatostatin recep
9	48	55.8	428	2 S30508	probable G protein
10	47	54.7	360	2 A57160	chemokine (C-C) re
11	47	54.7	374	2 S42628	G protein-coupled
12	47	54.7	374	2 S32785	G protein-coupled
13	47	54.7	380	2 I38435	angiotensin recept
14	46	53.5	327	2 S6162	MDCK15 protein - h
15	46	53.5	353	2 S28787	neurotrophin Y/pep
16	46	53.5	354	2 A23669	interleukin-8 rece
17	46	53.5	372	2 S26667	G protein-coupled
18	45	52.3	349	2 I59336	galanin receptor 1
19	45	52.3	355	2 G02436	chemokine (C-C) re
20	45	52.3	355	2 A45177	chemokine (C-C) re
21	45	52.3	355	2 I49339	macrophage inflam
22	45	52.3	359	2 I49341	MIP-1 alpha recept
23	45	52.3	367	2 J50349	interferon-inducib
24	45	52.3	383	2 S55594	G protein-coupled
25	44	51.2	350	2 A39445	interleukin-8 rece
26	44	51.2	355	2 J01231	interleukin-8 rece
27	44	51.2	358	2 A53752	interleukin-8 rece
28	44	51.2	360	2 A53611	interleukin-8 rece
29	44	51.2	360	2 JC4587	chemokine (C-C) re

30 43 50.0 355 2 JC5067 G protein-coupled
31 43 50.0 391 2 A41795 somatostatin recep
32 43 50.0 391 2 C41795 somatostatin recep
33 43 50.0 391 2 A39297 somatostatin recep
34 43 50.0 444 2 T27866 hypothetical prote
35 42.5 49.4 359 2 JC1104 angiotensin II rec
36 42.5 49.4 359 2 JC1194 angiotensin II rec
37 42.5 49.4 359 2 A48857 angiotensin II rec
38 42.5 49.4 359 2 A42656 angiotensin II rec
39 42.5 49.4 359 2 JQ1516 angiotensin II rec
40 42.5 49.4 359 2 S15403 angiotensin II rec
41 42.5 49.4 359 2 I39418 angiotensin II rec
42 42.5 49.4 359 2 JH0621 angiotensin II rec
43 42.5 49.4 359 2 JC2134 angiotensin II rec
44 42 48.8 72 2 PH0848 somatostatin recep
45 42 48.8 356 2 S42096 interleukin-8 rece

ALIGNMENTS

RESULT 1
JC5068
G protein-coupled receptor CKR-L3 - human
C:Species: Homo sapiens (man)
C:Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 21-Jul-2000
C:Accession: JC5068
R:Zaballos, A.; Varona, R.; Gutierrez, J.; Lind, P.; Marquez, G.
Biochem. Biophys. Res. Commun. 227, 846-853, 1996
A:Title: Molecular cloning and RNA expression of two new human chemokine receptor-lik
A:Reference number: JC5067; MUID:97040707
A:Accession: JC5068
A:Molecule type: DNA
A:Residues: 1-369 <ZAB>
A:Cross-references: EMBL:279784; NID:g1668737; PIDN:CAB02144.1; PID:g1668738
C:Comment: This protein belongs to the family of alpha chemokine receptors.
C:Genetics:
A:Gene: GDB:CMK9R6; STRL22; GPR29; CCR6; CKR-L3; GPR-CY4
A:Cross-references: GDB:5370639; OMIM:601835
A:Map position: 6q27-6q27
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; transmembrane protein
F:42-68/Domain: transmembrane #status predicted <TM1>
F:79-99/Domain: transmembrane #status predicted <TM2>
F:115-136/Domain: transmembrane #status predicted <TM3>
F:160-180/Domain: transmembrane #status predicted <TM4>
F:212-233/Domain: transmembrane #status predicted <TM5>
F:250-271/Domain: transmembrane #status predicted <TM6>
F:292-315/Domain: transmembrane #status predicted <TM7>

Query Match 100.0%; Score 86; DB 2; Length 369;
Best Local Similarity 100.0%; Pred. No. 3.8e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRYAIVQATKSPRLRSR 18
| | | | | | | | | | | | | | | | | | | | | |
Db 137 DRYAIVQATKSPRLRSR 154

RESULT 2
A45680
G protein-coupled peptide receptor EBI 1 - human
C:Species: Homo sapiens (man)
C:Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 24-Nov-1999
C:Accession: A45680
R: Birkenbach, M.; Josefsen, K.; Yalamanchili, R.; Lenoir, G.; Kieff, E.
J. Virol. 67, 2209-2220, 1993
A:Title: Epstein-Barr virus-induced genes: first lymphocyte-specific G protein-couple
A:Reference number: A45680; MUID:93188173
A:Accession: A45680
A:Status: preliminary
A:Molecule type: nucleic acid

A:Residues: 1-378 <BIR>
A:Cross-references: GB:L08176; NID:g183484; PID:g183485
A:Experimental source: B-lymphocytes
A:Note: sequence extracted from NCBI backbone (NCBIN:127094, NCBI:127095)
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 64.0%; Score 55; DB 2; Length 378;
Best Local Similarity 61.1%; Pred. No. 0.023;
Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 DRYIAIVQATKSFRLRSR 18
|||:||||| : ||:
Db 153 DRYVAIVQAVSAHRHRAR 170

RESULT 3
A55735
G protein-coupled receptor EB11 - human
N:Alternate names: Burkitt's lymphoma receptor 2; Epstein-Barr virus induced protein 1
C:Species: Homo sapiens (man)
C:Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 19-May-2000
C:Accession: B55735; S52443
R:Schweickart, V.L.; Raport, C.J.; Godiska, R.; Byers, M.G.; Eddy Jr., R.L.; Shows, T.B.
Genomics 23, 643-650, 1994
A:Title: Cloning of human and mouse EB11, a lymphoid-specific G-protein-coupled receptor
A:Reference number: A55735; MUID:95154835
A:Accession: B55735
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-378 <SCH>
A:Cross-references: GB:L31581; NID:g468319; PIDN:AAA74231.1; PID:g468320
R:Burgstahler, R.; Kempkes, B.; Staube, K.; Lipp, M.
submitted to the EMBL Data Library, February 1995
A:Description: The expression of the chemokine receptor BLR2/EB11 is specifically trans-
A:Reference number: S52443
A:Accession: S52443
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 21-378 <BUR>
A:Cross-references: EMBL:X84702
C:Genetics:
A:Gene: GDB:CMKBR7; EB11; BLR2; CCR7
R:Cross-references: GDB:342065; OMIM:600242
A:Map position: 17q12-17q21.2
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor

Query Match 64.0%; Score 55; DB 2; Length 378;
Best Local Similarity 61.1%; Pred. No. 0.023;
Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 DRYIAIVQATKSFRLRSR 18
|||:||||| : ||:
Db 153 DRYVAIVQAVSAHRHRAR 170

RESULT 4
A55735
G protein-coupled receptor EB11 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 24-Nov-1999
C:Accession: A55735
R:Schweickart, V.L.; Raport, C.J.; Godiska, R.; Byers, M.G.; Eddy Jr., R.L.; Shows, T.B.
Genomics 23, 643-650, 1994
A:Title: Cloning of human and mouse EB11, a lymphoid-specific G-protein-coupled receptor
A:Reference number: A55735; MUID:95154835
A:Accession: A55735
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-378 <SCH>

A:Cross-references: GB:L31580; NID:g468340; PIDN:AAA74232.1; PID:g468341
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor

Query Match 61.6%; Score 53; DB 2; Length 378;
Best Local Similarity 61.1%; Pred. No. 0.054;
Matches 11; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 DRYIAIVQATKSFRLRSR 18
|||:||||| : ||:
Db 153 DRYVAIVQAVSAHRHRAR 170

RESULT 5
G00048
fusin (LESTRA) - crab-eating macaque
C:Species: Macaca fascicularis (crab-eating macaque)
C:Date: 11-Apr-1997 #sequence_revision 11-Apr-1997 #text_change 26-Aug-1999
C:Accession: G00048
R:Tatsumi, M.
submitted to GenBank, July 1996
A:Reference number: H00048
A:Accession: G00048
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-352 <TAT>
A:Cross-references: GB:D86579; NID:g1468948; PID:g1468949
C:Superfamily: vertebrate rhodopsin

Query Match 57.0%; Score 49; DB 2; Length 352;
Best Local Similarity 68.8%; Pred. No. 0.28;
Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 DRYIAIVQATKSFRLR 16
|||:||||| : ||:
Db 133 DRYLAIVHATNSQRPR 148

RESULT 6
A45747
neuropeptide Y/peptide YY receptor Y3 - human
N:Alternate names: fusin; HM89; leukocyte-derived seven-transmembrane receptor LESTR;
C:Species: Homo sapiens (man)
C:Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 05-Nov-1999
C:Accession: A45747; A53103; I53006; I59444; I69203; S32761
R:Federspiel, B.; Melhado, I.G.; Duncan, A.M.V.; Delaney, A.; Schappert, K.; Clark-L-
Genomics 16, 707-712, 1993
A:Title: Molecular cloning of the cDNA and chromosomal localization of the gene for a
A:Reference number: A45747; MUID:93315164
A:Accession: A45747
A:Molecule type: mRNA
A:Residues: 1-352 <FED>
A:Cross-references: GB:M99293; NID:g292516; PIDN:AAA16617.1; PID:g292517
R:Loetscher, M.; Geiser, T.; O'Reilly, T.; Zwaalen, R.; Baggiolini, M.; Moser, B.
J. Biol. Chem. 269, 232-237, 1994
A:Title: Cloning of a human seven-transmembrane domain receptor, LESTR, that is highl
A:Reference number: A53103; MUID:94103215
A:Accession: A53103
A:Molecule type: mRNA
A:Residues: 1-352 <LOE>
A:Cross-references: EMBL:X71635; NID:g297099; PIDN:CAA50641.1; PID:g297100
R:Herzog, H.; Hort, Y.J.; Shine, J.; Selbie, L.A.
DNA Cell Biol. 12, 465-471, 1993
A:Title: Molecular cloning, characterization, and localization of the human homolog t
A:Reference number: I53006; MUID:93319629
A:Accession: I53006
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-352 <HER>
A:Cross-references: GB:L06797; NID:g414929; PIDN:AAA03209.1; PID:g414928
R:Jazin, E.E.; Yoo, H.; Blomqvist, A.G.; Yee, F.; Weng, G.; Walker, M.W.; Salton, J.;

F:151,251,317,332/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
F:251/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status predicted
F:256/Binding site: phosphate (Thr) (covalent) (by cAMP-dependent kinase) #status predicted
F:412/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted

Query Match 55.8%; Score 48; DB 2; Length 418;
Best Local Similarity 52.9%; Pred. No. 0.51;
Matches 9; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DRYIAIVQATKSFRLRS 17
| | | : | | : | | : | | :
Db 140 DRYLAVVHPTRSARWRT 156

RESULT 8
A44021
somatostatin receptor SSTR3 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 11-Jan-2000
C:Accession: A44021
R:Yasuda, K.; Rens-Domiano, S.; Breder, C.D.; Law, S.F.; Saper, C.B.; Reisine, T.; Berridge, M.J. J. Biol. Chem. 267, 20422-20428, 1992
A:Title: Cloning of a novel somatostatin receptor, SSTR3, coupled to adenylylcyclase.
A:Reference number: A44021; MUID:93015924
A:Accession: A44021
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-428 <YAS>
A:Cross-references: GB:M91000; NID:g201065; PIDN:AAA40144.1; PID:g201066
A:Note: sequence extracted from NCHI backbone (NCBIP:115746)
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 55.8%; Score 48; DB 2; Length 428;
Best Local Similarity 52.9%; Pred. No. 0.52;
Matches 9; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DRYIAIVQATKSFRLRS 17
| | | : | | : | | : | | :
Db 141 DRYLAVVHPTRSARWRT 157

RESULT 9
S30508
probable G protein-coupled receptor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 11-Jan-2000
C:Accession: S30508
R:Meierhof, W.; Wulfsen, I.; Schoenrock, C.; Fehr, S.; Richter, D. Proc. Natl. Acad. Sci. U.S.A. 89, 10267-10271, 1992
A:Title: Molecular cloning of a somatostatin-28 receptor and comparison of its expression with that of the rat SSTR3.
A:Reference number: S30508; MUID:93066220
A:Accession: S30508
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-428 <MEY>
A:Cross-references: EMBL:X63574; NID:g56315; PIDN:CAA5130.1; PID:g56316
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 55.8%; Score 48; DB 2; Length 428;
Best Local Similarity 52.9%; Pred. No. 0.52;
Matches 9; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DRYIAIVQATKSFRLRS 17
| | | : | | : | | : | | :
Db 141 DRYLAVVHPTRSARWRT 157

RESULT 10

A57160

Chemokine (C-C) receptor 4 - human
N:Alternate names: C-C CR-4
C:Species: Homo sapiens (man)
C:Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 21-Jul-2000
C:Accession: A57160
R:Power, C.A.; Meyer, A.; Nemeth, K.; Bacon, K.B.; Hoogewerf, A.J.; Proudfoot, A.E.I.; W
J. Biol. Chem. 270, 19495-19500, 1995
A:Title: Molecular cloning and functional expression of a novel CC chemokine receptor cd
A:Reference number: A57160; MUID:95370289
A:Accession: A57160
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-360 <POM>
A:CROSS-references: GB:X85740; NID:g1370103; PIDN:CAA59743.1; PID:g971452
C:Note: source clone K5-5
C:Genetics:
A:Gene: GDB:CMKBR4
A:CROSS-references: GDB:677463
A:Map position: 3p21-3p21
C:Superfamily: G protein-coupled rhodopsin
F:40-65/Domain: transmembrane #status predicted <TM1>
F:76-97/Domain: transmembrane #status predicted <TM2>
F:112-133/Domain: transmembrane #status predicted <TM3>
F:151-175/Domain: transmembrane #status predicted <TM4>
F:208-226/Domain: transmembrane #status predicted <TM5>
F:243-264/Domain: transmembrane #status predicted <TM6>
F:291-308/Domain: transmembrane #status predicted <TM7>
F:23-276,110-187/Disulfide bonds: #status predicted
F:74,350/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted
F:145/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
F:183,194/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted

Query Match 54.7%; Score 47; DB 2; Length 360;
Best Local Similarity 58.8%; Pred. No. 0.67;
Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 DRYIAIVQATKSFRLRS 17
| | | | | | | | | |
Db 134 DRYLAIVHAVFSRLRT 150

RESULT 11

S42628
G protein-coupled receptor Gpcr6 - mouse
N:Alternate names: Interleukin-8 receptor homolog; muBLR1 protein
C:Species: Mus musculus (house mouse)
C:Date: 07-Sep-1994 #sequence_revision 26-May-1995 #text_change 21-Jul-2000
C:Accession: S42628; C48909
R:Kaiser, E.; Foerster, K.; Wolf, I.; Ebensperger, C.; Kuehl, W.M.; Lipp, M.
Eur. J. Immunol. 23, 2532-2539, 1993
A:Title: The G protein-coupled receptor BLR1 is involved in murine B cell differentiation
A:Reference number: S42628; MUID:94009211
A:Accession: S42628
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-374 <KAI>
A:CROSS-references: EMBL:X71788; NID:g2598563; PIDN:CAA50673.1; PID:g433947
R:Wilkie, T.M.; Chen, Y.; Gilbert, D.J.; Moore, K.J.; Yu, L.; Simon, M.I.; Copeland, N.G
Genomics 18, 175-184, 1993
A:Title: Identification, chromosomal location, and genome organization of mammalian G-pr
A:Reference number: A48909; MUID:94116980
A:Accession: C48909
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 151-269 <WIL>
A:CROSS-references: GB:L20332; NID:g438798; PIDN:AAA16852.1; PID:g438799
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 54.7%; Score 47; DB 2; Length 374;
Best Local Similarity 56.2%; Pred. No. 0.7;
Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 DRYIAIVQATKSFRLR 16
| | | | | | | | | |
Db 148 DRYLAIVHAVYRRR 163

RESULT 12

S32785
G protein-coupled receptor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 24-Nov-1999
C:Accession: S32785
R:Kouba, M.; Vanetti, M.; Wang, X.; Schaefer, M.; Hoeltt, V.
FEBS Lett. 321, 173-178, 1993
A:Title: Cloning of a novel putative G-protein-coupled receptor (NLR) which is expres
A:Reference number: S32785; MUID:93238948
A:Accession: S32785
A:Molecule type: mRNA
A:Residues: 1-374 <KOU>
A:CROSS-references: GB:X71463; GB:S59748; NID:g599926; PIDN:CAA50582.1; PID:g599927
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 54.7%; Score 47; DB 2; Length 374;
Best Local Similarity 56.2%; Pred. No. 0.7;
Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 DRYIAIVQATKSFRLR 16
| | | | | | | | | |
Db 148 DRYLAIVHAVYRRR 163

RESULT 13

I38435
angiotensin receptor homolog APJ - human
C:Species: Homo sapiens (man)
C:Date: 15-Mar-1996 #sequence_revision 15-Mar-1996 #text_change 21-Jul-2000
C:Accession: I38435
R:O'Dowd, B.F.; Heiber, M.; Chan, A.; Heng, H.H.; Tsui, L.; Kennedy, J.L.; Shi, X.; P
Gene 136, 355-360, 1993
A:Title: A human gene that shows identity with the gene encoding the angiotensin rece
A:Reference number: I38435; MUID:94124031
A:Accession: I38435
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-380 <RES>
A:CROSS-references: EMBL:U03642; NID:g425351; PIDN:AAA18954.1; PID:g425352
C:Genetics:
A:Gene: APJ
A:Map position: 11q12
A:Introns: #status absent
C:Superfamily: vertebrate rhodopsin

Query Match 54.7%; Score 47; DB 2; Length 380;
Best Local Similarity 55.6%; Pred. No. 0.71;
Matches 10; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 DRYIAIVQATKSFRLSR 18
| | | | | | | | | |
Db 126 DRYLAIVRPVANRLRL 143

RESULT 14

S56162
MDCK15 protein - human
C:Species: Homo sapiens (man)
C:Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 08-Oct-1999

C;Accession: S56162
R;Barella, L.; Loetscher, M.; Tobler, A.; Baggiolini, M.; Moser, B.
Biochem. J. 309, 773-779, 1995
A;Title: Sequence variation of a novel heptahelical leucocyte receptor through alternati
A;Reference number: S56162; MUID:95366951
A;Accession: S56162
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-327 <BAR>
A;Cross-references: EMBL:X68829; NID:g840783; PIDN:CAA48723.1; PID:g840784
C;Superfamily: vertebrate rhodopsin

Query Match 53.5%; Score 46; DB 2; Length 327;
Best Local Similarity 56.2%; Pred. No. 0.93;
Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 DRYIAIVQATKSFRLR 16
|||:||||| :||
Db 101 DRYLAIVHAVYRHR 116

RESULT 15

S28787

neuropeptide Y/peptide YY receptor Y3 - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 26-Aug-1999
C;Accession: S28787
R;Rimland, J.; Xin, W.; Sweetnam, P.; Saijoh, K.; Nestler, E.J.; Duman, R.S.
Mol. Pharmacol. 40, 869-875, 1991
A;Title: Sequence and expression of a neuropeptide Y receptor cDNA.
A;Reference number: S28787; MUID:92100053
A;Accession: S28787
A;Molecule type: mRNA
A;Residues: 1-353 <RIM>
A;Cross-references: EMBL:M86739
C;Superfamily: vertebrate rhodopsin
C;Keywords: appetite; G protein-coupled receptor; transmembrane protein

Query Match 53.5%; Score 46; DB 2; Length 353;
Best Local Similarity 62.5%; Pred. No. 1;
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 DRYIAIVQATKSFRLR 16
|||:||||| :||
Db 134 DRYLAIVHAVYRHR 149

Search completed: May 23, 2001, 15:32:00
Job time: 507 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 23, 2001, 15:36:18 ; Search time 62.39 Seconds
(without alignments)
9.883 Million cell updates/sec

Title: US-08-887-977-10_COPY_133_150

Perfect score: 86
Sequence: 1 DRYIAIVQATKSFRLSR 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	86	100.0	374	1	CCR6_HUMAN
2	83	96.5	367	1	CCR6_MOUSE
3	55	64.0	378	1	CCR7_HUMAN
4	53	61.6	378	1	CCR7_MOUSE
5	49	57.0	192	1	CCR4_SHEEP
6	49	57.0	352	1	CCR4_HUMAN
7	49	57.0	352	1	CCR4_MACFA
8	49	57.0	353	1	CCR4_PAPAN
9	49	57.0	353	1	CCR4_FELCA
10	49	57.0	359	1	CCR4_MOUSE
11	48	55.8	369	1	CCR9_MOUSE
12	48	55.8	418	1	SSR3_HUMAN
13	48	55.8	428	1	SSR3_MOUSE
14	48	55.8	428	1	SSR3_RAT
15	47	54.7	339	1	GPRH_HUMAN
16	47	54.7	360	1	CCR4_HUMAN
17	47	54.7	374	1	CCR5_MOUSE
18	47	54.7	374	1	CCR5_RAT
19	47	54.7	377	1	APJ_MOUSE
20	47	54.7	380	1	APJ_HUMAN
21	47	54.7	380	1	APJ_MACMU
22	47	54.7	381	1	V03L_CAPVK
23	46	53.5	342	1	BONZ_CERAE
24	46	53.5	342	1	BONZ_HUMAN
25	46	53.5	342	1	BONZ_MACNE
26	46	53.5	343	1	BONZ_MACMU
27	46	53.5	352	1	CCR4_CERTO
28	46	53.5	352	1	CCR4_MACMU
29	46	53.5	353	1	CCR4_BOVIN
30	46	53.5	372	1	CCR5_HUMAN
31	45	52.3	346	1	GALR_RAT
32	45	52.3	348	1	GALR_MOUSE
33	45	52.3	349	1	CCR4_RAT

RESULT 1

ID	CCR6_HUMAN	STANDARD;	PRT;	374 AA.
AC	P51684; Q92846; P78553;			
DT	01-OCT-1996 (Rel. 34, Created)			
DT	15-JUL-1998 (Rel. 36, Last sequence update)			
DT	01-OCT-2000 (Rel. 40, Last annotation update)			
DE	C-C CHEMOKINE RECEPTOR TYPE 6 (C-C CCR-6) (CC-CCR-6) (CCR-6) (IARC RECEPTOR) (GPR-CY4) (GPCY4) (CHEMOKINE RECEPTOR-LIKE 3) (CCR-L3) (DRY6).			
GN	CCR6 OR CMKBR6 OR STRL22 OR GPR29 OR CCR6L3.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A., AND FUNCTION.			
RX	MEDLINE=97313465; PubMed=9169459;			
RA	Baba M., Imai T., Nishimura M., Kakizaki M., Takagi S., Hieshima K., Nomiya H., Yoshie O.;			
RT	"Identification of CCR6, the specific receptor for a novel lymphocyte-directed CC chemokine LARC.";			
RL	J. Biol. Chem. 272:14893-14898(1997).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	Lautens L.L., Modi W., Bonner T.I.;			
RL	Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=97040707; PubMed=8886020;			
RA	Zaballos A., Varona R., Gutierrez J., Lind P., Marquez G.;			
RT	"Molecular cloning and RNA expression of two new human chemokine receptor-like genes.";			
RL	Biochem. Biophys. Res. Commun. 227:846-853(1996).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RA	McCoy R., Perlmutter D.H.;			
RL	Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=97224503; PubMed=9070937;			
RA	Liao F., Lee H.-H., Farber J.M.;			
RT	"Cloning of STRL22, a new human gene encoding a G-protein-coupled receptor related to chemokine receptors and located on chromosome 6q27.";			
RL	Genomics 40:175-180(1997).			
CC	-!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-3-ALPHA/LARC AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.			
CC	-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.			
CC	-!- TISSUE SPECIFICITY: SPLEEN, LYMPH NODES, APPENDIX, AND FETAL LIVER. EXPRESSED IN LYMPHOCYTES, T CELLS AND B CELLS BUT NOT IN NATURAL KILLER CELLS, MONOCYTES, OR GRANULOCYTES.			
CC	-!- INDUCTION: INTERLEUKIN-2.			
CC	-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.			
CC	-!- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-6 IS THE INITIATOR.			

ALIGNMENTS

34	45	52.3	349	1	GALR_HUMAN	P47211 homo sapien
35	45	52.3	355	1	CKR1_HUMAN	P32246 homo sapien
36	45	52.3	355	1	CKR1_MACMU	P56482 macaca mula
37	45	52.3	355	1	CKR1_MOUSE	P51675 mus musculus
38	45	52.3	355	1	CKR3_CERAE	P56492 cercopithec
39	45	52.3	355	1	CKR3_HUMAN	P51677 homo sapien
40	45	52.3	355	1	CKR3_MACMU	P56483 macaca mula
41	45	52.3	358	1	CKR3_CAVPO	Q92213 cavia porce
42	45	52.3	359	1	CKR3_MOUSE	P51678 mus musculus
43	45	52.3	359	1	CKR3_RAT	O54814 rattus norv
44	45	52.3	367	1	CCR3_MOUSE	O88410 mus musculus
45	44	51.2	349	1	IL8A_RAT	P70612 rattus norv

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DR EMBL; U45984; AAB62714.1; -;
 DR EMBL; 279784; CAB02144.1; ALT_INIT.
 DR EMBL; U60000; AAB06949.1; -;
 DR EMBL; U68030; AAC51124.1; -;
 DR EMBL; U68032; AAC51125.1; -;
 DR HSSP; P34996; IDDD.
 DR GCRDB; GCR_1037; -;
 DR GCRDB; GCR_1075; -;
 DR GCRDB; GCR_1906; -;
 DR GCRDB; GCR_1919; -;
 DR GCRDB; GCR_1941; -;
 DR GCRDB; GCR_2110; -;
 DR MIM; 601835; -;
 DR InterPro; IPR000276; -;
 DR Pfam; PF00001; 7tm.1; 1.
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECF1_1; 1.
 DR PROSITE; PS0262; G_PROTEIN_RECF1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 47
 FT TRANSMEM 48 74
 FT DOMAIN 75 93
 FT TRANSMEM 84 104
 FT DOMAIN 105 119
 FT TRANSMEM 120 141
 FT DOMAIN 142 159
 FT TRANSMEM 160 180
 FT DOMAIN 181 211
 FT TRANSMEM 212 238
 FT DOMAIN 239 254
 FT TRANSMEM 255 279
 FT DOMAIN 280 303
 FT TRANSMEM 304 321
 FT DOMAIN 322 374
 FT DISULFID 118 197
 FT CARBOHYD 7 7
 FT CONFLICT 23 23
 FT CONFLICT 60 60
 FT CONFLICT 74 74
 FT CONFLICT 86 86
 FT CONFLICT 164 164
 FT CONFLICT 182 182
 FT CONFLICT 192 192
 FT CONFLICT 206 206
 FT CONFLICT 225 225
 FT CONFLICT 370 374
 SQ SEQUENCE 374 AA; 42494 MW; D7F963534E990BC4 CRC64;
 Query Match 100.0%; Score 86; DB 1; Length 374;
 Best Local Similarity 100.0%; Pred. No. 2.9e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRYIAIVQATKSFRLRSR 18
 |||||
 DB 142 DRYIAIVQATKSFRLRSR 159

RESULT 2
 ID_CKR6_MOUSE STANDARD; PRT; 367 AA.
 AC O54689;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE C-C CHEMOKINE RECEPTOR TYPE 6 (C-C CKR-6) (CCR-6) (KY411).
 GN CCR6 OR CKMR6.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RN SEQUENCE FROM N.A.
 RA Yanagihara S., Komura E., Yamaguchi Y.;
 RT "Mouse G protein-coupled receptor KY411.";
 RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=99077268; PubMed=9862452;
 RA Varona R., Zaballós A., Gutierrez J., Martin P., Roncal F.,
 RA Albar J.P., Ardavin C., Marquez G.;
 RT "Molecular cloning, functional characterization and mRNA expression
 RT analysis of the murine chemokine receptor CCR6 and its specific ligand
 RT MIP-3alpha.";
 RL FEBS Lett. 440:188-194(1998).
 CC -|- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-3-
 CC ALPHA/LARC AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE
 CC INTRACELLULAR CALCIUM IONS LEVEL.
 CC -|- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -|- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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 CC -----
 DR EMBL; AB009369; BAA23776.1; -;
 DR EMBL; AJ22714; CAA10956.1; -;
 DR MGD; MGI:1333797; Cmkbr6.
 DR InterPro; IPR000276; -;
 DR Pfam; PF00001; 7tm.1; 1.
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECF1_1; 1.
 DR PROSITE; PS0262; G_PROTEIN_RECF1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 39
 FT TRANSMEM 40 66
 FT DOMAIN 67 75
 FT TRANSMEM 76 96
 FT DOMAIN 97 111
 FT TRANSMEM 112 133
 FT DOMAIN 134 151
 FT TRANSMEM 152 172
 FT DOMAIN 173 203
 FT TRANSMEM 204 230
 FT DOMAIN 231 246
 FT TRANSMEM 247 271
 FT DOMAIN 272 295
 FT TRANSMEM 296 313
 FT DOMAIN 314 367
 FT DISULFID 110 189
 FT CARBOHYD 2 2
 FT CARBOHYD 35 35
 SQ SEQUENCE 367 AA; 42102 MW; 6A309AF83B1117E CRC64;
 Query Match 96.5%; Score 83; DB 1; Length 367;
 Best Local Similarity 94.4%; Pred. No. 9.9e-08;
 Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRYIAIVQATKSFRLRSR 18
 |||||
 DB 134 DRYIAIVQATKSFRLRSR 151

```

RESULT 3
CKR7_HUMAN
ID CKR7_HUMAN STANDARD; PRT; 378 AA.
AC P32248;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE C-C CHEMOKINE RECEPTOR TYPE 7 PRECURSOR (C-C CKR-7) (CCR-7)
DE (MIP-3 BETA RECEPTOR) (EBV-INDUCED G PROTEIN-COUPLED RECEPTOR 1)
DE (EB1) (BLR2).
GN CC7 OR CMKBR7 OR EB11 OR EV11.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93188173; PubMed=8383338;
RA Birkenbach M.P., Josefsen K., Yalamanchili R.R., Lenoir G.M.,
RA Elliott K.;
RT "Epstein-Barr virus-induced genes: first lymphocyte-specific G
RT protein-coupled peptide receptors.";
RL J. Virol. 67:2209-2220(1993).
RN [2]
RP SEQUENCE FROM N.A.
RX TISSUE=Placenta;
RN MEDLINE=95154835; PubMed=7851893;
RA Schweickart V.L., Raport C.J., Godiska R., Byers M.G., Eddy R.L. Jr.,
RA Shows T.B., Gray P.W.;
RT "Cloning of human and mouse EB11, a lymphoid-specific
RT G-protein-coupled receptor encoded on human chromosome 17q12-q21.2.";
RL Genomics 23:643-650(1994).
CC -1- FUNCTION: RECEPTOR FOR THE MIP-3-BETA CHEMOKINE. PROBABLE MEDIATOR
CC OF EBV EFFECTS ON B LYMPHOCYTES OR OF NORMAL LYMPHOCYTE FUNCTIONS.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN VARIOUS LYMPHOID TISSUES AND
CC ACTIVATED B AND T LYMPHOCYTES, STRONGLY UPREGULATED IN B CELLS
CC INFECTED WITH EPSTEIN-BARR VIRUS AND T CELLS INFECTED WITH
CC HERPESVIRUS 6 OR 7.
CC -1- INDUCTION: BY EBV.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC
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CC -----
CC EMBL; L08176; AAA58615.1; -
CC EMBL; L31584; AAA74230.1; -
CC EMBL; L31582; AAA74230.1; JOINED.
CC EMBL; L31583; AAA74230.1; JOINED.
CC EMBL; L31581; AAA74231.1; -
CC PIR; A45680; A45680.
CC HSP; P34996; 1DD0.
CC GCRDb; GCR_0492; -
CC GCRDb; GCR_0958; -
CC MIM; 600242; -
CC InterPro; IPR000276; -
CC InterPro; IPR001718; -
CC Pfam; PF00001; 7tm1.1; 1.
CC PRINTS; PR00237; GPCRHHODOPS.
CC PRINTS; PR00641; CHEMOKINER7.
CC PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
CC PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 378 C-C CHEMOKINE RECEPTOR TYPE 7.
FT DOMAIN 25 59 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 60 86 1 (POTENTIAL).

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FT DOMAIN 87 95 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 96 116 2 (POTENTIAL).
FT DOMAIN 117 130 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 131 152 3 (POTENTIAL).
FT DOMAIN 153 170 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 171 191 4 (POTENTIAL).
FT DOMAIN 192 219 5 (POTENTIAL).
FT TRANSMEM 220 247 6 (POTENTIAL).
FT DOMAIN 248 263 7 (POTENTIAL).
FT TRANSMEM 264 289 8 (POTENTIAL).
FT DOMAIN 290 313 9 (POTENTIAL).
FT TRANSMEM 314 331 10 (POTENTIAL).
FT DOMAIN 332 378 11 (POTENTIAL).
FT CARBOHYD 36 36 N-LINKED (GLCNAC. .) (POTENTIAL).
FT DISULFID 129 210 BY SIMILARITY.
FT CONFLICT 182 183 IW -> SA (IN REF. 1).
FT CONFLICT 337 337 L -> I (IN REF. 1).
SQ SEQUENCE 378 AA; 42874 MW; D4CB4213841A1BD4 CRC64;

Query Match 64.0%; Score 55; DB 1; Length 378;
Best Local Similarity 61.1%; Pred. No. 0.014;
Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 DRYIAIVQATKFKRLSR 18
   |||:||||| : ||:|
Db 153 DRYVAIVQAVSAHRHAR 170

RESULT 4
CKR7_MOUSE
ID CKR7_MOUSE STANDARD; PRT; 378 AA.
AC P47774;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE C-C CHEMOKINE RECEPTOR TYPE 7 PRECURSOR (C-C CKR-7) (CCR-7)
DE (MIP-3 BETA RECEPTOR) (EBV-INDUCED G PROTEIN-COUPLED RECEPTOR 1)
DE (EB11).
GN CC7 OR CMKBR7 OR EB11 OR EB1H.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=B6/CBA; TISSUE=Thymus;
RX MEDLINE=95134835; PubMed=7851893;
RA Schweickart V.L., Raport C.J., Godiska R., Byers M.G., Eddy R.L. Jr.,
RA Shows T.B., Gray P.W.;
RT "Cloning of human and mouse EB11, a lymphoid-specific
RT G-protein-coupled receptor encoded on human chromosome 17q12-q21.2.";
RL Genomics 23:643-650(1994).
CC -1- FUNCTION: RECEPTOR FOR THE MIP-3-BETA CHEMOKINE. PROBABLE MEDIATOR
CC OF EBV EFFECTS ON B LYMPHOCYTES OR OF NORMAL LYMPHOCYTE FUNCTIONS.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC
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CC -----
CC EMBL; L31580; AAA74232.1; -
CC MGD; MGI:103011; Cmkbr7.
CC InterPro; IPR000276; -
CC InterPro; IPR001718; -
CC Pfam; PF00001; 7tm1.1; 1.
CC PRINTS; PR00237; GPCRHHODOPS.
CC PRINTS; PR00641; CHEMOKINER7.

```

DR PROSITE; PS00237; G_PROTEIN_RECP_FL_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECP_FL_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 378 C-C CHEMOKINE RECEPTOR TYPE 7.
FT DOMAIN 25 59 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 60 86 1 (POTENTIAL).
FT DOMAIN 87 95 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 96 116 2 (POTENTIAL).
FT DOMAIN 117 130 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 131 152 3 (POTENTIAL).
FT DOMAIN 153 170 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 171 191 4 (POTENTIAL).
FT DOMAIN 192 219 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 220 247 5 (POTENTIAL).
FT DOMAIN 248 263 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 264 289 6 (POTENTIAL).
FT DOMAIN 290 313 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 314 331 7 (POTENTIAL).
FT DOMAIN 332 378 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 36 36 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 129 210 BY SIMILARITY.
SQ SEQUENCE 378 AA; 42941 MW; ACB1A422CF54AA54 CRC64;

Query Match 61.6%; Score 53; DB 1; Length 378;
Best Local Similarity 61.1%; Pred. No. 0.032;
Matches 11; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 DRYAIVQATKSFRLSR 18
|||:||||| |:
DB 153 DRYAIVQAVSRHRR 170

RESULT 5
CCR4_SHEEP STANDARD; PRT; 192 AA.
AC Q28553;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE C-X-C CHEMOKINE RECEPTOR TYPE 4 (CXCR-4) (SDF-1 RECEPTOR)
DE (STROMAL CELL-DERIVED FACTOR 1 RECEPTOR) (FUSIN) (LEUKOCYTE-DERIVED
SEVEN TRANSMEMBRANE DOMAIN RECEPTOR) (LESTR) (FRAGMENT).
GN CXCR4 OR LESTR.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Hypothalamus;
RA Dyer C.J., Matteri R.L., Keisler D.H.;
RT "Development of an ovine Y3 cDNA and expression of the Y3 receptor
mRNA in the ovine hypothalamus and pituitary.";
RL Abstr. Soc. Neurosci. 21:1890-1890(1995).
CC -!- FUNCTION: RECEPTOR FOR THE C-X-C CHEMOKINE SDF-1. TRANSDUCES A
SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -!- CAUTION: WAS ORIGINALLY THOUGHT TO BE A RECEPTOR FOR NEUROPEPTIDE
Y, TYPE 3 (NPY3-R).

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EMBL; U38942; AAA81347.1; .

DR GCRDB; GCR_1581; .
DR InterPro; IPR000276; .
DR Pfam; PF00001; 7tm.1; 1.
DR PROSITE; PS00237; G_PROTEIN_RECP_FL_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECP_FL_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT NON_TER 1 1
FT DOMAIN <1 29 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 30 53 1 (POTENTIAL).
FT DOMAIN 54 69 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 70 89 2 (POTENTIAL).
FT DOMAIN 90 100 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 101 122 3 (POTENTIAL).
FT DOMAIN 123 144 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 145 165 4 (POTENTIAL).
FT DOMAIN 166 190 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 191 >192 5 (POTENTIAL).
FT DISULFID 99 176 BY SIMILARITY.
FT NON_TER 192 192
SQ SEQUENCE 192 AA; 22178 MW; A8BCFE303C52BD98 CRC64;

Query Match 57.0%; Score 49; DB 1; Length 192;
Best Local Similarity 68.8%; Pred. No. 0.081;
Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 DRYAIVQATKSFRLR 16
|||:||||| |:
DB 123 DRYAIVQATNSQRP 138

RESULT 6
CCR4_HUMAN STANDARD; PRT; 352 AA.
AC P30991; P56438;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE C-X-C CHEMOKINE RECEPTOR TYPE 4 (CXCR-4) (SDF-1 RECEPTOR)
DE (STROMAL CELL-DERIVED FACTOR 1 RECEPTOR) (FUSIN) (LEUKOCYTE-DERIVED
SEVEN TRANSMEMBRANE DOMAIN RECEPTOR) (LESTR) (FB22) (NPYRL)
DE (HM89).
GN CXCR4.
OS Homo sapiens (Human), and Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606, 9598;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=Human; TISSUE=Lung;
RX MEDLINE=93319629; PubMed=8329116;
RA Herzog H., Hort Y.J., Shine J., Selbie L.A.;
RT "Molecular cloning, characterization, and localization of the human
homolog to the reported bovine NPY Y3 receptor: lack of NPY binding
and activation.";
RL DNA Cell Biol. 12:465-471(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=Human; TISSUE=Brain;
RX MEDLINE=94052833; PubMed=8234909;
RA Jazin E.E., Yoo H., Blomqvist G., Yee F., Weng G., Walker M.W.,
RA Salton J., Larhammar D., Wahlestedt C.R.;
RT "A proposed bovine neuropeptide Y (NPY) receptor cDNA clone, or its
human homologue, confers neither NPY binding sites nor NPY
responsiveness on transfected cells.";
RL Regul. Pept. 47:247-258(1993).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=Human; TISSUE=Spleen;
RX MEDLINE=93315164; PubMed=8325644;
RA Federspiel B., Delaney A.D., Clark-Lewis I., Jirik F., Duncan A.M.,
RA Schappert K.T., Melhado I.;
RT "Molecular cloning of the cDNA and chromosomal localization of the

RT gene for a putative seven-transmembrane segment (7-TMS) receptor
 RT isolated from human spleen.";
 RT Genomics 16:707-712(1993).
 [4]
 RN SEQUENCE FROM N.A.
 RC SPECIES=Human; TISSUE=Leukocyte;
 RX MEDLINE=94103215; PubMed=8276799;
 RA Loetscher M., Geisler T., O'Reilly T., Zwahlen R., Baggiolini M.,
 RA Moser B.;
 RT "Cloning of a human seven-transmembrane domain receptor, LESTR, that
 RT is highly expressed in leukocytes.";
 RL J. Biol. Chem. 269:232-237(1994).
 [5]
 RN SEQUENCE FROM N.A.
 RC SPECIES=Human; TISSUE=Monocytes;
 RX MEDLINE=94052629; PubMed=7505609;
 RA Nomura H., Nielsen B.W., Matsushima K.;
 RT "Molecular cloning of cDNAs encoding a LD78 receptor and putative
 RT leukocyte chemotactic peptide receptors.";
 RL Int. Immunol. 5:1239-1249(1993).
 [6]
 RN SEQUENCE FROM N.A.
 RC SPECIES=Human;
 RA Wegner S.A., Ehrenberg P.K., Chang G., Dayhoff D.E., Michael N.L.;
 RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
 [7]
 RN SEQUENCE FROM N.A.
 RC SPECIES=Human;
 RX MEDLINE=98238970; PubMed=9599023;
 RA Caruz A., Sansom M., Alonso J.M., Alcaml J., Baleux F.,
 RA Virelizier J.L., Parmentier M., Arenzana-Seisdedos F.;
 RT "Genomic organization and promoter characterization of human CXCR4
 RT gene.";
 RL FEBS Lett. 426:271-278(1998).
 [8]
 RN SEQUENCE FROM N.A.
 RC SPECIES=Human;
 RA Xiao L., Weiss S., Qari S., Rudolph D., Hodge T., Lal R.;
 RT "Partial resistance to infection by syncytium-inducing primary HIV-1
 RT in exposed uninfected individuals homozygous for CCR5 32bp
 RT deletion.";
 RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
 [9]
 RN SEQUENCE FROM N.A.
 RC SPECIES=Human; TISSUE=Blood;
 RA Frodl R., Moepes B., Gierschik P.;
 RT "Genomic organization and expression pattern of the human chemokine
 RT receptor CXCR4.";
 RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
 [10]
 RN SEQUENCE FROM N.A.
 RC SPECIES=Human; TISSUE=Blood;
 RX MEDLINE=98090115; PubMed=9430250;
 RA Pretet J.-L., Zerbib A., Girard M., Guillet J.-G., Butor C.;
 RT "Chimpanzee CXCR4 and CCR5 act as coreceptors for HIV type 1.";
 RL AIDS Res. Hum. Retroviruses 13:1583-1587(1997).
 [11]
 RN FUNCTION.
 RP MEDLINE=96351077; PubMed=8752280;
 RA Bleul C.C., Farzan M., Choe H., Parolin C., Clark-Lewis I.,
 RA Sodroski J., Springer T.A.;
 RT "The lymphocyte chemoattractant SDF-1 is a ligand for LESTR/fusin and
 RT blocks HIV-1 entry.";
 RL Nature 382:829-833(1996).
 [12]
 RN FUNCTION.
 RP MEDLINE=96351078; PubMed=8752281;
 RA Oberlin E., Amara A., Bachelierie F., Bessia C., Virelizier J.-L.,
 RA Arenzana-Seisdedos F., Schwartz O., Heard J.-M., Clark-Lewis I.,
 RA Legler D.F., Loetscher M., Baggiolini M., Moser B.;
 RT "The CXCR chemokine SDF-1 is the ligand for LESTR/fusin and prevents
 RT infection by T-cell-line-adapted HIV-1.";
 RL Nature 382:833-835(1996).

[13]
 RN ERRATUM.
 RA Oberlin E., Amara A., Bachelierie F., Bessia C., Virelizier J.-L.,
 RA Arenzana-Seisdedos F., Schwartz O., Heard J.-M., Clark-Lewis I.,
 RA Legler D.F., Loetscher M., Baggiolini M., Moser B.;
 RL Nature 384:288-288(1996).
 [14]
 RN CHARACTERIZATION OF ITS HIV-1 RECEPTOR FUNCTION.
 RX MEDLINE=96217947; PubMed=8629022;
 RA Feng Y., Broder C.C., Kennedy P.E., Berger E.A.;
 RT "HIV-1 entry cofactor: functional cDNA cloning of a
 RT seven-transmembrane, G protein-coupled receptor.";
 RL Science 272:872-877(1996).
 CC -!- FUNCTION: RECEPTOR FOR THE C-X-C CHEMOKINE SDF-1. TRANSDUCES A
 CC SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. ACTS AS
 CC A CO-RECEPTOR WITH CD4 FOR SYNCYTIIUM-INDUCING STRAINS (SI) (T-
 CC CELL-LINE-ADAPTED) OF HIV-1 VIRUS. IT PROMOTES ENV-MEDIATED FUSION
 CC OF THE VIRUS.
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -!- CAUTION: WAS ORIGINALLY THOUGHT TO BE A RECEPTOR FOR NEUROPEPTIDE
 CC Y, TYPE 3 (NPY3-R).

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 DR EMBL: L01639; AA16594.1; -
 DR EMBL: M9293; AA16617.1; -
 DR EMBL: X71635; CA50641.1; -
 DR EMBL: L06797; AA03209.1; -
 DR EMBL: D10924; BAA01722.1; -
 DR EMBL: AF050058; AAB93982.1; -
 DR EMBL: AF052572; AAC34581.1; -
 DR EMBL: AF025375; AAB81970.1; -
 DR EMBL: Y14739; CA75034.1; -
 DR EMBL: U89798; AAC03718.1; -
 DR PIR: S32761; S32761.
 DR PIR: A45747; A45747.
 DR GCRDB: GCR_0438; -
 DR GCRDB: GCR_0448; -
 DR GCRDB: GCR_0475; -
 DR GCRDB: GCR_0529; -
 DR GCRDB: GCR_0903; -
 DR GCRDB: GCR_2433; -
 DR GCRDB: GCR_2568; -
 DR MIM: 162643; -
 DR InterPro: IPR000276; -
 DR InterPro: IPR001277; -
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCRHHODOPHN.
 DR PRINTS: PR00645; LCR1ORPHANR.
 DR PROSITE: PS00237; G-PROTEIN_RECP_F1_1; 1.
 DR PROSITE: PS00262; G-PROTEIN_RECP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 39
 FT TRANSMEM 40 63
 FT DOMAIN 64 79
 FT TRANSMEM 80 99
 FT DOMAIN 100 110
 FT TRANSMEM 111 132
 FT DOMAIN 133 154
 FT TRANSMEM 155 175
 FT DOMAIN 176 200
 FT TRANSMEM 201 220
 FT DOMAIN 221 240
 FT TRANSMEM 241 261
 FT DOMAIN 262 285
 FT TRANSMEM 286 305

FT DOMAIN 306 352 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 11 11 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 109 186 BY SIMILARITY.
SQ SEQUENCE 352 AA: 39745 MW; 8C8476A18678B83 CRC64;

Query Match 57.0%; Score 49; DB 1; Length 352;
Best Local Similarity 68.8%; Pred. No. 0.16;
Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 DRYIAIVQATKSFRLR 16
|||:|||||
DB 133 DRYLAIVHATNSORPR 148

RESULT 7
CCR4_MACFA STANDARD; PRT; 352 AA.
AC Q28474;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE C-X-C CHEMOKINE RECEPTOR TYPE 4 (CXC-R4) (CXCR-4) (SDF-1 RECEPTOR)
DE (STROMAL CELL-DERIVED FACTOR 1 RECEPTOR) (FUSIN) (LESTR).
GN CXCR4.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RA Tatsumi M., Takahashi H.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: RECEPTOR FOR THE C-X-C CHEMOKINE SDF-1. TRANSDUCES A
CC SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; D86579; BAAL3126.1; -
CC GCRDB; GCR_1143; -
CC InterPro; IPR000276; -
CC InterPro; IPR001277; -
CC Pfam; PF00001; 7tm_1; 1.
CC PRINTS; PR00237; GPCRHDOPSN.
CC PRINTS; PR00645; LCR1ORPHAN.
CC PROSITE; PS00237; G_PROTEIN_RECEPTOR_FL_1; 1.
CC PROSITE; PS00237; G_PROTEIN_RECEPTOR_FL_2; 1.
CC PROSITE; PS00262; G_PROTEIN_RECEPTOR_FL_2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein.
CC DOMAIN 1 39
CC EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 40 63
CC 1 (POTENTIAL).
CC DOMAIN 64 79
CC CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 80 99
CC 2 (POTENTIAL).
CC DOMAIN 100 110
CC EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 111 132
CC 3 (POTENTIAL).
CC DOMAIN 133 154
CC CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 155 175
CC 4 (POTENTIAL).
CC DOMAIN 176 200
CC CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 201 220
CC EXTRACELLULAR (POTENTIAL).
CC DOMAIN 221 240
CC 5 (POTENTIAL).
CC TRANSMEM 241 261
CC CYTOPLASMIC (POTENTIAL).
CC DOMAIN 262 285
CC 6 (POTENTIAL).
CC TRANSMEM 286 305
CC EXTRACELLULAR (POTENTIAL).
CC DOMAIN 306 352
CC CYTOPLASMIC (POTENTIAL).
CC CARBOHYD 11 11
CC N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SQ SEQUENCE 352 AA: 39751 MW; 468E542E1851265A CRC64;

FT DISULFID 109 186 BY SIMILARITY.
SQ SEQUENCE 352 AA: 39753 MW; 432DA6C11859EF8A CRC64;

Query Match 57.0%; Score 49; DB 1; Length 352;
Best Local Similarity 68.8%; Pred. No. 0.16;
Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 DRYIAIVQATKSFRLR 16
|||:|||||
DB 133 DRYLAIVHATNSORPR 148

RESULT 8
CCR4_PAPAN STANDARD; PRT; 352 AA.
AC P56431;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE C-X-C CHEMOKINE RECEPTOR TYPE 4 (CXC-R4) (CXCR-4) (SDF-1 RECEPTOR)
DE (STROMAL CELL-DERIVED FACTOR 1 RECEPTOR) (FUSIN).
GN CXCR4.
OS Papio anubis (Olive baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Papio.
OX NCBI_TaxID=9555;
RN [1]
RP SEQUENCE FROM N.A.
RA Benton P.A., Timanus D.K., Shearer M.H., Lee D.R., Kennedy R.C.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: RECEPTOR FOR THE C-X-C CHEMOKINE SDF-1. TRANSDUCES A
CC SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CC
CC EMBL; AF031089; AAC63831.1; -
CC GCRDB; GCR_2512; -
CC InterPro; IPR000276; -
CC InterPro; IPR001277; -
CC Pfam; PF00001; 7tm_1; 1.
CC PRINTS; PR00237; GPCRHDOPSN.
CC PRINTS; PR00645; LCR1ORPHAN.
CC PROSITE; PS00237; G_PROTEIN_RECEPTOR_FL_1; 1.
CC PROSITE; PS00237; G_PROTEIN_RECEPTOR_FL_2; 1.
CC PROSITE; PS00262; G_PROTEIN_RECEPTOR_FL_2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein.
CC DOMAIN 1 39
CC EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 40 63
CC 1 (POTENTIAL).
CC DOMAIN 64 79
CC CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 80 99
CC 2 (POTENTIAL).
CC DOMAIN 100 110
CC EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 111 132
CC 3 (POTENTIAL).
CC DOMAIN 133 154
CC CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 155 175
CC 4 (POTENTIAL).
CC DOMAIN 176 200
CC EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 201 220
CC 5 (POTENTIAL).
CC DOMAIN 221 240
CC CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 241 261
CC EXTRACELLULAR (POTENTIAL).
CC DOMAIN 262 285
CC 6 (POTENTIAL).
CC TRANSMEM 286 305
CC EXTRACELLULAR (POTENTIAL).
CC DOMAIN 306 352
CC CYTOPLASMIC (POTENTIAL).
CC CARBOHYD 11 11
CC N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SQ SEQUENCE 352 AA: 39751 MW; 468E542E1851265A CRC64;

Query Match 57.0%; Score 49; DB 1; Length 352;
 Best Local Similarity 68.8%; Pred. No. 0.16;
 Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 DRYAIVQATKSFRLR 16
 |||:|||||
 Db 133 DRYLAIVHATNSQRPR 148

RESULT 9
 CCR4_FELCA STANDARD; PRT; 353 AA.
 AC P56498; P79172; O02700;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE C-X-C CHEMOKINE RECEPTOR TYPE 4 (CXCR-4) (SDF-1 RECEPTOR)
 DE (STROMAL CELL-DERIVED FACTOR 1 RECEPTOR) (FUSIN) (LESTR).
 GN CXCR4.
 OS Felis silvestris catus (Cat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
 OX NCBI_TaxID=9685;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97404646; PubMed=9261358;
 RA Willett B.J., Picard L., Hosie M.J., Turner J.D., Adema K.,
 RA Clapham P.R.;
 RT "Shared usage of the chemokine receptor CXCR4 by the feline and human
 RT immunodeficiency viruses.";
 RL J. Virol. 71:6407-6415(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Willett B.J.;
 RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Lerner D.L., Elder J.H.;
 RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: RECEPTOR FOR THE C-X-C CHEMOKINE SDF-1. TRANSDUCES A
 CC SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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 CC -----
 DR EMBL; U63558; AAC48852.1; -;
 DR EMBL; U92795; AAB51765.1; -;
 DR GCRdb; GCR_1113; -;
 DR GCRdb; GCR_1114; -;
 DR InterPro; IPR000276; -;
 DR InterPro; IPR001277; -;
 DR Pfam; PF00001; 7tm1.1;
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PRINTS; PR00645; LCRIORPHAN.
 DR PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS0262; G-PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 40 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 41 64
 FT DOMAIN 65 80 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 81 100
 FT DOMAIN 101 111 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 112 133
 FT DOMAIN 134 155 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 156 176
 FT DOMAIN 177 201 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 202 221 5 (POTENTIAL).
 FT DOMAIN 222 241 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 242 262 6 (POTENTIAL).
 FT DOMAIN 263 286 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 287 306 7 (POTENTIAL).
 FT DOMAIN 307 353 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 11 11 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT DISULFID 110 187 BY SIMILARITY.
 FT CONFLICT 67 67 Q -> H (IN REF. 3).
 FT CONFLICT 263 263 D -> E (IN REF. 3).
 SQ SEQUENCE 353 AA; 39935 MW; EA2BD46068A6C05B CRC64;

Query Match 57.0%; Score 49; DB 1; Length 353;
 Best Local Similarity 68.8%; Pred. No. 0.16;
 Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 DRYAIVQATKSFRLR 16
 |||:|||||
 Db 134 DRYLAIVHATNSQRPR 149

RESULT 10
 CCR4_MOUSE STANDARD; PRT; 359 AA.
 ID CCR4_MOUSE 009062; O09059; P70233;
 AC P70658; P70346; O09062; O09059; P70233;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE C-X-C CHEMOKINE RECEPTOR TYPE 4 (CXCR-4) (SDF-1 RECEPTOR)
 DE (STROMAL CELL-DERIVED FACTOR 1 RECEPTOR) (FUSIN) (LEUKOCYTE-DERIVED
 DE SEVEN TRANSMEMBRANE DOMAIN RECEPTOR) (LESTR).
 GN CXCR4 OR LESTR OR CMKAR4 OR SDFIR.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6 X CHA; TISSUE=Thymus;
 RA Moepps B., Prodl R., Kessler H., Gierschik P.;
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SV;
 RA Heesen M., Berman M.A., Gerard C., Dorf M.E.;
 RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J;
 RA Heesen M., Berman M.A., Benson J.D., Gerard C., Dorf M.E.;
 RL "Cloning of the mouse fusin gene, homologue to a human HIV-1
 RT co-factor";
 RT J. Immunol. 157:5455-5460(1996).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Bone marrow;
 RA Nagasawa T., Nakajima T., Tachibana K., Iizasa H., Bleul C.C.,
 RA Yoshie O., Matsushima K., Yoshida N., Springer T.A., Kishimoto T.;
 RT "Molecular cloning and characterization of a murine pre-B-cell
 RT growth-stimulating factor/stromal cell-derived factor 1 receptor, a
 RT murine homolog of the human immunodeficiency virus 1 entry coreceptor
 RT fusin";
 RL Proc. Natl. Acad. Sci. U.S.A. 93:14726-14729(1996).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Thymus;
 RA Suzuki G., Nakata Y., Uzawa A., Shirasawa T., Saito T., Mita K.;
 RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.

RN RC SEQUENCE FROM N.A.
 RA STRAIN=129/SV; TISSUE=Thymus;
 RL Submitted A., Burgstahler R., Lipp M.;
 CC -!- FUNCTION: RECEPTOR FOR THE C-X-C CHEMOKINE SDF-1. TRANSDUCE A
 CC SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC
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 CC
 CC EMBL; X99581; CAA67893.1; -
 CC EMBL; X99582; CAA67894.1; -
 CC EMBL; U59760; AAB07725.1; -
 CC EMBL; U65580; AAC52953.1; -
 CC EMBL; D87747; BAA13451.1; -
 CC EMBL; AB008003; BAA18187.1; -
 CC EMBL; Z80111; CAB02201.1; -
 CC EMBL; Z80112; CAB02202.1; -
 CC GCRDB; GCR_1138; -
 CC GCRDB; GCR_1387; -
 CC GCRDB; GCR_1646; -
 CC GCRDB; GCR_1730; -
 CC GCRDB; GCR_2592; -
 CC MGD; MGI:109563; Cmkar4.
 CC InterPro; IPR000276; -
 CC InterPro; IPR001277; -
 CC Pfam; PF00001; 7tm_1; 1.
 CC PRINTS; PR00237; GPCRHHODPSN.
 CC PRINTS; PR00645; LCRORPHANR.
 CC PROSITE; PS00237; G_PROTEIN_RECEPTOR_F1_1; 1.
 CC PROSITE; PS0262; G_PROTEIN_RECEPTOR_F1_2; 1.
 CC G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 41 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 42 65
 FT DOMAIN 66 81 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 82 101
 FT DOMAIN 102 112 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 113 134
 FT DOMAIN 135 156 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 157 177
 FT DOMAIN 178 207 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 208 227
 FT DOMAIN 228 247 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 248 268
 FT DOMAIN 269 292 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 293 312
 FT DOMAIN 313 359 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 111 193 BY SIMILARITY.
 FT CARBOHYD 13 13 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 6 7 MISSING (IN REF. 6).
 FT CONFLICT 216 216 I -> V (IN REF. 1 AND 5).
 FT SEQUENCE 359 AA; 40426 MW; 33DIB5552A31595B CRC64;

Query Match 57.0%; Score 49; DB 1; Length 359;
 Best Local Similarity 68.8%; Pred. No. 0.16;
 Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DRYIAIVQATKSFRLR 16
 |||:|||||
 Db 135 DRYLAIVHATNSQRP 150

RESULT 11
 CKR9_MOUSE

ID CKR9_MOUSE STANDARD; PRT; 369 AA.
 AC Q9WUT7;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE C-C CHEMOKINE RECEPTOR TYPE 9 (C-C CKR-9) (CCR-9)
 DE (CHEMOKINE C-C RECEPTOR 10).
 GN CCR9 OR CMKBR10.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
 RN NCBI_TaxID=10090;
 RX [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Thymus;
 RX MEDLINE=99248139; Pubmed=10229797;
 RA Zaballios A., Gutierrez J., Varona R., Ardavin C., Marquez G.;
 RT "Cutting edge: Identification of the orphan chemokine receptor GPR-9-6
 RL J. Immunol. 162:5671-5675(1999).
 CC -!- FUNCTION: RECEPTOR FOR CHEMOKINE SCYA25/TECK. SUBSEQUENTLY
 CC TRANSDUCE A SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS
 CC LEVEL.
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN THE THYMUS AND LOW IN
 CC LYMPH NODES AND SPLEEN.
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC
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 CC
 CC EMBL; AJ132336; CAB43480.1; -
 CC MGD; MGI:1341902; Cmkbr10.
 CC InterPro; IPR000174; -
 CC InterPro; IPR000248; -
 CC InterPro; IPR000276; -
 CC InterPro; IPR000355; -
 CC InterPro; IPR000496; -
 CC InterPro; IPR001277; -
 CC InterPro; IPR001718; -
 CC Pfam; PF00001; 7tm_1; 1.
 CC PRINTS; PR00237; GPCRHHODPSN.
 CC PRINTS; PR00241; ANGIOTENSINR.
 CC PRINTS; PR00425; BRADYKININR.
 CC PRINTS; PR00427; INTRLEUKIN8R.
 CC PRINTS; PR00641; CHEMOKINER7.
 CC PRINTS; PR00645; LCRORPHANR.
 CC PRINTS; PR00657; CCHEMOKINER.
 CC PROSITE; PS00237; G_PROTEIN_RECEPTOR_F1_1; 1.
 CC PROSITE; PS0262; G_PROTEIN_RECEPTOR_F1_2; 1.
 CC G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 49 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 50 76
 FT DOMAIN 77 85 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 86 106
 FT DOMAIN 107 120 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 121 142
 FT DOMAIN 143 160 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 161 181
 FT DOMAIN 182 210 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 211 238
 FT DOMAIN 239 254 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 255 280
 FT DOMAIN 281 304 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 305 322
 FT DOMAIN 323 369
 FT CARBOHYD 32 32 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT DISULFID 119 198 BY SIMILARITY.

SQ SEQUENCE 369 AA; 41913 MW; 6971F76F0A24B4AE CRC64;

Query Match 55.8%; Score 48; DB 1; Length 369;
Best Local Similarity 83.38; Pred. No. 0.26;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DRYIAIQAOKS 12
||||||| I:
Db 143 DRYIAIQAOKA 154

RESULT 12

ID SSR3_HUMAN STANDARD; PRT; 418 AA.
AC P32745;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE SOMATOSTATIN RECEPTOR TYPE 3 (SS3R) (SSR-28).
GN SSTR3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93149123; PubMed=1337145;
RA Yamada Y., Reisine T., Law S.F., Ihara Y., Kubota A., Kagimoto S.,
RA Seino M., Seino Y., Bell G.I., Seino S.;
RT "Somatostatin receptors, an expanding gene family: cloning and
RT functional characterization of human SSTR3, a protein coupled to
RT adenylyl cyclase.";
RL Mol. Endocrinol. 6:2136-2142(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=93238970; PubMed=8097479;
RA Corness J.D., Demchishyn L.L., Seeman P., van Tol H.H.M.,
RA Srikant C.B., Kent G., Patel Y.C., Niznik H.B.;
RT "A human somatostatin receptor (SSTR3), located on chromosome 22,
RT displays preferential affinity for somatostatin-14 like peptides.";
RL FEBS Lett. 321:279-284(1993).
RN [3]
RP SEQUENCE FROM N.A.
RA Connor R., Davis J.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: RECEPTOR FOR SOMATOSTATINS-14 AND -28. THIS RECEPTOR IS
CC COUPLED VIA PERTUSSIS TOXIN SENSITIVE G PROTEINS TO INHIBITION OF
CC ADENYLYL CYCLASE.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- TISSUE SPECIFICITY: BRAIN, PITUITARY AND PANCREAS.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC -----
DR EMBL; M96738; AAA60592.1; -;
DR EMBL; Z82188; CAB45263.1; -;
DR PIR; S32501; S32501.
DR PIR; A46226; A46226.
DR HSP; P34996; 1DD0.
DR GCRdb; GCR_0452; -;
DR GCRdb; GCR_0630; -;
DR MIN; 182453; -;
DR InterPro; IPR000276; -;
DR InterPro; IPR000586; -;
DR InterPro; IPR001856; -;
DR Pfam; PF00001; 7tm_1; 1.

DR PRINTS; PR00237; GPCRHHODPSN.
DR PRINTS; PR00246; SOMATOSTATNR.
DR PRINTS; PR00589; SOMATOSTATNR.
DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multigene family.
KW DOMAIN 1 43 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 44 69 1 (POTENTIAL).
FT DOMAIN 70 79 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 80 101 2 (POTENTIAL).
FT DOMAIN 102 116 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 117 138 3 (POTENTIAL).
FT DOMAIN 139 161 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 162 181 4 (POTENTIAL).
FT DOMAIN 182 205 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 206 231 5 (POTENTIAL).
FT DOMAIN 232 257 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 258 279 6 (POTENTIAL).
FT DOMAIN 280 293 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 294 316 7 (POTENTIAL).
FT DOMAIN 317 418 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 17 17 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 30 30 N-LINKED (GLCNAC. .) (POTENTIAL).
FT DISULFID 116 191 BY SIMILARITY.
FT DOMAIN 346 360 GLU-RICH (ACIDIC).
SQ SEQUENCE 418 AA; 45847 MW; 1227095F801190C4 CRC64;

Query Match 55.8%; Score 48; DB 1; Length 418;
Best Local Similarity 52.9%; Pred. No. 0.3;
Matches 9; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 DRYIAIQAOKSFRILRS 17
||||| I:
Db 140 DRYIAIQAOKSFRILRS 156

RESULT 13

ID SSR3_MOUSE STANDARD; PRT; 428 AA.
AC P30935;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE SOMATOSTATIN RECEPTOR TYPE 3 (SS3R) (SSR-28).
GN SSTR3 OR SMSTR3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93015924; PubMed=1328199;
RA Yasuda K., Rens-Domiano S., Breder C.D., Law S.F., Saper C.B.,
RA Reisine T., Bell G.I.;
RT "Cloning of a novel somatostatin receptor, SSTR3, coupled to
RT adenylyl cyclase.";
RL J. Biol. Chem. 267:20422-20428(1992).
CC -!- FUNCTION: RECEPTOR FOR SOMATOSTATINS-14 AND -28. THIS RECEPTOR IS
CC COUPLED VIA PERTUSSIS TOXIN SENSITIVE G PROTEINS TO INHIBITION OF
CC ADENYLYL CYCLASE.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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DR EMBL; M91000; AAA40144.1; -
DR PIR; A44021; A44021.
DR HSP; P34996; 1DDD.
DR GCRdb; GCR_0470; -
DR MGD; MGI:98329; Smstr3.
DR InterPro; IPR000276; -
DR InterPro; IPR000586; -
DR InterPro; IPR001856; -
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PRINTS; PR00246; SOMATOSTATNR.
DR PRINTS; PR00589; SOMATOSTATNR.
DR PROSITE; PS00237; G_PROTEIN_REC_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_REC_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multigene family.
FT DOMAIN 1 45 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 46 71 1 (POTENTIAL).
FT DOMAIN 72 81 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 82 103 2 (POTENTIAL).
FT DOMAIN 104 118 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 119 140 3 (POTENTIAL).
FT DOMAIN 141 162 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 163 182 4 (POTENTIAL).
FT DOMAIN 183 206 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 207 232 5 (POTENTIAL).
FT DOMAIN 233 266 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 267 288 6 (POTENTIAL).
FT DOMAIN 289 302 POLY-GLU.
FT TRANSMEM 303 325 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 326 428 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 18 18 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 31 31 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 117 192 BY SIMILARITY.
FT DOMAIN 358 373 POLY-GLU.
SQ SEQUENCE 428 AA; 47391 MW; D006E4B7BE501FAA CRC64;

Query Match 55.8%; Score 48; DB 1; Length 428;
Best Local Similarity 52.9%; Pred. No. 0.31;
Matches 9; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DRYIAVQATKSFRLRS 17
|||:|:| | | | |
Db 141 DRYLAVVHPTSRARWT 157

RESULT 14
SSR3_RAT STANDARD; PRT; 428 AA.
ID SSR3_RAT
AC P30936;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE SOMATOSTATIN RECEPTOR TYPE 3 (SSR3) (SSR-28).
GN SSR3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=Brain;
RX MEDLINE=93066220; PubMed=1279674;
RA Meyerhof W., Wulfsen I., Schoenrock C., Fehr S., Richter D.;
RT "Molecular cloning of a somatostatin-28 receptor and comparison of
RT its expression pattern with that of a somatostatin-14 receptor in rat
RT brain."
RL Proc. Natl. Acad. Sci. U.S.A. 89:10267-10271(1992).
CC -1- FUNCTION: RECEPTOR FOR SOMATOSTATINS-14 AND -28. THIS RECEPTOR IS
CC COUPLED VIA PERTUSSIS TOXIN SENSITIVE G PROTEINS TO INHIBITION OF
CC ADENYL CYCLASE.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

```

CC -1- TISSUE SPECIFICITY: DENSELY EXPRESSED IN CEREBELLUM AND IN MODERATE LEVELS IN THE AMYGDALA, CORTEX, STRIATUM, SPLEEN, LIVER, PITUITARY.

CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

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CC EMBL; X63574; CAA45130.1; -

CC PIR; S30508; S30508.

CC HSP; P34996; 1DDD.

CC GCRdb; GCR_0502; -

CC InterPro; IPR000276; -

CC InterPro; IPR000586; -

CC InterPro; IPR001856; -

CC Pfam; PF00001; 7tm.1; 1.

CC PRINTS; PR00237; GPCRHHODOPSN.

CC PRINTS; PR00246; SOMATOSTATNR.

CC PRINTS; PR00589; SOMATOSTATNR.

CC PROSITE; PS00237; G_PROTEIN_REC_F1_1; 1.

CC PROSITE; PS0262; G_PROTEIN_REC_F1_2; 1.

KW G-protein coupled receptor; Transmembrane; Glycoprotein;

KW Multigene family.

FT DOMAIN 1 45 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 46 71 1 (POTENTIAL).

FT DOMAIN 72 81 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 82 103 2 (POTENTIAL).

FT DOMAIN 104 118 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 119 140 3 (POTENTIAL).

FT DOMAIN 141 162 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 163 182 4 (POTENTIAL).

FT DOMAIN 183 206 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 207 232 5 (POTENTIAL).

FT DOMAIN 233 266 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 267 288 6 (POTENTIAL).

FT DOMAIN 289 302 POLY-GLU.

FT TRANSMEM 303 325 EXTRACELLULAR (POTENTIAL).

FT DOMAIN 326 428 CYTOPLASMIC (POTENTIAL).

FT CARBOHYD 18 18 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 31 31 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT DISULFID 117 192 BY SIMILARITY.

FT DOMAIN 358 373 POLY-GLU.

SQ SEQUENCE 428 AA; 47151 MW; BE0AA948840A9E9D CRC64;

Query Match 55.8%; Score 48; DB 1; Length 428;

Best Local Similarity 52.9%; Pred. No. 0.31;

Matches 9; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DRYIAVQATKSFRLRS 17

|||:|:| | | | |

Db 141 DRYLAVVHPTSRARWT 157

RESULT 15

GPRH_HUMAN STANDARD; PRT; 339 AA.

ID GPRH_HUMAN

AC Q13304;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 01-OCT-2000 (Rel. 40, Last annotation update)

DE PUTATIVE G PROTEIN-COUPLED RECEPTOR GPR17 (R12).

GN GPR17.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

```

RP SEQUENCE FROM N.A.
RX MEDLINE=96145150; PubMed=8558062;
RA Raport C.J., Schweickart V.L., Chantry D., Eddy R.L. Jr., Shows T.B.,
RT Godiska R., Gray P.W.;
RL "New members of the chemokine receptor gene family.";
RN J. Leukoc. Biol. 59:18-23(1996).
[2]
RP SEQUENCE FROM N.A.
RX TISSUE=Hippocampus;
RA MEDLINE=98181695; PubMed=9523551;
RA Blaesus R.H., Weber R.G., Lichter P., Ogilvie A.;
RT "A novel orphan G protein-coupled receptor primarily expressed in the
RL brain is localized on human chromosomal band 2q21.";
RL J. Neurochem. 70:1357-1365(1998).
CC -!- FUNCTION: ORPHAN RECEPTOR. POTENTIAL CHEMOKINE RECEPTOR.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- TISSUE SPECIFICITY: PRIMARILY EXPRESSED IN BRAIN.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC -----
DR EMBL; U33447; AAB16746.1; -
DR EMBL; Z94154; CAB08107.1; -
DR HSP; P34996; IDDD.
DR GCRdb; GCR_1968; -
DR GCRdb; GCR_2597; -
DR MIM; 603071; -
DR InterPro; IPR000276; -
DR Pfam; PF00001; 7cm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G-PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 36
FT TRANSMEM 37 57
FT DOMAIN 58 64
FT TRANSMEM 65 85
FT DOMAIN 86 105
FT TRANSMEM 106 126
FT DOMAIN 127 147
FT TRANSMEM 148 168
FT DOMAIN 169 195
FT TRANSMEM 196 216
FT DOMAIN 217 232
FT TRANSMEM 233 253
FT DOMAIN 254 280
FT TRANSMEM 281 301
FT DOMAIN 302 339
FT TRANSMEM 340 360
FT CARBOHYD 14 14
FT CARBOHYD 176 176
FT CARBOHYD 254 254
SQ SEQUENCE 339 AA; 37826 MW; BD2AEDB2FEBF15E1 CRC64;
Query Match 54.7%; Score 47; DB 1; Length 339;
Best Local Similarity 56.2%; Pred. No. 0.36;
Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
Qy 1 DRYTAIVQATKSFRLR 16
Db 128 DRELAIVHPVKSLKLR 143

```


GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 23, 2001, 15:35:14 ; Search time 189.03 Seconds
(without alignments)

11.161 Million cell updates/sec

Title: US-08-887-977-10_COPY_133_150

Perfect score: 86

Sequence: 1 DRYIAIVQATKSFRLRSR 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_15:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_unclassified:*
13: sp_vertebrate:*
14: sp_virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	83	96.5	367	11 Q9R1V0	Q9R1V0 mus musculus
2	54	62.8	303	13 P70058	P70058 xenopus lae
3	54	62.8	353	13 P79960	P79960 xenopus lae
4	52	60.5	380	5 Q9NFV3	Q9NFV3 lymphnaea sta
5	52	60.5	380	5 Q9NFV2	Q9NFV2 lymphnaea sta
6	52	60.5	380	5 Q9NFV1	Q9NFV1 lymphnaea sta
7	52	60.5	380	5 Q9NFV0	Q9NFV0 lymphnaea sta
8	51	59.3	353	13 Q9PTF7	Q9PTF7 brachydanio
9	50	58.1	357	13 O42445	O42445 oncorhynch
10	49	57.0	334	6 Q9N1P4	Q9N1P4 cercopithec
11	49	57.0	334	6 Q9N1P3	Q9N1P3 hylobates l
12	49	57.0	334	6 Q9N1P2	Q9N1P2 saquinus oe
13	49	57.0	334	6 Q9N130	Q9N130 saimiri bol
14	49	57.0	337	4 O75819	O75819 homo sapien
15	49	57.0	346	6 Q9M2M4	Q9M2M4 nycticebus
16	49	57.0	346	6 Q9M2M3	Q9M2M3 nycticebus
17	49	57.0	346	6 Q9M2M2	Q9M2M2 nycticebus
18	49	57.0	347	6 Q9M2N6	Q9M2N6 hylobates c
19	49	57.0	347	6 Q9M2N5	Q9M2N5 hylobates h

ALIGNMENTS

RESULT 1

Q9R1V0 ID Q9R1V0 PRELIMINARY; PRT; 367 AA.
AC Q9R1V0;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE CC CHEMOKINE LARC SPECIFIC RECEPTOR.
GN MCCR6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RA SEQUENCE FROM N.A.
RP Tanaka Y.;
RT "Molecular Cloning of Murine Homologue of CCR6, the Specific Receptor for CC Chemokine LARC."
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB016031; BAA82443.1;
DR INTERPRO; IPR000190;
DR INTERPRO; IPR000276;
DR INTERPRO; IPR000355;
DR PFAM; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PRINTS; PR00635; ANGIOTENSINR.
DR PRINTS; PR00657; CCHEMOKINER.
DR PROSITE; PS00237; G-PROTEIN-RECEPTOR; UNKNOWN_1.
KW Receptor.
SQ SEQUENCE 367 AA; 42082 MW; 207FD98B2F7A6DD3 CRC64;

Query Match 96.5%; Score 83; DB 11; Length 367;
Best Local Similarity 94.4%; Pred. No. 3.7e-07;
Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRYIAIVQATKSFRLRSR 18

Db 134 DRYIAIVQATKSFRLRSR 151

RESULT 2

Q9mzn4 hylobates l
Q9mzn3 hylobates s
Q9mzn2 pongo pygma
Q9mzn1 gorilla gor
Q9mzn0 atouatta se
Q9mzm9 ateles pani
Q9mzm7 callimico g
Q9mzm6 callicebus
Q9mzm1 eulemur mac
O77488 cercopithec
Q9ukn2 homo sapien
Q60835 homo sapien
Q9mzm5 pithecia pi
Q9pua0 acipenser r
Q9udz6 homo sapien
Q93247 cyprinus ca
Q9jly8 rattus norv
Q9uly7 homo sapien
Q9uly6 homo sapien
Q9ue21 homo sapien
Q9kv08 mus musculu
Q9jhg3 rattus norv
O97666 macaca mula
Q9tv16 pan troglod
Q9xt45 macaca mula
Q9n0z0 cercocebus

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P70058
ID P70058 PRELIMINARY; PRT; 303 AA.
AC P70058;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE ANGIOTENSIN RECEPTOR RELATED PROTEIN.
GN XANGI01.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Saha M.S., Oakes J.A., Miles R.R.;
RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; U72029; AAB17004.1; -.
DR INTERPRO; IPR000276; -.
DR PFAM; PF00001; 7tm.1.1.
DR PROSITE; PS00237; G-PROTEIN_RECEPTOR; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
SQ SEQUENCE 303 AA; 34088 MW; C4E2D902DDEFAF5D1 CRC64;

Query Match 62.8%; Score 54; DB 13; Length 303;
Best Local Similarity 61.1%; Pred. No. 0.067;
Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 DRYIAIVQATKSFRLRSR 18
DB 132 DRYLAIVHSLSSAKLRSR 149
||||| : | : |||

RESULT 3
P79960
ID P79960 PRELIMINARY; PRT; 353 AA.
AC P79960;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE MESENCHYME-ASSOCIATED SERPENTINE RECEPTOR.
GN X-MSR.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-97109511; PubMed-8951791;
RA Devic E., Paquereau L., Vernier P.;
RT "Expression of a new G protein-coupled receptor X-msr is associated with an endothelial lineage in Xenopus laevis.";
RL Mech. Dev. 59:129-140(1996).
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; X93045; CAA63612.1; -.
DR INTERPRO; IPR000276; -.
DR PFAM; PF00001; 7tm.1.1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G-PROTEIN_RECEPTOR; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
SQ SEQUENCE 353 AA; 40303 MW; 1BF757DB65057621 CRC64;

Query Match 62.8%; Score 54; DB 13; Length 353;
Best Local Similarity 61.1%; Pred. No. 0.079;
Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 DRYIAIVQATKSFRLRSR 18

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DB 132 DRYLAIVHSLSSAKLRSR 149
||||| : | : |||

RESULT 4
Q9NFV3
ID Q9NFV3 PRELIMINARY; PRT; 380 AA.
AC Q9NFV3;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE G-PROTEIN COUPLED RECEPTOR.
GN ORPH 1.
OS Lymnaea stagnalis (Great pond snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Basommatophora;
OC Lymnaeidae; Lymnaea.
OX NCBI_TaxID=6523;
RN [1]
RP SEQUENCE FROM N.A.
RA Saunders S.E., Burke J.F., Benjamin P.R.;
RT "Multimeric CREB binding sites in the promoter regions of a family of orphan G-protein coupled receptors related to the vertebrate galanin and nociceptin/orphanin-FQ receptor families.";
RT Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ270459; CAB77262.1; -.
DR KW Receptor; G-protein coupled receptor.
SQ SEQUENCE 380 AA; 42773 MW; DFB1E56A20C72629 CRC64;

Query Match 60.5%; Score 52; DB 5; Length 380;
Best Local Similarity 58.8%; Pred. No. 0.2;
Matches 10; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 DRYIAIVQATKSFRLRS 17
DB 143 DRYLAVVHAIRSMTLRS 159
||||| : | : |||

RESULT 5
Q9NFV2
ID Q9NFV2 PRELIMINARY; PRT; 380 AA.
AC Q9NFV2;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE G-PROTEIN COUPLED RECEPTOR.
GN ORPH 2.
OS Lymnaea stagnalis (Great pond snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Basommatophora;
OC Lymnaeidae; Lymnaea.
OX NCBI_TaxID=6523;
RN [1]
RP SEQUENCE FROM N.A.
RA Saunders S.E., Burke J.F., Benjamin P.R.;
RT "Multimeric CREB binding sites in the promoter regions of a family of orphan G-protein coupled receptors related to the vertebrate galanin and nociceptin/orphanin-FQ receptor families.";
RT Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ270460; CAB77263.1; -.
DR KW Receptor; G-protein coupled receptor.
SQ SEQUENCE 380 AA; 42595 MW; C1CEE818CF3AF1FC CRC64;

Query Match 60.5%; Score 52; DB 5; Length 380;
Best Local Similarity 58.8%; Pred. No. 0.2;
Matches 10; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 DRYIAIVQATKSFRLRS 17
DB 143 DRYLAVVHAIRSMTLRS 159
||||| : | : |||

RESULT 6

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Q9NFV1
ID Q9NFV1 PRELIMINARY; PRT; 380 AA.
AC Q9NFV1;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE G-PROTEIN COUPLED RECEPTOR.
GN ORPH 3.
OS Lymnaea stagnalis (Great pond snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;
OC Lymnaeidae; Lymnaea.
OX NCBI_TaxID=6523;
RN [1]
RP SEQUENCE FROM N.A.
RA Saunders S.E., Burke J.F., Benjamin P.R.;
RT "Multimeric CREB binding sites in the promoter regions of a family of
RT orphan G-protein coupled receptors related to the vertebrate galanin
RT and nociceptin/orphanin-FQ receptor families.";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ270461; CAB77264.1;
DR PRINTS; PR00657; CCHEMOKINER.
KW Receptor; G-protein coupled receptor.
SQ SEQUENCE 380 AA; 42604 MW; A072ADFCD89028D3 CRC64;

Query Match 60.5%; Score 52; DB 5; Length 380;
Best Local Similarity 58.8%; Pred. No. 0.2;
Matches 10; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DRYIAIVQATKSFRLR 17
|||:|:|:|:|
Db 143 DRYLAVVHAIRSMTLRS 159

RESULT 7
Q9NFV0
ID Q9NFV0 PRELIMINARY; PRT; 380 AA.
AC Q9NFV0;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE G-PROTEIN COUPLED RECEPTOR.
GN ORPH 4.
OS Lymnaea stagnalis (Great pond snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;
OC Lymnaeidae; Lymnaea.
OX NCBI_TaxID=6523;
RN [1]
RP SEQUENCE FROM N.A.
RA Saunders S.E., Burke J.F., Benjamin P.R.;
RT "Multimeric CREB binding sites in the promoter regions of a family of
RT orphan G-protein coupled receptors related to the vertebrate galanin
RT and nociceptin/orphanin-FQ receptor families.";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ270462; CAB77265.1;
DR PRINTS; PR00657; CCHEMOKINER.
KW Receptor; G-protein coupled receptor.
SQ SEQUENCE 380 AA; 42723 MW; D54F5BE2BBFE4EC4 CRC64;

Query Match 60.5%; Score 52; DB 5; Length 380;
Best Local Similarity 58.8%; Pred. No. 0.2;
Matches 10; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DRYIAIVQATKSFRLR 17
|||:|:|:|:|
Db 143 DRYLAVVHAIRSMTLRS 159

RESULT 8
Q9PTF7
ID Q9PTF7 PRELIMINARY; PRT; 353 AA.
AC Q9PTF7;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)

DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE CHEMOKINE RECEPTOR CXCR4.
GN CXCR4.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Rasbora; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Tseng S., Rollins B.J.;
RT "Chemokines and chemokine receptors in zebrafish.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF201451; AAF17561.1;
DR INTERPRO; IPR000276;
DR INTERPRO; IPR000355;
DR INTERPRO; IPR001277;
DR PFAM; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHHODOPS.
DR PRINTS; PR00645; LCR1ORPHANR.
DR PRINTS; PR00657; CCHEMOKINER.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; 1.
KW Receptor.
SQ SEQUENCE 353 AA; 39444 MW; 410F9A7F75D631BE CRC64;

Query Match 59.3%; Score 51; DB 13; Length 353;
Best Local Similarity 62.5%; Pred. No. 0.28;
Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DRYIAIVQATKSFRLR 16
|||:|:|:|:|
Db 131 DRYLAVVHAIRSMTLRS 146

RESULT 9
Q42445
ID Q42445 PRELIMINARY; PRT; 357 AA.
AC Q42445;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE CXCR4 CHEMOKINE RECEPTOR.
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE FROM N.A.
RA Daniels G.D., Charlemagne J., Secombes C.J.;
RT "Cloning and sequencing of a rainbow trout, Oncorhynchus mykiss,
RT chemokine receptor homolog.";
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; AJ001039; CAA04493.1;
DR INTERPRO; IPR000276;
DR PFAM; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHHODOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
SQ SEQUENCE 357 AA; 39817 MW; 14EC2F01DA1222C4 CRC64;

Query Match 58.1%; Score 50; DB 13; Length 357;
Best Local Similarity 58.8%; Pred. No. 0.43;
Matches 10; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DRYIAIVQATKSFRLR 17
|||:|:|:|:|
Db 135 DRYLAVVHAIRSMTLRS 151

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RESULT 10
Q9NIP4
ID Q9NIP4 PRELIMINARY; PRT; 334 AA.
AC Q9NIP4;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE CXC CHEMOKINE RECEPTOR 4 (FRAGMENT).
GN CXCR4.
OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9534;
RN [1]
RP SEQUENCE FROM N.A.
RA Zubair S., Metzberg S.;
RT "CXCR4 homologs of Gibbon ape, African green monkey, and Cotton-top
marmoset."
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF178082; AAF42990.1;
KW Receptor.
FT NON_TER 1 1
FT NON_TER 334 334
SQ SEQUENCE 334 AA; 37752 MW; 8C91CED8AB54D131 CRC64;

Query Match 57.0%; Score 49; DB 6; Length 334;
Best Local Similarity 68.8%; Pred. No. 0.62;
Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DRYIAIQAATKSFRLR 16
|||:|||||
Db 120 DRYLAIVHATNSQRP 135

RESULT 11
Q9NIP3
ID Q9NIP3 PRELIMINARY; PRT; 334 AA.
AC Q9NIP3;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE CXC CHEMOKINE RECEPTOR 4 (FRAGMENT).
GN CXCR4.
OS Hylobates lar (Common gibbon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
OX NCBI_TaxID=9580;
RN [1]
RP SEQUENCE FROM N.A.
RA Zubair S., Metzberg S.;
RT "CXCR4 homologs of Gibbon ape, African green monkey, and Cotton-top
marmoset."
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF178083; AAF42991.1;
KW Receptor.
FT NON_TER 1 1
FT NON_TER 334 334
SQ SEQUENCE 334 AA; 37725 MW; C8813B0CB3CF9A61 CRC64;

Query Match 57.0%; Score 49; DB 6; Length 334;
Best Local Similarity 68.8%; Pred. No. 0.62;
Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DRYIAIQAATKSFRLR 16
|||:|||||
Db 120 DRYLAIVHATNSQRP 135

RESULT 12
Q9NIP2
ID Q9NIP2 PRELIMINARY; PRT; 334 AA.
AC Q9NIP2;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE CXC CHEMOKINE RECEPTOR 4 (FRAGMENT).
GN CXCR4.
OS Saguinus oedipus (Cotton-top tamarin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Saguinus.
OX NCBI_TaxID=9490;
RN [1]
RP SEQUENCE FROM N.A.
RA Zubair S., Metzberg S.;
RT "CXCR4 homologs of Gibbon ape, African green monkey, and Cotton-top
marmoset."
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF178084; AAF42992.1;
KW Receptor.
FT NON_TER 1 1
FT NON_TER 334 334
SQ SEQUENCE 334 AA; 37877 MW; EB2362E88D0997C5 CRC64;

Query Match 57.0%; Score 49; DB 6; Length 334;
Best Local Similarity 68.8%; Pred. No. 0.62;
Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DRYIAIQAATKSFRLR 16
|||:|||||
Db 120 DRYLAIVHATNSQRP 135

RESULT 13
Q9N130
ID Q9N130 PRELIMINARY; PRT; 334 AA.
AC Q9N130;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE CXCR4 RECEPTOR (FRAGMENT).
OS Saimiri boliviensis (Bolivian squirrel monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Saimiri.
OX NCBI_TaxID=27679;
RN [1]
RP SEQUENCE FROM N.A.
RA Zubair S., Metzberg S.;
RT TISSUE-BLOOD;
RC "CXCR4 homologs of Gibbon ape, African green monkey, Cotton-top
marmoset, and Bolivian squirrel monkey."
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF229128; AAF37288.1;
KW Receptor.
FT NON_TER 1 1
FT NON_TER 334 334
SQ SEQUENCE 334 AA; 37943 MW; 277227E898098DB5 CRC64;

Query Match 57.0%; Score 49; DB 6; Length 334;
Best Local Similarity 68.8%; Pred. No. 0.62;
Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DRYIAIQAATKSFRLR 16
|||:|||||
Db 120 DRYLAIVHATNSQRP 135

RESULT 14
O75819
ID O75819 PRELIMINARY; PRT; 337 AA.

```

```

AC 075819;
DT 01-NOV-1998 (TReMBLrel. 08, Created)
DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
DT 01-JUN-2000 (TReMBLrel. 14, Last annotation update)
DE T CELL-DEATH ASSOCIATED PROTEIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98317948; PubMed=9655242;
RA Kyaw H., Zeng Z., Su K., Fan P., Shell B.K., Carter K.C., Li Y.;
RT "Cloning, characterization, and mapping of human homolog of mouse T-
RL DNA Cell Biol. 17:493-500(1998).
DR EMBL; U95218; AAC31794.1; -
DR INTERPRO; IPR000276; -
DR INTERPRO; IPR000504; -
DR PFAM; PF00001; 7tm_1; 1.
DR PROSITE; PS00030; RNP_1; UNKNOWN_1.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
SQ SEQUENCE 337 AA; 39339 MW; 05DA739457B079A2 CRC64;

Query Match 57.0%; Score 49; DB 4; Length 337;
Best Local Similarity 55.6%; Pred. No. 0.63;
Matches 10; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 DRYIAIVQATKSFRLRSR 18
   |||:|:| | | | |
Db 111 DRYLAIVVPLKFFFLRTR 128

RESULT 15
Q9MZM4
ID Q9MZM4 PRELIMINARY; PRT; 346 AA.
AC Q9MZM4;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DE 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
DE CHEMOKINE RECEPTOR CXCR4 (FRAGMENT).
GN CXCR4.
OS Nycticebus coucang (Slow loris).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Strepsirhini; Loridae; Nycticebus.
OX NCBI_TaxID=9470;
RN [1]
RP SEQUENCE FROM N.A.
RA Zheng X.-Z., Zhang Y.-P., Geng Z.-C.;
RT "Molecular Evolution of the Chemokine Receptor CXCR4 Gene Sequences in
RT Primates.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF172239; AAF89359.1; -
KW Receptor.
FT NON_TER.
FT SEQUENCE 1 1
SQ SEQUENCE 346 AA; 39235 MW; BC176D2E634CCEE CRC64;

Query Match 57.0%; Score 49; DB 6; Length 346;
Best Local Similarity 68.8%; Pred. No. 0.64;
Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 DRYIAIVQATKSFRLR 16
   |||:|:| | | | |
Db 128 DRYLAIVHATNSQRP 143

```

Search completed: May 23, 2001, 15:35:14
Job time: 620 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 23, 2001, 15:28:29 ; Search time 184.73 Seconds
(without alignments)
8.045 Million cell updates/sec

Title: US-08-887-977-10_COPY_151_176

Perfect score: 129

Sequence: 1 TLPKRIICLVWGLSVIISSTFV 26

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 390729 seqs, 57163235 residues

Total number of hits satisfying chosen parameters: 390729

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_0401.*
1: /SID56/gcgdata/geneseq/geneseq/AA1980.DAT.*
2: /SID56/gcgdata/geneseq/geneseq/AA1981.DAT.*
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6: /SID56/gcgdata/geneseq/geneseq/AA1985.DAT.*
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9: /SID56/gcgdata/geneseq/geneseq/AA1988.DAT.*
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13: /SID56/gcgdata/geneseq/geneseq/AA1992.DAT.*
14: /SID56/gcgdata/geneseq/geneseq/AA1993.DAT.*
15: /SID56/gcgdata/geneseq/geneseq/AA1994.DAT.*
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21: /SID56/gcgdata/geneseq/geneseq/AA2000.DAT.*
22: /SID56/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	129	100.0	365	19	Human dendritic ce
2	129	100.0	365	21	Primate (human) ch
3	60	46.5	354	15	Interleukin 8 (IL-
4	60	46.5	355	13	Sequence in a high
5	60	46.5	355	16	Recombinant high a
6	58	45.0	312	15	G-protein coupled
7	58	45.0	312	17	G-protein coupled
8	58	45.0	355	14	Human IL-8 recepto
9	58	45.0	355	17	Human IL-8 recepto
10	58	45.0	360	13	Sequence in a low
11	58	45.0	360	16	Interleukin 8 rece

12	58	45.0	1064	16	R70124	IL8-R type 2-GSP 1
13	57	44.2	358	13	R28274	Sequence in a low
14	57	44.2	358	16	R80952	Recombinant high a
15	55	42.6	342	20	W97784	African green monk
16	55	42.6	342	20	W97785	Pig-tailed macaque
17	55	42.6	368	19	W54371	Human IP-10/Mig re
18	55	42.6	368	21	Y90614	Human G protein-co
19	55	42.6	368	21	Y90648	Human mutant G-pro
20	55	42.6	378	20	Y50129	Human chemokine re
21	55	42.6	415	18	W19780	Human G-protein ch
22	54	41.9	49	21	B27602	Human secreted pro
23	54	41.9	73	19	W69998	Rodent chemokine r
24	54	41.9	350	13	R27791	Interleukin-8 rece
25	54	41.9	350	16	R68811	Interleukin-8 rece
26	54	41.9	350	16	R80756	Interleukin 8 rece
27	54	41.9	350	16	R80951	Recombinant high a
28	54	41.9	350	17	B09989	Human IL-8 recepto
29	54	41.9	367	19	W69999	Rodent chemokine r
30	54	41.9	1060	16	R70123	IL8-R type 1-GSP 1
31	53	41.1	176	22	B45701	Human 7TM clone H7
32	53	41.1	322	20	Y30164	Human dorsal root
33	53	41.1	322	21	Y87663	Human G protein-co
34	53	41.1	322	21	Y87664	Human G protein-co
35	51	39.5	395	19	W44703	Human Th2/B19. Ho
36	50	38.8	302	19	W70001	Rodent chemokine r
37	50	38.8	338	21	Y77736	Seven times membra
38	50	38.8	351	20	Y23825	A7 times membrane
39	50	38.8	372	20	W86323	Kidney injury asso
40	49	38.0	304	15	R48714	G-protein coupled
41	49	38.0	304	17	W02686	G-protein coupled
42	49	38.0	316	15	R48725	G-protein coupled
43	49	38.0	316	17	W02697	G-protein coupled
44	49	38.0	325	8	P70428	Polypeptide encode
45	49	38.0	360	16	R80953	Recombinant high a

ALIGNMENTS

RESULT	1
W48086	
ID	W48086 standard; Protein; 365 AA.
AC	
XX	W48086;
XX	
DF	11-JUN-1998 (first entry)
XX	Human dendritic cell chemokine receptor.
DE	
DE	Human; thymus expressed chemokine; TECK; MIP-3alpha; MIP-3beta;
KW	receptor; dendritic cell; macrophage; inflammation; asthma.
KW	
XX	Homo sapiens.
OS	
XX	
Key	Location/Qualifiers
FT	Misc-difference 193
FT	/note= "encoded by CAN"
XX	
PN	WO9801557-A2.
XX	
PD	15-JAN-1998.
XX	
PF	02-JUL-1997; 97WO-US10819.
XX	
PR	04-JUN-1997; 97US-0048593.
PR	05-JUL-1996; 96US-0675814.
PR	11-OCT-1996; 96US-0028329.
XX	
XX	(SCHE) SCHERING CORP.
PA	
PI	Gish KC, Schall TJ, Vicari A, Wang W, Zlotnik A;
XX	
XX	WPI; 1998-101054/09.
DR	

DR N-PSDB; V15418.
 XX Novel chemokines, e.g. thymus expressed chemokine - used for
 PT treating inflammatory conditions including asthma.
 XX
 XX
 PS Claim 3; Page 94-95; 202pp; English.
 XX
 CC The present sequence represents human dendritic cell chemokine receptor.
 CC Antibodies which bind to the protein can be used in detecting or
 CC diagnosing various immunological conditions related to expression
 CC of the protein. The nucleic acid can be used for screening and
 CC isolating DNA clones for the chemokines, especially from other
 CC species. The chemokine can be used in the treatment of conditions
 CC associated with abnormal physiology or development, including
 CC inflammatory conditions such as asthma.
 XX
 XX Sequence 365 AA;
 SQ

Query Match 100.0%; Score 129; DB 19; Length 365;
 Best Local Similarity 100.0%; Pred. No. 2.1e-12;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TLPRSKIICLVWGLSVIISSTFVF 26
 DB 151 tlprskilclvwglsviisstfvf 176

RESULT 2
 Y97077
 ID Y97077 standard; Protein; 365 AA.
 XX
 AC Y97077;
 XX
 DT 04-DEC-2000 (first entry)
 XX
 DE Primate (human) chemokine receptor CCR6.
 XX
 XX MIP-3-alpha; chemokine; CCR6 receptor; ligand; cytostatic; agonist;
 KW antagonist; anti-psoriatic; dermatological; immunosuppressive;
 KW anti-inflammatory.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FT Misc-difference 193 /note= "Encoded by CAN#"
 FT
 XX WO200046248-A1.
 PN
 PD 10-AUG-2000.
 XX
 XX 02-FEB-2000; 2000WO-US00511.
 PF
 XX 03-FEB-1999; 99US-0244281.
 PR
 XX (SCHE) SCHERING CORP.
 PA
 XX Oldham ER, Honey B, Dieu-Nosjean M, Caux C, Zlotnik A;
 PI
 XX WPI; 2000-543477/49.
 DR
 XX N-PSDB; A51971.
 DR
 XX Novel methods for modulating the migration of cells within or to the
 PT skin using MIP-3-alpha or CCR6 agonists or antagonists, useful for
 PT treating skin disorders, e.g. cancer
 PT
 XX Disclosure; Page 53-54; 61pp; English.
 PS
 XX The MIP-3-alpha chemokine is expressed in inflamed skin cells. This
 CC chemokine is the ligand for the CCR6 receptor. MIP-3-alpha or CCR6
 CC agonists or antagonists can be used to modulate the migration of a cell
 CC within or to the skin of a mammal. MIP-3-alpha can be used to purify a

CC population of cells expressing a MIP-3-alpha receptor. The methods are
 CC useful for treating a mammalian subject with a skin disease or condition,
 CC e.g. cancer, metastasis, psoriasis, atopic or contact dermatitis,
 CC systemic lupus erythematosus and lichen ruber planus, or for treating
 CC skin transplants or grafts.
 XX
 XX Sequence 365 AA;
 SQ

Query Match 100.0%; Score 129; DB 21; Length 365;
 Best Local Similarity 100.0%; Pred. No. 2.1e-12;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TLPRSKIICLVWGLSVIISSTFVF 26
 DB 151 tlprskilclvwglsviisstfvf 176

RESULT 3
 R53932
 ID R53932 standard; Protein; 354 AA.
 XX
 AC R53932;
 XX
 DT 23-FEB-1995 (first entry)
 XX
 DE Interleukin 8 (IL-8) receptor.
 XX
 KW Interleukin; receptor; antiinflammatory; psoriasis; reperfusion;
 KW rheumatoid arthritis; allograft; graft rejection.
 XX
 OS Homo sapiens.
 XX
 XX JP06100595-A.
 PN
 PD 12-APR-1994.
 XX
 XX 27-MAY-1991; 91JP-0149245.
 PF
 XX 27-MAY-1991; 91JP-0149245.
 PR
 XX (UYBO-) UNIV BOSTON.
 PA
 XX WPI; 1994-156656/19.
 DR
 XX N-PSDB; Q63919.
 DR
 XX Recombinant interleukin-8 receptor polypeptide - having
 PT antiinflammatory properties
 PT
 XX Claim 1; Figure 1; 13pp; Japanese.
 PS
 XX Anti-inflammatory agents containing the interleukin-8 receptor
 CC polypeptide can be used for the treatment of psoriasis, rheumatoid
 CC arthritis and other acute and chronic inflammatory diseases,
 CC including reperfusion and allograft rejection.
 XX
 XX Sequence 354 AA;
 SQ

Query Match 46.5%; Score 60; DB 15; Length 354;
 Best Local Similarity 52.4%; Pred. No. 0.15;
 Matches 11; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
 QY 6 KIICLVWGLSVIISSTFVF 26
 DB 158 kfclgiwalsilslpfllf 178

RESULT 4
 R28272
 ID R28272 standard; Protein; 355 AA.
 XX
 AC R28272;

XX 04-APR-1993 (first entry)
 XX Sequence in a high affinity recombinant rabbit interleukin-8
 DE (IL-8) receptor polypeptide in F3R.
 XX
 XX IL-8 receptor polypeptide; G-protein-coupled receptor.
 XX
 XX Oryctolagus cuniculus.
 OS
 XX WO9218641-A.
 PN
 XX 29-OCT-1992.
 PD
 XX
 XX 10-APR-1992; 92WO-US02977.
 PF
 XX
 XX 10-APR-1991; 91US-0685101.
 PR
 XX 09-JUL-1991; 91US-0726606.
 PR
 XX 09-DEC-1991; 91US-0803842.
 PR
 XX (REP K) REPLIGEN CORP.
 PA (UYBO-) UNIV BOSTON.
 PA
 XX Navarro J, Thomas KM, Witt DP;
 PI
 XX WPI; 1992-382123/46.
 DR
 XX N-PSDB; Q30011.
 DR
 XX Recombinant mammalian interleukin-8 receptor - used for screening
 PT interleukin-8 binding antagonists, used to treat inflammation
 PT
 XX Claim 2; Fig 1; 71pp; English.
 PS
 XX Rabbit high affinity IL-8 receptor gene was isolated from rabbit
 CC peritoneal neutrophils and used as a source of poly(A)+ RNA, to
 CC produce a rabbit neutrophil cDNA library. 250,000 recombinant
 CC plaques were screened for those which hybridized to an antisense
 CC oligonucleotide (Q30015). This probe was designed based on the
 CC sequence derived from the second transmembrane domain of G-protein-
 CC coupled receptors. After tertiary screening, six plaques were
 CC isolated. The insert of one of these plaques, termed F3R was of 2.5
 CC kb in size. This insert was sequenced. The protein deduced from
 CC the F3R clone demonstrates that it belongs to the family of
 CC G-protein-coupled receptors. The deduced protein sequence
 CC indicates seven putative transmembrane segments.
 CC
 XX Sequence 355 AA;
 SQ

Query Match 46.5%; Score 60; DB 13; Length 355;
 Best Local Similarity 52.4%; Pred. No. 0.15;
 Matches 11; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
 QY 6 KIICLVWGLSVIISSTFVF 26
 Db 159 kfclgiwalslslpfflf 179

RESULT 5
 R80950
 ID R80950 standard; Protein; 355 AA.
 XX
 XX R80950;
 AC
 XX 24-APR-1996 (first entry)
 DT
 XX Recombinant high affinity interleukin-8 receptor subtype A.
 DE
 XX IL-8A; IL-8B; receptor; monoclonal antibody; inflammatory disorder;
 KW anaphylaxis; systemic lupus erythematosus; rheumatoid arthritis;
 KW systemic necrotizing vasculitis; psoriasis; asthma; allergy; ARDS;
 KW adult respiratory distress syndrome; neutrophil detection.
 XX

OS Oryctolagus cuniculus.
 XX
 XX WO9525126-A1.
 PN
 XX 21-SEP-1995.
 PD
 XX
 XX 09-MAR-1995; 95WO-US03032.
 PF
 XX
 XX 02-MAY-1994; 94US-0237937.
 PR
 XX 15-MAR-1994; 94US-0210250.
 PR
 XX (REP K) REPLIGEN CORP.
 PA (UYBO-) UNIV BOSTON.
 PA
 XX Greenfield EA, Larosa GJ, Navarro J, Thomas KM;
 PI Witt DT;
 PI
 XX WPI; 1995-336945/43.
 DR
 XX N-PSDB; Q99949.
 DR
 XX Monoclonal antibody against recombinant IL-8 receptor polypeptide -
 PT useful for treating inflammatory disorders, for detecting
 PT neutrophil(s) and for isolating IL-8 receptor from liq.mixt.
 PT
 XX Claim 2; Fig 1A-B; 74pp; English.
 PS
 XX Monoclonal antibodies were raised against recombinant interleukin-8
 CC (IL-8) receptor subtypes A and B from both human and rabbit sources
 CC (R80950-53 encoded by 099949-52). The A subtype receptor (IL-8rA) is
 CC a high affinity receptor and the B subtype receptor (IL-8rB) is a
 CC low affinity receptor. The monoclonal antibody (mAb) pref. binds to
 CC the IL-8 binding domain thus blocking its activation. The mAbs are
 CC useful for treating inflammatory disorders (see key words) and for
 CC detecting the presence of neutrophils in a biological sample. The
 CC mAbs are also useful in the isolation of IL-8 receptors from a mixture.
 CC
 XX Sequence 355 AA;
 SQ

Query Match 46.5%; Score 60; DB 16; Length 355;
 Best Local Similarity 52.4%; Pred. No. 0.15;
 Matches 11; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
 QY 6 KIICLVWGLSVIISSTFVF 26
 Db 159 kfclgiwalslslpfflf 179

RESULT 6
 R48717
 ID R48717 standard; Protein; 312 AA.
 XX
 XX R48717;
 AC
 XX 06-JUN-1996 (first entry)
 DT
 XX G-protein coupled human interleukin-8 receptor protein.
 DE
 XX G-protein coupled receptor; ligand binding assay; transmembrane domain;
 KW psychotic disorder; schizophrenia; dopamine; cAMP; adenosine; thrombin;
 KW muscarinic acetylcholine; adrenergic; endothelin; bombesin; endocrine;
 KW rhodopsin; opsin; odorant; cytomegalovirus.
 KW
 XX Homo sapiens.
 OS
 XX WO9405695-A1.
 PN
 XX 17-MAR-1994.
 PD
 XX 09-SEP-1993; 93WO-US08528.
 PF
 XX 10-SEP-1992; 92US-0943236.
 PR
 XX

PA (UUNY) UNIV NEW YORK STATE.
 XX Murphy RB, Schuster DI;
 PI
 XX WPI; 1994-101120/12.
 DR
 XX Polypeptides of G-coupled receptor proteins (GPRs) - useful for
 PT binding GPR ligands or modulating GPR binding
 PT
 XX Disclosure; Page 92; 160pp; English.
 PS
 XX Proteins R48685-R48758 represent a range of G-protein coupled receptor
 CC proteins selected from cAMP, adenosine, muscarinic acetylcholine,
 CC adrenergic, thrombin, endothelin, bombesin, endocrine, rhodopsin, opsin,
 CC odorant, cytomagaloviral and other G-protein coupled receptors. The
 CC receptor proteins were used to design polypeptides, pref. based on the
 CC transmembrane domains, for use in G-protein coupled receptor ligand
 CC binding assays. The polypeptide fragments retain biological activity
 CC such as binding a GPR ligand or modulating GPR ligand binding to a GPR
 CC (see R48759-R48758, R50569-R50807 and R89189-R89195 for examples of
 CC polypeptide fragments). The polypeptide fragments can be used in
 CC compositions for treating subjects suffering from a pathology related to
 CC a GPR abnormality e.g. a psychotic disorder such as schizophrenia.
 XX
 XX Sequence 312 AA;
 SQ

Query Match 45.0%; Score 58; DB 15; Length 312;
 Best Local Similarity 42.9%; Pred. No. 0.27;
 Matches 9; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 6 KIICLVVWGLSVIISSTFEV 26
 | | | | : | | | | : : |
 Db 115 kficlsiwglslilalpvlif 135

RESULT 7
 W02689
 ID W02689 standard; peptide; 312 AA.
 AC
 XX W02689;
 XX
 DT 12-NOV-1996 (first entry)
 XX
 DE G-protein coupled human interleukin-8 receptor.
 XX
 KW G-protein coupled receptor; ligand binding assay; transmembrane domain;
 KW schizophrenia; dopamine; cAMP; adenosine; thrombin; adrenergic; opsin;
 KW muscarinic acetylcholine; endothelin; bombesin; endocrine; rhodopsin;
 KW odorant; cytomagalovirus; serotonergic.
 XX
 OS Homo sapiens.
 XX
 PN US5508384-A.
 XX
 PD 16-APR-1996.
 XX
 PF 10-SEP-1992; 92US-0943236.
 XX
 PR 09-SEP-1993; 93US-0118270.
 PR 10-SEP-1992; 92US-0943236.
 XX
 PA (UUNY) UNIV NEW YORK STATE.
 XX
 XX Murphy RB, Schuster DI;
 PI
 XX WPI; 1996-208785/21.
 DR
 XX New dopamine receptor peptide - useful as antipsychotic agent, e.g.
 PT for treating schizophrenia
 PT
 XX Disclosure; Column 103-106; 184pp; English.
 PS
 XX

CC Proteins W02657-W02730 represent a range of G-protein coupled receptor
 CC (GPR) proteins selected from cAMP, adenosine, muscarinic acetylcholine,
 CC adrenergic, thrombin, endothelin, bombesin, endocrine, rhodopsin, opsin,
 CC odorant, cytomagaloviral and other GPR proteins. The receptor proteins
 CC were used to design polypeptides, pref. based on the transmembrane
 CC domains, for use in G-protein coupled receptor ligand binding assays.
 CC The polypeptide fragments retain biological activity such as binding a
 CC GPR ligand or modulating GPR ligand binding to a GPR (see W02747-W02999
 CC for examples of polypeptide fragments). The polypeptide fragments can
 CC be used in compositions for treating subjects suffering from a pathology
 CC related to a GPR abnormality e.g. a psychotic disorder such as
 CC schizophrenia.
 XX
 XX Sequence 312 AA;
 SQ

Query Match 45.0%; Score 58; DB 17; Length 312;
 Best Local Similarity 42.9%; Pred. No. 0.27;
 Matches 9; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 6 KIICLVVWGLSVIISSTFEV 26
 | | | | : | | | | : |
 Db 115 kficlsiwglslilalpvlif 135

RESULT 8
 R33420
 ID R33420 standard; Protein; 355 AA.
 XX
 AC R33420;
 XX
 DT 26-JUL-1993 (first entry)
 XX
 DE Human IL-8 receptor from clone p2.
 XX
 KW Interleukin-8 receptor; probes; gene therapy; gro receptor;
 KW intracellular-calcium mobilising; ligand-binding; MIP-2 receptor.
 XX
 OS Homo sapiens.
 XX
 PN W09306229-A.
 XX
 PD 01-APR-1993.
 XX
 PF 14-SEP-1992; 92WO-US07641.
 XX
 PR 13-SEP-1991; 91US-0759568.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICE.
 XX
 PI Murphy PM;
 XX
 DR WPI; 1993-117549/14.
 DR N-PSDB; Q38747.
 XX
 PT New interleukin-8 receptor aminoacid sequence - and corresp. cDNA
 PT expressed in Xenopus laevis oocytes or transfected host cells,
 PT for screening ligands of IL-8 receptor and gene therapy.
 XX
 PS Claim 1; Fig 3; 39pp; English.
 XX
 CC cDNA libraries from 2 and 3.5 kb fractions of poly(A)+ RNA from HL60
 CC neutrophils sepd. of a sucrose gradient were made in Unizap. The
 CC libraries were screened with F3R oligonucleotide probe (from rabbit
 CC IL-8 receptor) and under low stringency with a p2 cDNA probe
 CC synthesised from random primers, to isolated the clone p2, encoding
 CC human IL-8 receptor protein. The presence or absence of the DNA
 CC encoding IL-8R or related MIP-2 receptor may be detected using
 CC portions of the p2 clone as probes. P2 may also be used to screen
 CC for ligands of IL-8R and may also be used in gene therapy to treat a
 CC patient deficient in IL-8R. The IL-8R is a gro receptor and has
 CC intracellular calcium-mobilising and ligand-binding properties.
 XX

SQ Sequence 355 AA;

Query Match 45.0%; Score 58; DB 14; Length 355;
Best Local Similarity 42.9%; Pred. No. 0.32; Length 355;
Matches 9; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 6 KIICLVWGLSVIISSTFVF 26
| | | : | | | : | : |
Db 158 kfclsiwglslilalpvlif 178

RESULT 9

ID B09990 standard; Protein; 355 AA.

XX AC B09990;

DT 20-OCT-2000 (first entry)

XX Human IL-8 receptor protein hIL8RB.

XX IL-8 receptor protein; hIL8RA; hIL8RB; human; interleukin-8; drug;
KW treatment; inflammatory disease; anti-tumor.

XX OS Homo sapiens.

XX JP08103276-A.

XX 23-APR-1996.

XX 06-OCT-1994; 94JP-0242534.

XX 06-OCT-1994; 94JP-0242534.

XX (TAKE) TAKEDA CHEM IND LTD.

XX WPI; 1996-253878/26.

XX N-PSDB; A40128.

XX Recombinant human interleukin 8 receptor protein, - its prepn. and
PT application.

XX Example 2; Fig 4; 22pp; Japanese.

XX This invention describes a novel expression vector which carries a DNA
CC encoding human interleukin 8 receptor protein and is expressed by
CC pAKK01.11/hIL8RA or pAKK01.11/hIL8RB. Also claimed are (I) CHO cell
CC containing the above expression vector, (II) the preparation of a
CC recombinant human interleukin 8 receptor protein in which the above CHO
CC cell is cultured under a condition enabling the expression of a DNA
CC coding human interleukin 8 receptor protein, (III) a CHO cell
CC containing a recombinant human interleukin 8 receptor protein which can
CC be prepared, by culturing the above CHO cell under a condition enabling
CC the expression of a DNA coding human interleukin 8 receptor protein or
CC its cell membrane fraction, (IV) a recombinant human interleukin 8
CC receptor protein isolated from a CHO cell containing the above
CC recombinant human interleukin 8 receptor protein, its partial peptide or
CC their salt, (V) the screening of human interleukin 8 receptor agonist or
CC antagonist in which the above CHO cell or its cell membrane fraction is
CC used or the above recombinant human interleukin 8 receptor protein, its
CC partial peptide or their salt is used (VI) a kit for screening the human
CC interleukin 8 receptor agonist or antagonist containing the above CHO
CC cell or its cell membrane fraction or the above recombinant human
CC interleukin 8 receptor protein, its partial peptide or their salt, (VII)
CC a human interleukin 8 receptor agonist or antagonist prepared by using
CC the above screening method or the above screening kit or its salt, (VII)
CC an activation promoter or a migration promoter of neutrophils containing
CC the above agonist or its salt, and an activation inhibitor or a migration
CC inhibitor containing the above agonist or its salt. The agonist or the
CC antagonist can be used in drug compositions for the prevention and
CC treatment of inflammatory diseases and anti-tumor agents. The screening
CC method can select an agonist or an antagonist advantageously. This

CC sequence represents the human IL-8 receptor protein hIL8RB which is
CC described in the method of the invention.

XX SQ Sequence 355 AA;

Query Match 45.0%; Score 58; DB 17; Length 355;
Best Local Similarity 42.9%; Pred. No. 0.32;
Matches 9; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 6 KIICLVWGLSVIISSTFVF 26
| | | : | | | : | : |
Db 158 kfclsiwglslilalpvlif 178

RESULT 10

ID R28273 standard; Protein; 360 AA.

XX AC R28273;

XX 04-APR-1993 (first entry)

XX Sequence in a low affinity recombinant human interleukin-8
DE (IL-8) receptor polypeptide in 4AB.

XX IL-8 receptor polypeptide; G-protein-coupled receptor.

XX OS Homo sapiens.

XX WO9218641-A.

XX 29-OCT-1992.

XX 10-APR-1992; 92WO-US02977.

XX 10-APR-1991; 91US-0685101.

XX 09-JUL-1991; 91US-0726606.

XX 09-DEC-1991; 91US-0803842.

XX (REPK) REPLIGEN CORP.

XX (UYBO-) UNIV BOSTON.

XX Navarro J, Thomas KM, Witt DP;

XX WPI; 1992-382123/46.

XX N-PSDB; Q30012.

XX Recombinant mammalian interleukin-8 receptor - used for screening

XX interleukin-8 binding antagonists, used to treat inflammation

XX Disclosure; Fig 2; 71pp; English.

XX Rabbit high affinity IL-8 receptor gene was isolated from rabbit
CC peritoneal neutrophils and used as a source of poly(A)+ RNA, to
CC produce a rabbit neutrophil cDNA library. 250,000 recombinant
CC plaques were screened for those which hybridized to an antisense
CC oligonucleotide (Q30015). This probe was designed based on the
CC sequence derived from the second transmembrane domain of G-protein-
CC coupled receptors. After tertiary screening, six plaques were
CC isolated. The insert of one of these plaques, termed F3R was of 2.5
CC kb in size. This insert was sequenced. The protein deduced from
CC the F3R clone demonstrates that it belongs to the family of
CC G-protein-coupled receptors. The deduced protein sequence
CC indicates seven putative transmembrane segments. A human
CC peripheral blood leukocyte lambda gt10 cDNA library (5' stretch) was
CC screened with a 652 bp EcoRI/BamHI fragment (including nucleotides
CC -27 to 625) of the rabbit F3R clone. After tertiary screening
CC several human clones which hybridized to the rabbit IL-8 probe
CC were isolated. The insert of one such clone, termed 4AB was
CC sequenced (Q30012).

XX SQ Sequence 360 AA;

Query Match 45.0%; Score 58; DB 13; Length 360;
 Best Local Similarity 42.9%; Pred. No. 0.32;
 Matches 9; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

OY 6 KIICLVWGLSVIISSSTFVF 26
 | ||| : ||| : : : : :
 Db 163 kfciiswglslilalpvlif 183

RESULT 11

R80758
 ID R80758 standard; Protein; 360 AA.

XX
 AC R80758;

DT 26-MAR-1996 (first entry)

DE Interleukin 8 receptor B.

KW Interleukin; IL-8; inflammation; psoriasis; dermatitis;
 KW rheumatoid arthritis; inflammatory bowel disease;
 KW chronic lung inflammation; treatment; antibody;
 KW affinity purification; detection.

XX Homo sapiens.

XX US5440021-A.

PN 08-AUG-1995.

XX 29-MAR-1991; 91US-0677211.

XX 25-FEB-1994; 94US-0202056.

PR 29-MAR-1991; 91US-0677211.

XX (CHUN/) CHUNTHARAPAI A.

PA (HEBE/) HEBERT C.

PA (KIMK/) KIM K J.

PA (LEEJ/) LEE J.

XX Chuntharapai A, Hebert C, Kim KJ, Lee J;

PI WPI; 1995-283151/37.

DR N-PSDB; Q99008.

XX New antibodies against interleukin 8 type B receptor - used to treat
 PT or prevent inflammation, also for detecting receptor expression and
 PT purificn.

PS Disclosure; Columns 53-56; 62pp; English.

XX Antibodies directed against the interleukin-8 receptor B can be used
 CC to treat or prevent inflammation e.g. psoriasis, dermatitis,
 CC rheumatoid arthritis and particularly inflammatory bowel disease and
 CC chronic lung inflammation. When immobilised, these antibodies may
 CC be used to detect interleukin-8 receptor B expression in cells and
 CC tissues and for affinity purification of interleukin-8 receptor B
 CC from cells.

XX Sequence 360 AA;

Query Match 45.0%; Score 58; DB 16; Length 360;
 Best Local Similarity 42.9%; Pred. No. 0.32;
 Matches 9; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

OY 6 KIICLVWGLSVIISSSTFVF 26
 | ||| : ||| : : : : :
 Db 163 kfciiswglslilalpvlif 183

RESULT 12

R70124

ID R70124 standard; Protein; 1064 AA.

XX
 AC R70124;

XX 14-FEB-1996 (first entry)

DE IL8-R type 2-GBP 130 fusion protein.

KW Hybrid peptide; malaria parasite; Plasmodium falciparum; fusion protein;
 KW red blood cell; cytokine receptor; glycoporphin binding peptide 130;
 KW GBP 130; GBPH; glycoporphin binding peptide homologue; glycoporphin A.

XX Chimeric Homo sapiens.

OS Chimeric Plasmodium falciparum.

XX WO9506737-A.

PN 09-MAR-1995.

XX 01-SEP-1994; 94WO-GB01900.

XX 03-SEP-1993; 93GB-0018350.

PR 23-AUG-1994; 94GB-0017021.

XX (PREN/) PRENDERGAST K F.

XX Prendergast KF;

XX WPI; 1995-115452/15.

XX New hybrid peptide(s) for binding cytokine(s) - comprising a
 PT malaria parasite peptide capable of binding a red blood cell and
 PT a receptor peptide.

XX Example A; Page 80-82; 93pp; English.

XX Hybrid peptides for binding cytokines, comprising a malaria parasite
 CC (Plasmodium falciparum) peptide (capable of binding to a red blood
 CC cell (RBC)) and a receptor peptide are claimed. R70103-25 are examples
 CC of these hybrid peptides. R70124 is a fusion of interleukin 8 receptor
 CC type 2 and glycoporphin binding protein (GBP) 130. The use of cytokine
 CC receptors not normally found on RBCs means that the cytokine can bind
 CC harmlessly to the RBC without deleterious effect. The RBC protects the
 CC hybrid peptides from excretion from the kidney, and due to steric
 CC hindrance prevents the cytokines binding to a receptor in another cell.
 CC GBP 130 or GBPH (GBP homologue) are the pref. malaria parasite peptides
 CC used, others include EBA 175 (175 kDa erythrocyte binding antigen),
 CC PMNSA (pre major merozoite surface antigen) and the Duffy binding
 CC receptor molecule (eg. exhibited by Plasmodium vivax). These peptides
 CC bind to pref. glycoporphin A, B and C, sialo glycoproteins, found on
 CC the surface of RBCs. The hybrid peptides are thus used to lower
 CC the levels of free cytokines in the circulation to reduce pathological
 CC damage.

XX Sequence 1064 AA;

Query Match 45.0%; Score 58; DB 16; Length 1064;
 Best Local Similarity 42.9%; Pred. No. 1.1;
 Matches 9; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

OY 6 KIICLVWGLSVIISSSTFVF 26
 | ||| : ||| : : : : :
 Db 157 kfciiswglslilalpvlif 177

RESULT 13

R28274

ID R28274 standard; Protein; 358 AA.

XX
 AC R28274;

```

XX 04-APR-1993 (first entry)
XX Sequence in a low affinity recombinant rabbit interleukin-8
XX (IL-8) receptor polypeptide in 5bla.
XX IL-8 receptor polypeptide; G-protein-coupled receptor.
XX Oryctolagus cuniculus.
XX WO9218641-A.
XX 29-OCT-1992.
XX 10-APR-1992; 92WO-US02977.
XX 10-APR-1991; 91US-0685101.
XX 09-JUL-1991; 91US-0726606.
XX 09-DEC-1991; 91US-0803842.
XX (REPK ) REPLIGEN CORP.
XX (UYBO-) UNIV BOSTON.
XX Navarro J, Thomas KM, Witt DP;
XX WPI; 1992-382123/46.
XX N-PSDB; Q30013.
XX Recombinant mammalian Interleukin-8 receptor - used for screening
XX Interleukin-8 binding antagonists, used to treat inflammation
XX Claim 4; Fig 9; 71pp; English.
XX Rabbit high affinity IL-8 receptor gene was isolated from rabbit
XX peritoneal neutrophils and used as a source of poly(A)+ RNA, to
XX produce a rabbit neutrophil cDNA library. 250,000 recombinant
XX plaques were screened for those which hybridized to an antisense
XX oligonucleotide (Q30015). This probe was designed based on the
XX sequence derived from the second transmembrane domain of G-protein-
XX coupled receptors. After tertiary screening, six plaques were
XX isolated. The insert of one of these plaques, termed F3R was of 2.5
XX kb in size. This insert was sequenced. The protein deduced from
XX the F3R clone demonstrates that it belongs to the family of
XX G-protein-coupled receptors. The deduced protein sequence
XX indicates seven putative transmembrane segments. Using the methods
XX described above, a cDNA encoding the rabbit low affinity IL-8
XX receptor was also identified and isolated from the rabbit neutrophil
XX library. This cDNA was subcloned into the EcoRI site of pUC19 to
XX produce plasmid 5bla. Its nucleic acid sequence was determined by
XX standard techniques and found to be similar, but not identical, to the
XX high affinity receptor clone F3R.
XX Sequence 358 AA;

Query Match 44.2%; Score 57; DB 13; Length 358;
Best Local Similarity 47.6%; Pred. No. 0.46;
Matches 10; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 6 KIICLVWGLSVIISSSTFFV 26
DB 161 kfcismwgvslilspilff 181

RESULT 14
R80952
ID R80952 standard; Protein; 358 AA.
XX R80952;
XX 24-APR-1996 (first entry)
XX Recombinant high affinity interleukin-8 receptor subtype B.

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XX IL-8A; IL-8B; receptor; monoclonal antibody; inflammatory disorder;
XX anaphylaxis; systemic lupus erythematosus; rheumatoid arthritis;
XX systemic necrotizing vasculitis; psoriasis; asthma; allergy; ARDS;
XX adult respiratory distress syndrome; neutrophil detection.
XX Oryctolagus cuniculus.
XX WO9525126-A1.
XX 21-SEP-1995.
XX 09-MAR-1995; 95WO-US03032.
XX 02-MAY-1994; 94US-0237937.
XX 15-MAR-1994; 94US-0210250.
XX (REPK ) REPLIGEN CORP.
XX (UYBO-) UNIV BOSTON.
XX Greenfield EA, Larosa GJ, Navarro J, Thomas KM,
XX Witt DT;
XX WPI; 1995-336945/43.
XX N-PSDB; Q99951.
XX Monoclonal antibody against recombinant IL-8 receptor polypeptide -
XX useful for treating inflammatory disorders, for detecting
XX neutrophil(s) and for isolating IL-8 receptor from liq.mixt.
XX Claim 6; Fig 3A-B; 74pp; English.
XX Monoclonal antibodies were raised against recombinant interleukin-8
XX (IL-8) receptor subtypes A and B from both human and rabbit sources
XX (880950-53 encoded by Q99949-52). The A subtype receptor (IL-8A) is
XX a high affinity receptor and the B subtype receptor (IL-8B) is a
XX low affinity receptor. The monoclonal antibody (mAb) pref. binds to
XX the IL-8 binding domain thus blocking its activation. The mAbs are
XX useful for treating inflammatory disorders (see key words) and for
XX detecting the presence of neutrophils in a biological sample. The
XX mAbs are also useful in the isolation of IL-8 receptors from a mixture.
XX Sequence 358 AA;

Query Match 44.2%; Score 57; DB 16; Length 358;
Best Local Similarity 47.6%; Pred. No. 0.46;
Matches 10; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 6 KIICLVWGLSVIISSSTFFV 26
DB 161 kfcismwgvslilspilff 181

RESULT 15
W97784
ID W97784 standard; Protein; 342 AA.
XX W97784;
XX 21-MAY-1999 (first entry)
XX African green monkey HIV/SIV receptor protein Bonzo.
XX SIV receptor; HIV receptor; Bonzo; translocation promoting agent;
XX G protein coupled receptor; chemokine receptor; AIDS; infection;
XX virus transmission; African green monkey.
XX Cercopithecus aethiops.
XX WO9903888-A1.
XX 28-JAN-1999.

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XX 17-JUL-1998; 98WO-US14857.
XX
XX 17-JUL-1997; 97US-0896155.
XX
XX (UYNV ) UNIV NEW YORK STATE.
XX
XX Deng H, Kewalramani VN, Littman DR, Unutmaz D;
XX
XX WPI; 1999-132164/11.
XX
XX N-PSDB; X07290.
XX
XX New nucleic acid encoding the human translocation promoter Bonzo -
XX used to screen for potential agents for treating acquired immune
XX deficiency syndrome
XX
XX Disclosure; Page 80-81; 97pp; English.
XX
XX This is the amino acid sequence of African green monkey Bonzo, a
XX novel HIV/SIV translocation promoting agent that acts in conjunction
XX with CD4 to serve as a receptor for the entry into a cell of a virus
XX having a specific viral envelope glycoprotein. Bonzo is a member of
XX the 7-transmembrane G-protein coupled receptor family, is closely
XX related to the chemokine receptor family, and is expressed in
XX lymphoid tissues. The invention provides the amino acid sequences
XX (see W87783-88) and DNA sequences (see X07289-94) of human,
XX African green monkey and pig-tailed macaque Bonzo and Bob (brother
XX of Bonzo) translocation promoting agents. These novel receptors
XX were identified using an expression cloning strategy. They were
XX found to be used by particular strains of HIV-2 and M-tropic HIV-1.
XX The invention also includes: mammalian cells transfected with Bonzo
XX and/or Bob and human CD4, which can be used to screen potential
XX therapeutic agents and identify ligands; antibodies to Bonzo, which
XX can be used therapeutically, e.g. as antagonists or to target
XX toxins or radioisotopes to HIV-permissive cells; transgenic
XX animals; and antisense and ribozyme molecules, which may also be
XX used therapeutically, particularly expressed from a gene therapy
XX vector.
XX
XX Sequence 342 AA;
XX
Query Match 42.6%; Score 55; DB 20; Length 342;
Best Local Similarity 33.3%; Pred. NO. 0.9;
Matches 7; Conservative 9; Mismatches 5; Indels 0; Gaps 0;
QY 6 KIICLVWGLSVIISSTFVF 26
Db 149 kvicllwvslslvslpqiyl 169

```

Search completed: May '23, 2001, 15:28:29
Job time: 406 sec

RESULT 2
US-08-118-270-38
; Sequence 38, Application US/08118270
; Patent No. 5508384
; GENERAL INFORMATION:
; APPLICANT: Murphy, Randall B.
; APPLICANT: Schuster, David I.
; TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
; TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
; NUMBER OF SEQUENCES: 348
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 09-SEP-1993
; APPLICATION NUMBER: US/08/118,270
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/943,236
; FILING DATE: 10-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Townsend, Kevin G.
; REGISTRATION NUMBER: 34,033
; REFERENCE/DOCKET NUMBER: MURPHY-2A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 312 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-118-270-38

Query Match 45.0%; Score 58; DB 1; Length 312;
Best Local Similarity 42.9%; Pred. No. 0.2;
Matches 9; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

Qy 6 KIICLVWGLSVIISSSTFVF 26
| | | | : | | | | : | |
Db 115 KFCILSIWGLSLLALPVLFF 135

RESULT 3
PCT-US93-08528-38
; Sequence 38, Application PC/TUS9308528
; GENERAL INFORMATION:
; APPLICANT: New York University
; TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
; TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
; NUMBER OF SEQUENCES: 348
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/759,568
; FILING DATE: 19910913
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Scott, Watson T.
; REGISTRATION NUMBER: 26581
; REFERENCE/DOCKET NUMBER: WTS/5683/91535/WB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3000
; TELEFAX: 202-822-0944
; TELEX: 6714627 cush
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/08528
; FILING DATE: 09-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/943,236
; FILING DATE: 10-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Townsend, Kevin G.
; REGISTRATION NUMBER: 34,033
; REFERENCE/DOCKET NUMBER: MURPHY-2 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 312 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
PCT-US93-08528-38

Query Match 45.0%; Score 58; DB 5; Length 312;
Best Local Similarity 42.9%; Pred. No. 0.2;
Matches 9; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

Qy 6 KIICLVWGLSVIISSSTFVF 26
| | | | : | | | | : | |
Db 115 KFCILSIWGLSLLALPVLFF 135

RESULT 4
US-07-759-568-1
; Sequence 1, Application US/07759568
; Patent No. 5374506
; GENERAL INFORMATION:
; APPLICANT: Murphy, Philip M.
; TITLE OF INVENTION: Cloning of cDNA Encoding a Functional
; TITLE OF INVENTION: Human Interleukin-8 Receptor
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cushman, Darby & Cushman
; STREET: 1615 L Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036-5601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/759,568
; FILING DATE: 19910913
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Scott, Watson T.
; REGISTRATION NUMBER: 26581
; REFERENCE/DOCKET NUMBER: WTS/5683/91535/WB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3000
; TELEFAX: 202-822-0944
; TELEX: 6714627 cush
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids

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; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-759-568-1

Query Match 45.0%; Score 58; DB 1; Length 355;
Best Local Similarity 42.9%; Pred. No. 0.23;
Matches 9; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 6 KIICLVWGLSVIISSTFFV 26
   | | | | : | | | : | |
Db 158 KFICLSIWGLSLLLALPVL 178

RESULT 5
US-08-450-393A-8
; Sequence 8, Application US/08450393A
; Patent No. 5707815
; GENERAL INFORMATION:
; APPLICANT: Charo, Israel
; APPLICANT: Coughlin, Shaun
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
; TITLE OF INVENTION: PROTEIN RECEPTORS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
; STREET: 5 Palo Alto Square
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,393A
; FILING DATE: May 25, 1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Cseri, Luann
; REGISTRATION NUMBER: 31,822
; REFERENCE/DOCKET NUMBER: UCAL-237/02US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5165
; TELEFAX: 415-8857-0663
; TELEX: 380816COOLEYPA
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-450-393A-8

Query Match 45.0%; Score 58; DB 1; Length 355;
Best Local Similarity 42.9%; Pred. No. 0.23;
Matches 9; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 6 KIICLVWGLSVIISSTFFV 26
   | | | | : | | | : | |
Db 158 KFICLSIWGLSLLLALPVL 178

RESULT 6
US-08-390-000A-5
; Sequence 5, Application US/08390000A
; Patent No. 5985583
```

```
; GENERAL INFORMATION:
; APPLICANT: Sealton, Stuart C.
; TITLE OF INVENTION: Cloning and Expression of
; TITLE OF INVENTION: Gonadotropin-Releasing Hormone Receptor
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/390,000A
; FILING DATE: 17-FEB-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 6923-052
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-390-000A-5

Query Match 45.0%; Score 58; DB 2; Length 355;
Best Local Similarity 42.9%; Pred. No. 0.23;
Matches 9; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 6 KIICLVWGLSVIISSTFFV 26
   | | | | : | | | : | |
Db 158 KFICLSIWGLSLLLALPVL 178

RESULT 7
US-08-446-669-8
; Sequence 8, Application US/08446669
; Patent No. 6132987
; GENERAL INFORMATION:
; APPLICANT: Charo, Israel
; APPLICANT: Coughlin, Shaun
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
; TITLE OF INVENTION: PROTEIN RECEPTORS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
; STREET: 5 Palo Alto Square
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,669
; FILING DATE: May 25, 1995
; CLASSIFICATION: 435
```


Query Match 45.0%; Score 58; DB 5; Length 355;
Best Local Similarity 42.9%; Pred. NO. 0.23;
Matches 9; Conservative 6; Mismatches 6; Indels

APPLICANT: Loetscher, Marcel
APPLICANT: Moser, Bernhard
TITLE OF INVENTION: IP-10/MIG RECEPTOR DESIGNATED CXCR3,
TITLE OF INVENTION: NUCLEIC ACIDS, AND METHODS OF USES THEREFOR
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive

;; CITY: Lexington
;; STATE: MA
;; COUNTRY: USA
;; ZIP: 02173
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentin Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/709,838
;; FILING DATE:
;; CLASSIFICATION: 530
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Brook Esq., David E.
;; REGISTRATION NUMBER: 22,592
;; REFERENCE/DOCKET NUMBER: TK196-01
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (617) 861-6240
;; TELEFAX: (617) 861-9540
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 368 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-709-838-2

Query Match 42.6%; Score 55; DB 4; Length 368;
Best Local Similarity 39.1%; Pred. No. 0.7;
Matches 9; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

QY 4 RSKIIICLVWGLSVIISSTFVF 26
| : || |||| : : ||
Db 167 RVTLTCLAVWGLCLLFPDFIF 189

RESULT 11

US-08-829-839-2
;; Sequence 2, Application US/08829839
;; Patent No. 6184358
;; GENERAL INFORMATION:
;; APPLICANT: Loetscher, Marcel
;; APPLICANT: Moser, Bernhard
;; APPLICANT: Qin, Shixin
;; APPLICANT: Mackay, Charles R.
;; TITLE OF INVENTION: IP-10/MIG RECEPTOR DESIGNATED CXCR3,
;; TITLE OF INVENTION: ANTIBODIES, NUCLEIC ACIDS, AND METHODS OF USE THEREFOR
;; NUMBER OF SEQUENCES: 4
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
;; STREET: Two Militia Drive
;; CITY: Lexington
;; STATE: MA
;; COUNTRY: USA
;; ZIP: 02173
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentin Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/829,839
;; FILING DATE: 31-MAR-1997
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/709,838
;; FILING DATE: 10-SEP-1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Brook Esq., David E.
;; REGISTRATION NUMBER: 22,592
;; REFERENCE/DOCKET NUMBER: TK196-01A

;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (617) 861-6240
;; TELEFAX: (617) 861-9540
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 368 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-829-839-2

Query Match 42.6%; Score 55; DB 4; Length 368;
Best Local Similarity 39.1%; Pred. No. 0.7;
Matches 9; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

QY 4 RSKIIICLVWGLSVIISSTFVF 26
| : || |||| : : ||
Db 167 RVTLTCLAVWGLCLLFPDFIF 189

RESULT 12

US-08-202-056-1
;; Sequence 1, Application US/08202056
;; Patent No. 5440021
;; GENERAL INFORMATION:
;; APPLICANT: Chuntharapai, Anan
;; APPLICANT: Hebert, Caroline
;; APPLICANT: Kim, Kyung Jin
;; APPLICANT: Lee, James
;; TITLE OF INVENTION: Antibodies to Human IL-8 Type B Receptor
;; NUMBER OF SEQUENCES: 8
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Genentech, Inc.
;; STREET: 460 Point San Bruno Blvd
;; CITY: South San Francisco
;; STATE: California
;; COUNTRY: USA
;; ZIP: 94080
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: patin (Genentech)
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/202,056
;; FILING DATE: 25-FEB-1994
;; CLASSIFICATION: 436
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/677211
;; FILING DATE: 29-MAR-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Love, Richard B.
;; REGISTRATION NUMBER: 34,659
;; REFERENCE/DOCKET NUMBER: 706P3
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 415/225-5530
;; TELEFAX: 415/952-9881
;; TELEX: 910/371-7168
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 350 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; US-08-202-056-1

Query Match 41.9%; Score 54; DB 1; Length 350;
Best Local Similarity 47.6%; Pred. No. 0.93;
Matches 10; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 6 KIICLVWGLSVIISSTFVF 26
| : || |||| : : ||

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Db 154 KFCVLCGCGLSMNLSPFLF 174
;
; STREET: 5 Palo Alto Square
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,393A
; FILING DATE: May 25, 1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Cserr, Luann
; REGISTRATION NUMBER: 31,822
; REFERENCE/DOCKET NUMBER: UCAL-237/020S
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5165
; TELEFAX: 415-8857-0663
; TELEX: 380816CooLevPA
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 350 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-450-393A-7

Query Match 41.9% Score 54; DB 1; Length 350;
Best Local Similarity 47.6%; Pred. No. 0.93;
Matches 10; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 6 KIICLVVWGLSVIISSSTFVF 26
|:|:| |::|:| |:|
Db 154 KFCVLCGCGLSMNLSPFLF 174

RESULT 15
US-08-410-453A-1
; Sequence 1, Application US/08410453A
; Patent No. 5767063
; GENERAL INFORMATION:
; APPLICANT: Lee, James,
; APPLICANT: Holmes, William E.,
; APPLICANT: Woods, William I.
; TITLE OF INVENTION: Human P4A Receptors and Their Use
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/410,453A
; FILING DATE: 24-Mar-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/234494
; FILING DATE: 28-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/677211

Db 154 KFCVLCGCGLSMNLSPFLF 174
;
; STREET: 5 Palo Alto Square
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,393A
; FILING DATE: May 25, 1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Cserr, Luann
; REGISTRATION NUMBER: 31,822
; REFERENCE/DOCKET NUMBER: UCAL-237/020S
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5165
; TELEFAX: 415-8857-0663
; TELEX: 380816CooLevPA
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 350 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-450-393A-7

Query Match 41.9% Score 54; DB 1; Length 350;
Best Local Similarity 47.6%; Pred. No. 0.93;
Matches 10; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 6 KIICLVVWGLSVIISSSTFVF 26
|:|:| |::|:| |:|
Db 154 KFCVLCGCGLSMNLSPFLF 174

RESULT 14
US-08-450-393A-7
; Sequence 7, Application US/08450393A
; Patent No. 5707815
; GENERAL INFORMATION:
; APPLICANT: Charo, Israel
; APPLICANT: Coughlin, Shaun
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
; TITLE OF INVENTION: PROTEIN RECEPTORS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
```

```

; FILING DATE: 29-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P0706C1D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5530
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 350 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-410-453A-1

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Query Match      41.98; Score 54; DB 1; Length 350;
Best Local Similarity 47.6%; Pred. No. 0.93;
Matches 10; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

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QY      6 KIICLVVWGLSVIISSSTVF 26
       1:|||||:|:|
Db     154 KVCICGCGWGLSMNLSLPFLF 174

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Search completed: May 23, 2001, 15:30:06
Job time: 413 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 23, 2001, 15:32:00 ; Search time 110.15 seconds
(without alignments)
16.221 Million cell updates/sec

Title: US-08-887-977-10_COPY_151_176

Perfect score: 129

Sequence: 1 TLPRSKIICLVWGLSVIISSSTFEV 26

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 198801 seqs, 68722935 residues

Total number of hits satisfying chosen parameters: 198801

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_67: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	129	100.0	369	2 JC5068	G protein-coupled
2	60	46.5	354	2 A23669	interleukin-8 rece
3	60	46.5	355	2 JQ1231	interleukin-8 rece
4	58	45.0	360	2 A53611	interleukin-8 rece
5	58	45.0	371	2 G69827	conserved hypothet
6	57	44.2	358	2 A53752	interleukin-8 rece
7	55	42.6	364	2 JQ1488	bradykinin B2 rece
8	55	42.6	366	2 I49519	bradykinin B2 rece
9	54	41.9	350	2 A39445	interleukin-8 rece
10	54	41.9	367	2 JE0349	interleukin-8 rece
11	51	39.5	350	1 A37963	complement C5a ana
12	51	39.5	356	2 S42096	interleukin-8 rece
13	49	38.0	325	1 TVHVAS	transforming prote
14	49	38.0	366	1 OORFB2	bradykinin recepto
15	49	38.0	369	2 S48332	probable membrane
16	49	38.0	1515	2 T52081	MRP-like ABC trans
17	48	37.2	346	2 S10188	NADH dehydrogenase
18	48	37.2	483	2 A25896	beta-adrenergic re
19	47	36.4	305	2 B33465	11c-1 protein B -
20	47	36.4	324	1 TVRTAS	transforming prote
21	47	36.4	355	2 G02436	chemokine (C-C) re
22	47	36.4	357	2 S28058	serotonin receptor
23	47	36.4	357	2 B47472	5-hydroxytryptamin
24	47	36.4	359	2 S44425	angiotensin II rec
25	47	36.4	415	2 T35834	probable transcrip
26	47	36.4	425	2 A37912	thrombin receptor
27	47	36.4	427	2 S17148	alpha-thrombin rec
28	47	36.4	1027	2 T46481	hypothetical prote
29	47	36.4	1102	2 JC6316	probable protein k.

30 47 36.4 1233 2 T30989
31 46.5 36.0 315 2 S25581
32 46.5 36.0 419 2 T36272
33 46.5 36.0 905 2 T40015
34 46 35.7 279 2 B71894
35 46 35.7 334 2 JC4681
36 46 35.7 359 2 A48921
37 46 35.7 734 2 B83405
38 46 35.7 875 1 A57080
39 45.5 35.3 369 2 B41795
40 45 34.9 116 2 E71202
41 45 34.9 247 2 S42739
42 45 34.9 354 2 I58186
43 45 34.9 359 2 S15403
44 45 34.9 378 2 A39485
45 45 34.9 449 1 NBHUHS

ALIGNMENTS

RESULT 1

JC5068
G protein-coupled receptor CKR-L3 - human
C:Species: Homo sapiens (man)
C:Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 21-Jul-2000
C:Accession: JC5068
R:Zaballos, A.; Varona, R.; Gutierrez, J.; Lind, P.; Marquez, G.
Biochem. Biophys. Res. Commun. 227, 846-853, 1996
A:Title: Molecular cloning and RNA expression of two new human chemokine receptor-11k
A:Reference number: JC5067; MUID:97040707
A:Accession: JC5068
A:Molecule type: DNA
A:Residues: 1-369 <ZAB>
A:Cross-references: EMBL:279784; NID:gl668737; PIDN:CAB02144.1; PID:gl668738
C:Comment: This protein belongs to the family of alpha chemokine receptors.
C:Genetics:
A:Gene: GDB:CMKBR6; SFRSL22: GPR29; CCR6: CKR-L3; GPR-CY4
A:Cross-references: GDB:5370839; OMIM:601835
A:Map position: 6q27-6q27
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; transmembrane protein
F:42-68/Domain: transmembrane #status predicted <TM1>
F:79-99/Domain: transmembrane #status predicted <TM2>
F:115-135/Domain: transmembrane #status predicted <TM3>
F:160-180/Domain: transmembrane #status predicted <TM4>
F:212-233/Domain: transmembrane #status predicted <TM5>
F:250-271/Domain: transmembrane #status predicted <TM6>
F:292-315/Domain: transmembrane #status predicted <TM7>

Query Match 100.0%; Score 129; DB 2; Length 369;
Best Local Similarity 100.0%; Pred. No. 1.9e-11;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TLPRSKIICLVWGLSVIISSSTFEV 26

Db 155 TLPRSKIICLVWGLSVIISSSTFEV 180

RESULT 2

A23669
Interleukin-8 receptor, high affinity - rabbit
N:Alternate names: fMLP receptor
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 05-Nov-1999
R:Accession: A23669
R:Thomas, K.M.; Pyun, H.Y.; Navarro, J.
J. Biol. Chem. 265, 20061-20064, 1990
A:Title: Molecular cloning of the fMet-Leu-Phe receptor from neutrophils.
A:Reference number: A23669; MUID:91056034
A:Accession: A23669
A:Molecule type: mRNA

serine/threonine p
melanocyte-stimula
hypothetical prote
phosphatidylethano
hypothetical prote
bradykinin B1 rece
interleukin-8 rece
probable hydroxyla
cell surface antig
somatostatin recep
hypothetical prote
cytochrome-c oxida
probable G protein
angiotensin II rec
transforming prote
complement factor

11876; NID:g511816; PID:g511817; EMBL:U11877; NID:g511818; PID:g511819; EMBL:U11878;
R:Sprengrer, H.; Lloyd, A.R.; Lautens, L.L.; Bonner, T.I.; Kelvin, D.J.
J. Biol. Chem. 269, 11065-11072, 1994
A:Title: Structure, genomic organization, and expression of the human interleukin-8 r
A:Reference number: A53611; MUID:94209273
A:Accession: A53611
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 6-360 <SPR>
A:Cross-references: GB:M99412; GB:L19593
R:Murphy, P.M.; Tiffany, H.L.
Science 253, 1280-1283, 1991
A:Title: Cloning of complementary DNA encoding a functional human interleukin-8 recep
A:Reference number: A39446; MUID:91368200
A:Accession: A39446
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 6-360 <MUR>
A:Cross-references: GB:M73969
C:Comment: This receptor, unlike IL8RA, binds several peptides besides interleukin-8 r
C:Genetics:
A:Gene: GDB:IL8RB; IL8RA
A:Cross-references: GDB:127868; OMIM:145928
A:Map position: 2q35-2q35
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 45.0%; Score 58; DB 2; Length 360;
Best Local Similarity 42.9%; Pred. No. 0.47;
Matches 9; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

OY 6 KIICLVWGLSVIISSSTVFV 26
| III :|||||: :|
DB 163 KFCISINGLSLLLPVLLF 183

RESULT 5
G69827
conserved hypothetical protein yhdY - Bacillus subtilis
C:Species: Bacillus subtilis
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000
C:Accession: G69827
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber
C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari,
A:Authors: Foulger, D.R.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gal
teich, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.;
Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau
Y. M.; Ogawa, K.; Ogihara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portete
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanl
A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Se
keuchi, M.; Tanakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiya
T.; Winters, P.; Wipat, A.; Yamamoto, K.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida
A:Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; danchin, A.
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtili
A:Reference number: A69580; MUID:98044033
A:Accession: G69827
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-371 <KUN>
A:Cross-references: GB:Z99109; GB:AL009126; NID:g2633260; PIDN:CAB12803.1; PID:g26332
A:Experimental source: strain 168
C:Genetics:
A:Gene: yhdY
C:Superfamily: conserved hypothetical protein MJ0170

Query Match 45.0%; Score 58; DB 2; Length 371;
Best Local Similarity 43.5%; Pred. No. 0.48;
Matches 10; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

QY 4 RSKICLVWGLSVIISSSTVFV 26
| | | | : : : : :
Db 96 RSLIVALLWGLNLTATSSRF 118

RESULT 6

A53752
Interleukin-8 receptor (clone 5Bla) - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C:Accession: A53752
R:Prado, G.N.; Thomas, K.M.; Suzuki, H.; LaRosa, G.J.; Wilkinson, N.; Folco, E.; Navarro
J. Biol. Chem. 269, 12391-12394, 1994
A:Title: Molecular characterization of a novel rabbit interleukin-8 receptor isotype.
A:Reference number: A53752; MUID:94230294
A:Accession: A53752
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-358 <PRA>
A:Cross-references: GB:L24445; NID:g437661; PIDN:AAA31378.1; PID:g437662
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 44.2%; Score 57; DB 2; Length 358;
Best Local Similarity 47.6%; Pred. No. 0.66;
Matches 10; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 6 KIICLVWGLSVIISSSTVFV 26
| | | | : : : : :
Db 161 KFICLMMGVSLILSLPILF 181

RESULT 7

JQ1488
bradykinin B2 receptor - human
C:Species: Homo sapiens (man)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 13-Aug-1999
C:Accession: JQ0712; A46022; A55559; JQ1488; JCI400
R:Eggerickx, D.; Raspe, E.; Bertrand, D.; Vassart, G.; Parmentier, M.
Biochem. Biophys. Res. Commun. 187, 1306-1313, 1992
A:Title: Molecular cloning, functional expression and pharmacological characterization of
A:Reference number: JQ0712; MUID:93038601
A:Accession: JQ0712
A:Molecule type: DNA
A:Residues: 1-364 <EGG>
A:Cross-references: GB:S45489; NID:g256536; PIDN:AAB23467.1; PID:g256537
R:Powell, S.J.; Slyn, G.; Thomas, C.; Hopkins, B.; Briggs, I.; Graham, A.
Genomics 15, 435-438, 1993
A:Title: Human bradykinin B2 receptor: nucleotide sequence analysis and assignment to ch
A:Reference number: A46022; MUID:93194199
A:Accession: A46022
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-364 <POW>
A:Cross-references: GB:S56772; NID:g298604; PIDN:AAB25765.1; PID:g298605
A:Note: sequence extracted from NCBI backbone (NCBI:127280, NCBIP:1127284)
R:Ma, J.; Wang, D.; Ward, D.C.; Chen, L.; Dessai, T.; Chao, J.; Chao, L.
Genomics 23, 362-369, 1994
A:Title: Structure and chromosomal localization of the gene (BDKRB2) encoding human brad
A:Reference number: A55559; MUID:95137582
A:Accession: A55559
A:Molecule type: DNA
A:Residues: 1-364 <MAA>
A:Cross-references: GB:L27594
R:Hess, J.F.; Borkowski, J.A.; Young, G.S.; Strader, C.D.; Ransom, R.W.
Biochem. Biophys. Res. Commun. 184, 260-268, 1992
A:Title: Cloning and pharmacological characterization of a human bradykinin (BK-2) recep
A:Reference number: JQ1488; MUID:92231936
A:Accession: JQ1488
A:Molecule type: mRNA
A:Residues: 1-364 <HES>

A:Cross-references: GB:M88714; NID:g1387999; PIDN:AAB02793.1; PID:g1388000
C:Genetics:
A:Gene: GDB:BDKRB2
A:Cross-references: GDB:135713; OMIM:113503
A:Map position: 14q32.1-14q32.2
A:Introns: #status absent
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane p
F:34-56/Domain: transmembrane #status predicted <TM1>
F:66-92/Domain: transmembrane #status predicted <TM2>
F:104-127/Domain: transmembrane #status predicted <TM3>
F:148-171/Domain: transmembrane #status predicted <TM4>
F:195-221/Domain: transmembrane #status predicted <TM5>
F:241-266/Domain: transmembrane #status predicted <TM6>
F:285-309/Domain: transmembrane #status predicted <TM7>
F:3, 12, 180/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:170, 237, 342/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status
F:242/Binding site: phosphate (Thr) (covalent) (by protein kinase A) #status predicte
F:316/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status predicte

Query Match 42.6%; Score 55; DB 2; Length 364;
Best Local Similarity 40.9%; Pred. No. 1.3;
Matches 9; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

QY 5 SKIICLVWGLSVIISSSTVFV 26
| | | | : : : : :
Db 147 AKLYSLVWGCTLLLSFPLVF 168

RESULT 8

I49519
bradykinin B2 receptor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 13-Aug-1999
C:Accession: I49519; I49525; I48270; JCI2187
R:Hess, J.F.; Borkowski, J.A.; MacNeil, T.; Stonesifer, G.Y.; Fraher, J.; Strader, C.
Mol. Pharmacol. 45, 1-8, 1994
A:Title: Differential pharmacology of cloned human and mouse B2 bradykinin receptors.
A:Reference number: I49519; MUID:94134047
A:Accession: I49519
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-366 <HES>
A:Cross-references: GB:L26047; NID:g415711; PIDN:AAA19797.1; PID:g415712
R:Ma, J.X.; Wang, D.Z.; Chao, L.; Chao, J.
Gene 149, 283-289, 1994
A:Title: Cloning, sequence analysis and expression of the gene encoding the mouse bra
A:Reference number: I49525; MUID:95047489
A:Accession: I49525
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-271, 'A', 273-366 <MAJ>
A:Cross-references: GB:L27595; NID:g508524; PIDN:AAA62616.1; PID:g691756
A:Note: in GenBank entry MUSBB2R, release 106.0, the source is designated as Mus musc
R:McIntyre, P.; Phillips, E.; Skidmore, E.; Brown, M.; Webb, M.
Mol. Pharmacol. 44, 346-355, 1993
A:Title: Cloned murine bradykinin receptor exhibits a mixed B1 and B2 pharmacological
A:Reference number: I48270; MUID:93360929
A:Accession: I48270
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-271, 'A', 273-366 <MCI>
A:Cross-references: EMBL:X69676; NID:g440551; PIDN:CAA49357.1; PID:g440552
A:Note: submitted to the EMBL/GenBank/DBJ databases December 1992; this sequence has
R:McIntyre, P.; Phillips, E.; Skidmore, E.; Brown, M.; Webb, M.
Mol. Pharmacol. 45, 561-1994
A:Reference number: A58857
A:Contents: annotation; erratum; sequence correction
A:Note: submitted to the EMBL/GenBank/DBJ databases January 1994
R:Yokoyama, S.; Kimura, Y.; Taketo, M.; Black, J.A.; Ransom, B.R.; Higashida, H.
Biochem. Biophys. Res. Commun. 200, 634-641, 1994
A:Title: B2 bradykinin receptors in NG108-15 cells: cDNA cloning and functional expre

A:Reference number: JC2187; MUID:94220152
A:Accession: JC2187
A:Molecule type: mRNA
A:Residues: 1-366 <YOK>
A:Cross-references: GB:X78438; NID:9474937; PIDN:CAA55202.1; PID:9474938
A:Experimental source: GB:Neuroblastoma-glioma hybrid cell, strain NG 108-15
C:Genetics:
A:Gene: B2R
A:Introns: #status absent
A:Note: the two introns occur before the initiator codon
C:Superfamily: vertebrate rhodopsin
C:Keywords: bradykinin; glycoprotein; lipoprotein; phosphoprotein; receptor; transmembrane
F:36-59/Domain: transmembrane #status predicted <TM1>
F:69-93/Domain: transmembrane #status predicted <TM2>
F:107-128/Domain: transmembrane #status predicted <TM3>
F:151-173/Domain: transmembrane #status predicted <TM4>
F:197-223/Domain: transmembrane #status predicted <TM5>
F:243-267/Domain: transmembrane #status predicted <TM6>
F:287-311/Domain: transmembrane #status predicted <TM7>
F:3,14,182/Binding site: carboxylate (Asn) (covalent) #status predicted
F:318/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status predicted

Query Match 42.6%; Score 55; DB 2; Length 366;
Best Local Similarity 40.9%; Pred. NO. 1.3;
Matches 9; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

QY 5 SKIICLVWGLSVIISSSTFVF 26
I : ||| : : : ||| ||
Db 149 AKLYSLVWGCTLLSSPMLVF 170

RESULT 9
A39445
interleukin-8 receptor type A - human
N:Alternate names: interleukin-8 receptor, high-affinity
C:Species: Homo sapiens (man)
C:Date: 22-Jan-1993 #sequence_revision 12-Apr-1996 #text_change 05-Nov-1999
C:Accession: I37449; I38710; I38711; A39445
R:Mollereau, C.; Muscatelli, F.; Mattei, M.G.; Vassart, G.; Parmentier, M.
Genomics 16, 248-251, 1993
A:Title: The high-affinity interleukin 8 receptor gene (IL8RA) maps to the 2q33-q36 region
A:Reference number: I37449; MUID:93252387
A:Accession: I37449
A:Molecule type: DNA
A:Residues: 1-350 <RES>
A:Cross-references: EMBL:X65958; NID:g312046; PIDN:CAA45688.1; PID:g312047
R:Anuja, S.K.; Shetty, A.; Tiffany, H.L.; Murphy, P.M.
J. Biol. Chem. 269, 26381-26389, 1994
A:Title: Comparison of the genomic organization and promoter function for human interleukin 8 receptor
A:Reference number: I37898; MUID:95014476
A:Accession: I38710
A:Molecule type: DNA
A:Residues: 1-350 <RES>
A:Cross-references: EMBL:U11870; NID:g511804; PIDN:AAA64378.1; PID:g511805
R:Holmes, W.E.; Lee, J.; Kuang, W.J.; Rice, G.C.; Wood, W.I.
Science 253, 1278-1280, 1991
A:Title: Structure and functional expression of a human interleukin-8 receptor.
A:Reference number: A39445; MUID:91368199
A:Accession: A39445
A:Molecule type: mRNA
A:Residues: 1-275, 'T', 277-350 <HOL>
A:Cross-references: GB:M68932; NID:g186369; PIDN:AAA59159.1; PID:g186370
C:Genetics:
A:Gene: GDB:IL8RA
A:Cross-references: GDB:I35039; OMIM:146929
A:Map position: 2q35-2q35
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; glycoprotein; membrane protein

Query Match 41.9%; Score 54; DB 2; Length 350;
Best Local Similarity 47.6%; Pred. NO. 1.8;
Matches 10; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 6 KIICLVWGLSVIISSSTFVF 26
I : ||| ||| : : ||| ||
Db 154 KFCVLCGCGLSMNLSPFLF 174

RESULT 10
JE0349
interferon-inducible protein 10 (IP-10) receptor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 21-Jul-2000
C:Accession: JE0349
R:Tamaru, M.; Tominaga, Y.; Yatsunami, K.; Narumi, S.
Biochem. Biophys. Res. Commun. 251, 41-48, 1998
A:Title: Cloning of the murine interferon-inducible protein 10 (IP-10) receptor and its expression in human cells
A:Reference number: JE0349; MUID:95009219
A:Accession: JE0349
A:Molecule type: mRNA
A:Residues: 1-367 <TAM>
A:Cross-references: DDBJ:AB003174; NID:g3798731; PIDN:BAA34045.1; PID:g3798732
C:Comment: This protein is important for lymphocyte trafficking to lymphoid organs.
C:Superfamily: vertebrate rhodopsin

Query Match 41.9%; Score 54; DB 2; Length 367;
Best Local Similarity 34.8%; Pred. NO. 1.8;
Matches 8; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 4 RSKIICLVWGLSVIISSSTFVF 26
I : ||| ||| : : ||| ||
Db 166 RVAUTCIVWGLCLLFPDFIY 188

RESULT 11
A37963
complement C5a anaphylatoxin receptor - human
C:Species: Homo sapiens (man)
C:Date: 22-Jan-1993 #sequence_revision 14-Feb-1997 #text_change 21-Jul-2000
C:Accession: A37963; S13646; I52417; S30518
R:Boulay, F.; Mery, L.; Tardif, M.; Bouchon, L.; Vignais, P.
Biochemistry 30, 2993-2999, 1991
A:Title: Expression cloning of a receptor for C5a anaphylatoxin on differentiated HL-60 cells
A:Reference number: A37963; MUID:91175748
A:Accession: A37963
A:Molecule type: mRNA
A:Residues: 1-350 <BOU>
A:Cross-references: GB:J05327; NID:g179699; PIDN:AAA62831.1; PID:g179700
R:Gerard, N.P.; Gerard, C.
Nature 349, 614-617, 1991
A:Title: The chemotactic receptor for human C5a anaphylatoxin.
A:Reference number: S13646; MUID:91156029
A:Accession: S13646
A:Molecule type: mRNA
A:Residues: 1-350 <GER>
A:Cross-references: EMBL:X58674; NID:g29568; PIDN:CAB37830.1; PID:g4467832
R:Gerard, N.P.; Bao, L.; Xiao-Ping, H.; Eddy, R.L.
Biochemistry 32, 1243-1250, 1993
A:Title: Human chemotaxis receptor genes cluster at 19q13.3-13.4. Characterization of the human C5a anaphylatoxin receptor
A:Reference number: I52417; MUID:93192225
A:Accession: I52417
A:Status: translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-3 <RES>
A:Cross-references: GB:S56556; GB:S56557; NID:g298577; NID:g298578
C:Genetics:
A:Gene: GDB:C5AR1; C5A; CSAR
A:Cross-references: GDB:I28856; OMIM:113995
A:Map position: 19q13.3-19q13.4

A: Molecule type: DNA
A: Residues: 1-325 <YOU>
A: Cross-references: GB:MI3150; NID:g187388; PIDN:AAA36199.1; PID:g307158
C: Genetics:
A: Gene: GDB:MAS1
A: Cross-references: GDB:120166; OMIM:165180
C: Map position: 6q24-6q27
C: Superfamily: mas transforming protein
C: Keywords: G protein-coupled receptor; glycoprotein; proto-oncogene; transforming pr
F: 31-61/Domain: transmembrane #status predicted <TM1>
F: 66-97/Domain: transmembrane #status predicted <TM2>
F: 105-135/Domain: transmembrane #status predicted <TM3>
F: 150-172/Domain: transmembrane #status predicted <TM4>
F: 186-214/Domain: transmembrane #status predicted <TM5>
F: 225-250/Domain: transmembrane #status predicted <TM6>
F: 258-286/Domain: transmembrane #status predicted <TM7>
F: 5,16,22,272/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 38.0%; Score 49; DB 1; Length 325;
Best Local Similarity 27.3%; Pred. No. 9;
Matches 6; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

QY 4 RSKIIIVVGLSVIIISSTFV 25
: | : : | : : | : : : : |
Db 148 QSALVCALLWALSCLVTTMEY 169

RESULT 14
OORTB2
bradykinin receptor type B-2 - rat
C: Species: Rattus norvegicus (Norway rat)
C: Date: 30-Sep-1992 #sequence-revision 30-Sep-1992 #text_change 22-Jun-1999
C: Accession: A41283; A55079; S47529
F: McEachern, A.E.; Shelton, E.R.; Bhakta, S.; Ohernolte, R.; Bach, C.; Zuppan, P.; Fu
Proc. Natl. Acad. Sci. U.S.A. 88, 7724-7728, 1991
A: Title: Expression cloning of a rat B-2 bradykinin receptor.
A: Reference number: A41283; MUID:91352062
A: Accession: A41283
A: Molecule type: mRNA
A: Residues: 1-366 <MCE>
A: Cross-references: GB:M59967
R. Pesquero, J.B.; Lindsey, C.J.; Zeh, K.; Paiva, A.C.M.; Ganten, D.; Bader, M.
J. Biol. Chem. 269, 26920-26925, 1994
A: Title: Molecular structure and expression of rat bradykinin B2 receptor gene. Evid
A: Reference number: A55079; MUID:95014558
A: Accession: A55079
A: Status: preliminary; not compared with conceptual translation
A: Molecule type: DNA
A: Residues: 1-75, 'A', '77-366 <PES>
A: Cross-references: GB:X80187; GB:X80188; GB:X80189; GB:X80190
E; Wang, D.; Ma, J.; Chao, L.; Chao, J.
Biochim. Biophys. Acta 1219, 171-174, 1994
A: Title: Molecular cloning and sequence analysis of rat bradykinin B(2) receptor gene
A: Reference number: S47529; MUID:94368850
A: Accession: S47529
A: Status: preliminary
A: Molecule type: DNA
A: Residues: 1-366 <WAN>
A: Cross-references: EMBL:L26173; NID:g476749; PIDN:AAA62492.1; PID:g685244
C: Comment: This G protein-coupled receptor binds the nonapeptide bradykinin.
C: Superfamily: vertebrate rhodopsin
C: Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; lipoprote
F: 31-48/Domain: transmembrane #status predicted <TM1>
F: 79-96/Domain: transmembrane #status predicted <TM2>
F: 107-126/Domain: transmembrane #status predicted <TM3>
F: 154-170/Domain: transmembrane #status predicted <TM4>
F: 197-215/Domain: transmembrane #status predicted <TM5>
F: 245-261/Domain: transmembrane #status predicted <TM6>
F: 3,14,182/Binding site: carbohydrate (Asn) (covalent) #status predicted
F: 105-186/Disulfide bonds: #status predicted
F: 326/Binding site: palmitate (Cys) (covalent) #status predicted

Query Match 38.0%; Score 49; DB 1; Length 366;
 Best Local Similarity 36.4%; Pred. No. 10;
 Matches 8; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 5 SKIICLVWGLSVIISSTFVF 26
 DB 149 AKLYSLVINSCTLLSSPMLVF 170

RESULT 15

S48332
 probable membrane protein YML066c - Yeast (Saccharomyces cerevisiae)
 C:Species: Saccharomyces cerevisiae
 C:Date: 02-Dec-1994 #sequence_revision 02-Dec-1994 #text_change 04-Mar-2000
 C:Accession: S48332
 R: Bowman, S.: Church, C.
 submitted to the EMBL Data Library, August 1994
 A:Reference number: S48326
 A:Accession: S48332
 A:Molecule type: DNA
 A:Residues: 1-369 <BOW>
 A:Cross-references: EMBL:Z38114; NID:g558402; PID:g558409; GSPDB:GN00013; MIPS:YML066c
 C:Genetics:
 A:Gene: MIPS:YML066c
 A:Map position: 13L
 C:Superfamily: Saccharomyces cerevisiae probable membrane protein YML066c
 C:Keywords: transmembrane protein
 F:7-23/Domain: transmembrane #status predicted <TM1>
 F:209-225/Domain: transmembrane #status predicted <TM2>
 F:226-242/Domain: transmembrane #status predicted <TM3>
 F:267-283/Domain: transmembrane #status predicted <TM4>
 F:324-340/Domain: transmembrane #status predicted <TM5>

Query Match 38.0%; Score 49; DB 2; Length 369;
 Best Local Similarity 56.2%; Pred. No. 10;
 Matches 9; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 10 LVVWGLSVIISSTFV 25
 DB 7 LIVWGVLLILSLSQFV 22

Search completed: May 23, 2001, 15:32:01
 Job time: 508 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 23, 2001, 15:36:18 ; Search time 62.39 Seconds
(without alignments)
14.275 Million cell updates/sec

Title: US-08-887-977-10_COPY_151_176
Perfect score: 129
Sequence: 1 TLPRSKIIICLVVWGLSVISSTFVF 26

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34253486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	129	100.0	374	1 CCR6_HUMAN	P51684 homo sapien
2	90	69.8	367	1 CCR6_MOUSE	O54689 mus musculus
3	64	49.6	356	1 IL8B_CANFA	O97571 canis famil
4	63	48.8	360	1 IL8B_BOVIN	Q28003 bos taurus
5	61	47.3	350	1 IL8A_GORGO	P55919 gorilla gor
6	60	46.5	355	1 IL8A_RABIT	P21109 oryctolagus
7	58	45.0	353	1 IL8B_GORGO	Q28422 gorilla gor
8	58	45.0	353	1 IL8B_MACMU	Q28519 macaca mula
9	58	45.0	353	1 IL8B_PANTR	Q28807 pan troglod
10	58	45.0	360	1 IL8B_HUMAN	P25025 homo sapien
11	58	45.0	371	1 YHDY_BACSU	O07594 bacillus su
12	57	44.2	358	1 IL8B_RABIT	P35344 oryctolagus
13	55	42.6	342	1 BONZ_CERAE	O18983 cercopithec
14	55	42.6	342	1 BONZ_MACNE	O19024 macaca neme
15	55	42.6	343	1 BONZ_MACMU	Q9xt45 macaca mula
16	55	42.6	367	1 BRB2_RABIT	Q28642 oryctolagus
17	55	42.6	368	1 CCR3_HUMAN	P49682 homo sapien
18	55	42.6	372	1 BRB2_CAVPO	O70525 cavia porce
19	55	42.6	391	1 BRB2_HUMAN	P30411 homo sapien
20	54	42.6	392	1 BRB2_MOUSE	P32299 mus musculus
21	54	41.9	349	1 IL8A_RAT	P70612 rattus norv
22	54	41.9	350	1 IL8A_HUMAN	P25024 homo sapien
23	54	41.9	350	1 IL8A_PANTR	P55920 pan troglod
24	54	41.9	367	1 CCR3_MOUSE	O88410 mus musculus
25	51	39.5	340	1 C5AR_GORGO	P79175 gorilla gor
26	51	39.5	340	1 C5AR_MACMU	P79188 macaca mula
27	51	39.5	340	1 C5AR_PANTR	P79240 pan troglod
28	51	39.5	340	1 C5AR_PONPY	P79234 pongo pygma
29	51	39.5	350	1 C5AR_HUMAN	P21730 homo sapien
30	51	39.5	355	1 CCR3_CERAE	P36492 cercopithec
31	51	39.5	359	1 IL8B_RAT	P35407 rattus norv
32	50	38.8	371	1 CH23_HUMAN	O75748 homo sapien
33	50	38.8	373	1 CML1_HUMAN	Q99788 homo sapien

34	49	38.0	325	1 MAS_HUMAN	P04201 homo sapien
35	49	38.0	369	1 YMG6_YEAST	Q04658 saccharomyc
36	49	38.0	382	1 CRH2_MOUSE	Q92316 mus musculus
37	49	38.0	396	1 BRB2_RAT	P25023 rattus norv
38	48	37.2	346	1 NU2M_CHICK	P18937 gallus gall
39	48	37.2	477	1 OAR_HELVI	Q25188 heliothis v
40	48	37.2	483	1 BIAR_MELGA	P07700 meleagris g
41	47	36.4	292	1 LICB_HAFIN	P14182 haemophilus
42	47	36.4	324	1 MAS_RAT	P12526 rattus norv
43	47	36.4	355	1 CCR3_HUMAN	P51677 homo sapien
44	47	36.4	355	1 CCR3_MACMU	P56483 macaca mula
45	47	36.4	357	1 SH5A_MOUSE	P30966 mus musculus

ALIGNMENTS

RESULT	1
CCR6_HUMAN	
ID	CCR6_HUMAN STANDARD; PRT; 374 AA.
AC	P51684: Q92846; P78553;
DT	01-OCT-1996 (Rel. 34, Last sequence update)
DT	15-JUL-1998 (Rel. 36, Last annotation update)
DT	01-OCT-2000 (Rel. 40, Last annotation update)
DE	C-C CHEMOKINE RECEPTOR TYPE 6 (C-C CCR-6) (CCR-6) (LARC
DE	RECEPTOR) (GPR-CY4) (GPCY4) (CHEMOKINE RECEPTOR-LIKE 3) (CCR-L3)
DE	(DRY6).
GN	CCR6 OR CCR6R6 OR STRL22 OR GPR29 OR CCR6L3.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A., AND FUNCTION.
RX	MEDLINE=97313465; PubMed=9169459;
RA	Baba M., Imai T., Nishimura M., Kakizaki M., Takagi S., Hieshima K.,
RA	Nomiyama H., Yoshie O.;
RT	"Identification of CCR6, the specific receptor for a novel
RT	lymphocyte-directed CC chemokine LARC.";
RL	J. Biol. Chem. 272:14893-14898(1997).
RN	[2]
RP	SEQUENCE FROM N.A.
RA	Lautens L.L., Modi W., Bonner T.I.;
RL	Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
RN	[3]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=97040707; PubMed=8886020;
RA	Zaballos A., Varona R., Gutierrez J., Lind P., Marquez G.;
RT	"Molecular cloning and RNA expression of two new human chemokine
RT	receptor-like genes.";
RL	Biochem. Biophys. Res. Commun. 227:846-853(1996).
RN	[4]
RP	SEQUENCE FROM N.A.
RA	McCoy R., Perlmutter D.H.;
RL	Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
RN	[5]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=97224503; PubMed=9070937;
RA	Liao F., Lee H.-H., Farber J.M.;
RT	"Cloning of STRL22, a new human gene encoding a G-protein-coupled
RT	receptor related to chemokine receptors and located on chromosome
RT	6q27.";
RL	Genomics 40:175-180(1997).
CC	-!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-3-
CC	ALPHA/LARC AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE
CC	INTRACELLULAR CALCIUM IONS LEVEL.
CC	-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN
CC	LIVER. EXPRESSED IN LYMPHOCYTES, T CELLS AND B CELLS BUT NOT IN
CC	NATURAL KILLER CELLS, MONOCYTES, OR GRANULOCYTES.
CC	-!- INDUCTION: INTERLEUKIN-2.
CC	-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC	-!- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-6 IS THE INITIATOR.

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DR EMBL; U45984; AAB62714.1; -
 DR EMBL; 279784; CAB02144.1; ALT_INIT.
 DR EMBL; U60000; AAB06949.1; -
 DR EMBL; U68030; AAC51124.1; -
 DR EMBL; U68032; AAC51125.1; -
 DR HSSP; P34996; 1DDD.
 DR GCRDB; GCR_1037; -
 DR GCRDB; GCR_1075; -
 DR GCRDB; GCR_1906; -
 DR GCRDB; GCR_1919; -
 DR GCRDB; GCR_1941; -
 DR GCRDB; GCR_2110; -
 DR MIM; 601835; -
 DR InterPro; IPR000276; -
 DR Pfam; PF00001; 7tm1.1; -
 DR PRINTS; PR00237; GPCRHHODOPSN.
 DR PROSITE; PS00237; G-PROTEIN_RECF_FL_1; 1.
 DR PROSITE; PS0262; G-PROTEIN_RECF_FL_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 47
 FT TRANSMEM 48 74
 FT DOMAIN 75 83
 FT TRANSMEM 84 104
 FT DOMAIN 105 119
 FT TRANSMEM 120 141
 FT DOMAIN 142 159
 FT TRANSMEM 160 180
 FT DOMAIN 181 211
 FT TRANSMEM 212 238
 FT DOMAIN 239 254
 FT TRANSMEM 255 279
 FT DOMAIN 280 303
 FT TRANSMEM 304 321
 FT DOMAIN 322 374
 FT DISULFID 118 197
 FT CARBOHYD 7 7
 FT CARBOHYD 23 23
 FT CONFLICT 60 60
 FT CONFLICT 74 74
 FT CONFLICT 86 86
 FT CONFLICT 164 164
 FT CONFLICT 182 182
 FT CONFLICT 192 192
 FT CONFLICT 206 206
 FT CONFLICT 225 225
 FT CONFLICT 370 374
 FT CONFLICT 374 374
 SQ SEQUENCE 374 AA; 42494 MW; D7F963534E990BC4 CRC64;

Query Match 100.0%; Score 129; DB 1; Length 374;
 Best Local Similarity 100.0%; Pred. No. 1.9e-11;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TLPRSKIICLVWGLSVIISSTFFV 26
 |||||
 Db 160 TLPRSKIICLVWGLSVIISSTFFV 185

RESULT 2
 CCR6_MOUSE
 ID CCR6_MOUSE STANDARD; PRT; 367 AA.
 AC O54689;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE C-C CHEMOKINE RECEPTOR TYPE 6 (C-C CKR-6) (CCR-6) (KY411).
 GN CCR6 OR CCR6.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Yanagihara S., Komura E., Yamaguchi Y.;
 RT "Mouse G protein-coupled receptor KY411.";
 RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99077268; PubMed=9862452;
 RA Varona R., Zaballos A., Gutierrez J., Martin P., Roncal F.,
 RA Albar J.P., Ardavin C., Marquez G.;
 RT "Molecular cloning, functional characterization and mRNA expression
 RT analysis of the murine chemokine receptor CCR6 and its specific ligand
 RT MIP-3alpha.";
 RL FEBS Lett. 440:188-194(1998).
 CC -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-3-
 CC ALPHA/LARC AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE
 CC INTRACELLULAR CALCIUM IONS LEVEL.
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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 CC or send an email to license@isb-sib.ch).

DR EMBL; AB009369; BAA23776.1; -
 DR EMBL; AJ222714; CAA10956.1; -
 DR MGD; MGI:1333797; Cmkbr6.
 DR InterPro; IPR000276; -
 DR Pfam; PF00001; 7tm1.1; 1.
 DR PRINTS; PR00237; GPCRHHODOPSN.
 DR PROSITE; PS00237; G-PROTEIN_RECF_FL_1; 1.
 DR PROSITE; PS0262; G-PROTEIN_RECF_FL_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 39
 FT TRANSMEM 40 66
 FT DOMAIN 67 75
 FT TRANSMEM 76 96
 FT DOMAIN 97 111
 FT TRANSMEM 112 133
 FT DOMAIN 134 151
 FT TRANSMEM 152 172
 FT DOMAIN 173 203
 FT TRANSMEM 204 230
 FT DOMAIN 231 246
 FT TRANSMEM 247 271
 FT DOMAIN 272 295
 FT TRANSMEM 296 313
 FT DOMAIN 314 367
 FT DISULFID 110 189
 FT CARBOHYD 2 2
 FT CARBOHYD 35 35
 FT CONFLICT 367 367
 SQ SEQUENCE 367 AA; 42102 MW; 6A309AF833B117E CRC64;

Query Match 69.8%; Score 90; DB 1; Length 367;
 Best Local Similarity 61.5%; Pred. No. 7.4e-06;
 Matches 16; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 TLPRSKIICLVWGLSVIISSTFFV 26
 |||||
 Db 152 TLTHSKVICVAVWFISIIISSTFFIF 177

```
RESULT 3
IL8B_CANFA
ID IL8B_CANFA STANDARD; PRT; 356 AA.
AC O97571.
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE HIGH AFFINITY INTERLEUKIN-8 RECEPTOR B (IL-8R B) (CXCR-2) (GRO/MSGA
DE RECEPTOR).
GN IL8RB OR CXCR2.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BEAGLE;
RA Chang Y.F., Novosel V., Chang C.F.;
RT "The isolation and sequence of canine interleukin-8 receptor
RT homolog."
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
CC !- FUNCTION: RECEPTOR TO INTERLEUKIN-8, WHICH IS A POWERFUL
CC NEUTROPHILS CHEMOTACTIC FACTOR. BINDING OF IL-8 TO THE RECEPTOR
CC CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA A
CC G-PROTEIN THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND
CC MESSENGER SYSTEM. THE AFFINITY OF THIS RECEPTOR IS IL-8 >> NAP-2 >
CC MSGA (GRO).
CC !- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC !- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF047047; AAC98968.1; -
CC InterPro; IPR000057; -
CC InterPro; IPR000174; -
CC InterPro; IPR000276; -
CC InterPro; IPR000355; -
CC InterPro; IPR001277; -
CC Pfam; PF00001; 7tm1.1; 1.
CC PRINTS; PR00237; GPCRHHODPSN.
CC PRINTS; PR00427; INTRLEUKIN8R.
CC PRINTS; PR00573; INTRLEUKIN8R.
CC PRINTS; PR00645; LCRIORPHANR.
CC PRINTS; PR00657; CCHEMOKINR.
CC PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
CC PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein;
CC Chemotaxis.
CC
CC DOMAIN 1 46 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 47 73 1 (POTENTIAL).
CC DOMAIN 74 82 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 83 103 2 (POTENTIAL).
CC DOMAIN 104 118 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 119 140 3 (POTENTIAL).
CC DOMAIN 141 161 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 162 181 4 (POTENTIAL).
CC DOMAIN 182 206 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 207 229 5 (POTENTIAL).
CC DOMAIN 230 249 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 250 269 6 (POTENTIAL).
CC DOMAIN 270 290 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 291 311 7 (POTENTIAL).
CC DOMAIN 312 356 CYTOPLASMIC (POTENTIAL).
CC CARBOHYD 8 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC TRANSMEM 20 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC DISULFID 117 194 BY SIMILARITY.
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SQ SEQUENCE 356 AA; 40505 MW; 2B67DD4E8DD39B15 CRC64;
Query Match 49.6%; Score 64; DB 1; Length 356;
Best Local Similarity 57.1%; Pred. No. 0.039;
Matches 12; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
OY 6 KIICLVWGLSVIISSTFVF 26
DB 161 KFICIGIWSLILSLPIEFV 181
RESULT 4
IL8B_BOVIN
ID IL8B_BOVIN STANDARD; PRT; 360 AA.
AC Q28003;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE HIGH AFFINITY INTERLEUKIN-8 RECEPTOR B (IL-8R B) (CXCR-2).
GN IL8RB OR CXCR2.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Li Y., Feng J., Templeton J.W.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
CC !- FUNCTION: RECEPTOR TO INTERLEUKIN-8, WHICH IS A POWERFUL
CC NEUTROPHILS CHEMOTACTIC FACTOR. BINDING OF IL-8 TO THE RECEPTOR
CC CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA A
CC G-PROTEIN THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND
CC MESSENGER SYSTEM. THIS RECEPTOR BINDS TO IL-8 WITH A HIGH AFFINITY
CC AND TO GRO/MSGA AND NAP-2 ALSO WITH A HIGH AFFINITY (BY
CC SIMILARITY).
CC !- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC !- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC
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CC
CC EMBL; U19947; AAA84996.1; -
CC GCRDB; GCR.1224; -
CC InterPro; IPR000174; -
CC InterPro; IPR000276; -
CC Pfam; PF00001; 7tm1.1; 1.
CC PRINTS; PR00237; GPCRHHODPSN.
CC PRINTS; PR00427; INTRLEUKIN8R.
CC PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
CC PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein;
CC Chemotaxis.
CC
CC DOMAIN 1 48 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 49 75 1 (POTENTIAL).
CC DOMAIN 76 84 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 85 105 2 (POTENTIAL).
CC DOMAIN 106 120 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 121 142 3 (POTENTIAL).
CC DOMAIN 143 163 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 164 183 4 (POTENTIAL).
CC DOMAIN 184 208 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 209 231 5 (POTENTIAL).
CC DOMAIN 232 251 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 252 273 6 (POTENTIAL).
CC DOMAIN 274 294 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 295 315 7 (POTENTIAL).
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FT TRANSMEM 112 133 3 (POTENTIAL).
FT DOMAIN 134 154 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 155 174 4 (POTENTIAL).
FT DOMAIN 175 199 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 200 220 5 (POTENTIAL).
FT DOMAIN 221 242 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 243 264 6 (POTENTIAL).
FT DOMAIN 265 285 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 286 308 7 (POTENTIAL).
FT DOMAIN 309 350 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 3 3 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 16 16 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 110 187 BY SIMILARITY.
SQ SEQUENCE 350 AA; 39790 MW; DB99591CD6C10757 CRC64;

Query Match 47.3%; Score 61; DB 1; Length 350;
Best Local Similarity 52.4%; Pred. No. 0.1;
Matches 11; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 6 KIICLVWGLSVIISSSTVFV 26
   I : I I I I I I I I I I
Db 154 KVCIGCWGLSMILSLPFFLF 174

RESULT 6
IL8A_RABIT STANDARD; PRT: 355 AA.
ID IL8A_RABIT
AC P21109;
DT 01-FEB-1991 (Rel. 17, Created)
DI 01-MAY-1992 (Rel. 22, Last sequence update)
DR 01-NOV-1997 (Rel. 35, Last annotation update)
DE HIGH AFFINITY INTERLEUKIN-8 RECEPTOR A (IL-8R A) (CXCR-1).
GN IL8RA OR CXCR1.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91378994; PubMed=1898400;
RA Beckmann M.P., Munger W.E., Kozlosky C., Vandenbos T., Price V.,
RA Lyman S., Gerard N.P., Gerard C., Cerretti D.P.;
RT "Molecular characterization of the interleukin-8 receptor.";
RL Biochem. Biophys. Res. Commun. 179:784-789(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=ALBINO; TISSUE=Neutrophils;
RX MEDLINE=91056034; PubMed=1700779;
RA Thomas K.M., Pyun H.Y., Navarro J.;
RT "Molecular cloning of the fmet-Leu-Phe receptor from neutrophils.";
RL J. Biol. Chem. 265:20061-20064(1990).
RN [3]
RP SEQUENCE FROM N.A.
RX TISSUE=Neutrophils;
RX MEDLINE=92148149; PubMed=1737938;
RA Lee J., Kuang W.-J., Rice G.C., Wood W.I.;
RT "Characterization of complementary DNA clones encoding the rabbit
  IL-8 receptor.";
RL J. Immunol. 148:1261-1264(1992).
CC -1- FUNCTION: RECEPTOR TO INTERLEUKIN-8, WHICH IS A POWERFUL
CC NEUTROPHILS CHEMOTACTIC FACTOR. BINDING OF IL-8 TO THE RECEPTOR
CC CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA A
CC G-PROTEIN THAT ACTIVATES A PHOSPHATIDYLINOSITOL-CALCIUM SECOND
CC MESSENGER SYSTEM.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: NEUTROPHILS.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -1- CAUTION: WAS ORIGINALLY (REF.2) THOUGHT TO BE THE RECEPTOR FOR
CC FMET-LEU-PHE (N-FORMYL PEPTIDE RECEPTOR).
CC -----
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[illegible]

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OX NCBI_TaxID=9595;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96175151; PubMed=9110929;
RA Alvarez V., Coto E., Setien F., Gonzalez S., Gonzalez-Roces S.,
RA Lopez-Larrea C.;
RT "Characterization of interleukin-8 receptors in non-human primates.";
RL Immunogenetics 43:261-267(1996).
CC -!- FUNCTION: RECEPTOR TO INTERLEUKIN-8, WHICH IS A POWERFUL
CC NEUTROPHILS CHEMOTACTIC FACTOR. BINDING OF IL-8 TO THE RECEPTOR
CC CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA A
CC G-PROTEIN THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND
CC MESSENGER SYSTEM. THIS RECEPTOR BINDS TO IL-8 WITH A HIGH AFFINITY
CC AND TO GRO/MGSA AND NAP-2 ALSO WITH A HIGH AFFINITY.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CC -----
CC EMBL: X91114; CAA62564.1; -
CC HSSP; P34996; 1DDD.
CC InterPro: IPR000276; -.
CC Pfam: PF00001; 7tm.1; 1.
CC PROSITE; PS00237; G_PROTEIN_RECEP_FL_1; 1.
CC PROSITE; PS0262; G_PROTEIN_RECEP_FL_2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein;
CC Chemotaxis.
CC
FT FT 1 1
FT FT <1 45 EXTRACELLULAR (POTENTIAL).
FT FT DOMAIN 46 72 1 (POTENTIAL).
FT FT TRANSMEM 73 81 CYTOPLASMIC (POTENTIAL).
FT FT TRANSMEM 82 102 2 (POTENTIAL).
FT FT DOMAIN 103 117 EXTRACELLULAR (POTENTIAL).
FT FT TRANSMEM 118 139 3 (POTENTIAL).
FT FT DOMAIN 140 160 CYTOPLASMIC (POTENTIAL).
FT FT TRANSMEM 161 180 4 (POTENTIAL).
FT FT DOMAIN 181 205 EXTRACELLULAR (POTENTIAL).
FT FT TRANSMEM 206 228 5 (POTENTIAL).
FT FT DOMAIN 229 248 6 (POTENTIAL).
FT FT TRANSMEM 249 270 6 (POTENTIAL).
FT FT DOMAIN 271 291 EXTRACELLULAR (POTENTIAL).
FT FT TRANSMEM 292 312 7 (POTENTIAL).
FT FT DOMAIN 313 >353 CYTOPLASMIC (POTENTIAL).
FT FT DISULFID 116 193 BY SIMILARITY.
FT FT CARBOHYD 19 19 N-LINKED (GLCNAC. .) (POTENTIAL).
FT FT NON_TER 353 353
SQ SEQUENCE 353 AA; 39919 MW; 1FF04E31A7E825E4 CRC64;

Query Match 45.0%; Score 58; DB 1; Length 353;
Best Local Similarity 42.9%; Pred. No. 0.28;
Matches 9; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 6 KIICLVWGLSVIIISSTFFV 26
1 ||| :|||::: :|
Db 160 KFICLSINGSLLLALPVLFF 180

RESULT 8
IL8B_MACMU STANDARD; PRT; 353 AA.
ID IL8B_MACMU
AC Q28519;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
GN HIGH AFFINITY INTERLEUKIN-8 RECEPTOR B (IL-8R B) (CXCR-2) (FRAGMENT).
GN IL8RB OR CXCR2.

```

OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96175151; PubMed=9110929;
RA Alvarez V., Coto E., Setien F., Gonzalez S., Gonzalez-Roces S.,
RA Lopez-Larrea C.;
RT "Characterization of interleukin-8 receptors in non-human primates.";
RL Immunogenetics 43:261-267(1996).
CC -!- FUNCTION: RECEPTOR TO INTERLEUKIN-8, WHICH IS A POWERFUL
CC NEUTROPHILS CHEMOTACTIC FACTOR. BINDING OF IL-8 TO THE RECEPTOR
CC CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA A
CC G-PROTEIN THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND
CC MESSENGER SYSTEM. THIS RECEPTOR BINDS TO IL-8 WITH A HIGH AFFINITY
CC AND TO GRO/MGSA AND NAP-2 ALSO WITH A HIGH AFFINITY.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CC
DR EMBL; X91116; CAA62565.1; -
DR HSP; P34996; IDDD.
DR InterPro: IPR000276; -
DR Pfam: PF00001; 7tm_1; 1.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEPTOR_F2_1; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Chemotaxis.
FT NON_TER 1 1
FT DOMAIN <1 45 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 46 72 1 (POTENTIAL).
FT DOMAIN 73 81 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 82 102 2 (POTENTIAL).
FT DOMAIN 103 117 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 118 139 3 (POTENTIAL).
FT DOMAIN 140 160 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 161 180 4 (POTENTIAL).
FT DOMAIN 181 205 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 206 228 5 (POTENTIAL).
FT DOMAIN 229 248 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 249 270 6 (POTENTIAL).
FT DOMAIN 271 291 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 292 312 7 (POTENTIAL).
FT DOMAIN 313 >353 CYTOPLASMIC (POTENTIAL).
FT DISULFID 116 193 BY SIMILARITY.
FT CARBOHYD 19 19 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT NON_TER 353 353
SQ SEQUENCE 353 AA; 39947 MW; EC8B38130657C713 CRC64;

Query Match 45.0%; Score 58; DB 1; Length 353;
Best Local Similarity 42.9%; Pred. No. 0.28;
Matches 9; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

Qy 6 KIICLVWGLSVIISSSTFVF 26
| ||| :||||: :
Db 160 KFCISIWGLSLALLPVLFF 180

RESULT 9
IL8B_PANTR STANDARD; PRT; 353 AA.
ID IL8B_PANTR
AC Q28807;
DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE HIGH AFFINITY INTERLEUKIN-8 RECEPTOR B (IL-8R B) (CXCR-2) (FRAGMENT).
GN IL8RB OR CXCR2.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96175151; PubMed=9110929;
RA Alvarez V., Coto E., Setien F., Gonzalez S., Gonzalez-Roces S.,
RA Lopez-Larrea C.;
RT "Characterization of interleukin-8 receptors in non-human primates.";
RL Immunogenetics 43:261-267(1996).
CC -!- FUNCTION: RECEPTOR TO INTERLEUKIN-8, WHICH IS A POWERFUL
CC NEUTROPHILS CHEMOTACTIC FACTOR. BINDING OF IL-8 TO THE RECEPTOR
CC CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA A
CC G-PROTEIN THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND
CC MESSENGER SYSTEM. THIS RECEPTOR BINDS TO IL-8 WITH A HIGH AFFINITY
CC AND TO GRO/MGSA AND NAP-2 ALSO WITH A HIGH AFFINITY.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC
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CC or send an email to license@isb-sib.ch).
CC
DR EMBL; X91113; CAA62563.1; -
DR HSP; P34996; IDDD.
DR InterPro: IPR000276; -
DR Pfam: PF00001; 7tm_1; 1.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEPTOR_F2_1; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Chemotaxis.
FT NON_TER 1 1
FT DOMAIN <1 45 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 46 72 1 (POTENTIAL).
FT DOMAIN 73 81 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 82 102 2 (POTENTIAL).
FT DOMAIN 103 117 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 118 139 3 (POTENTIAL).
FT DOMAIN 140 160 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 161 180 4 (POTENTIAL).
FT DOMAIN 181 205 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 206 228 5 (POTENTIAL).
FT DOMAIN 229 248 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 249 270 6 (POTENTIAL).
FT DOMAIN 271 291 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 292 312 7 (POTENTIAL).
FT DOMAIN 313 >353 CYTOPLASMIC (POTENTIAL).
FT DISULFID 116 193 BY SIMILARITY.
FT CARBOHYD 19 19 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT NON_TER 353 353
SQ SEQUENCE 353 AA; 39998 MW; E745ACD9EC10C1E2 CRC64;

Query Match 45.0%; Score 58; DB 1; Length 353;
Best Local Similarity 42.9%; Pred. No. 0.28;
Matches 9; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

Qy 6 KIICLVWGLSVIISSSTFVF 26
| ||| :||||: :
Db 160 KFCISIWGLSLALLPVLFF 180

RESULT 10
IL8B_HUMAN

ID IL8B_HUMAN STANDARD; PRT: 360 AA.
AC P25025;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE HIGH AFFINITY INTERLEUKIN-8 RECEPTOR B (IL-8R B) (CXCR-2) (GRO/MGSA
DE RECEPTOR) (IL-8 RECEPTOR TYPE 2) (CDW128B).
GN IL8RB OR CXCR2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A.
RP MEDLINE=91368200; PubMed=1891716;
RA Murphy P.M., Tiffany H.L.;
RT "Cloning of complementary DNA encoding a functional human
RT Interleukin-8 receptor.";
RL Science 253:1280-1283(1991).
[2]
RN SEQUENCE FROM N.A., AND CHARACTERIZATION.
RP MEDLINE=91205012; PubMed=8384312;
RA Carretti D.P., Kozlosky C.J., Vanden Bos T., Nelson N., Gearing D.P.,
RA Beckmann M.P.;
RT "Molecular characterization of receptors for human interleukin-8,
RT GRO/melanoma growth-stimulatory activity and neutrophil activating
RT peptide-2.";
RL Mol. Immunol. 30:359-367(1993).
[3]
RN SEQUENCE FROM N.A.
RP MEDLINE=94209273; PubMed=7512557;
RA Sprenger H., Lloyd A.R., Lautens L.L., Bonner T.I., Kelvin D.J.;
RT "Structure, genomic organization, and expression of the human
RT interleukin-8 receptor B gene.";
RL J. Biol. Chem. 269:11065-11072(1994).
[4]
RN SEQUENCE FROM N.A.
RP TISSUE=Placenta;
RA MEDLINE=95014476; PubMed=7929358;
RA Anuja S.K., Shetty A., Tiffany H.L., Murphy P.M.;
RT "Comparison of the genomic organization and promoter function for
RT human interleukin-8 receptors A and B.";
RL J. Biol. Chem. 269:26381-26389(1994).
[5]
RN CHARACTERIZATION.
RP MEDLINE=92355587; PubMed=1379593;
RA Lee J., Horuk R., Rice G.C., Bennett G.L., Camerato T., Wood W.I.;
RT "Characterization of two high affinity human interleukin-8
RT receptors.";
RL J. Biol. Chem. 267:16283-16287(1992).
CC -!- FUNCTION: RECEPTOR TO INTERLEUKIN-8, WHICH IS A POWERFUL
CC NEUTROPHILS CHEMOTACTIC FACTOR. BINDING OF IL-8 TO THE RECEPTOR
CC CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA A
CC G-PROTEIN THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND
CC MESSENGER SYSTEM. THIS RECEPTOR BINDS TO IL-8 WITH A HIGH AFFINITY
CC AND TO GRO/MGSA AND NAP-2 ALSO WITH A HIGH AFFINITY.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -!- DATABASE: NAME=PROW; NOTE=CD guide cdw128b entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cdw128b.htm".
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; M73969; AAA83148.1; -
CC EMBL; M94582; AAA36108.1; -
CC EMBL; M99412; AAC14460.1; -
CC EMBL; L19593; AAB59437.1; -

DR EMBL; U11869; AAB60656.1; -
DR PIR; A39446; A39446.
DR PIR; A53611; A53611.
DR HSSP; P34996; 1DDO.
DR GCRDB; GCR_0077; -
DR GCRDB; GCR_0610; -
DR GCRDB; GCR_1001; -
DR GCRDB; GCR_1339; -
DR GCRDB; GCR_1831; -
DR MIM; 146928; -
DR InterPro; IPR000057; -
DR InterPro; IPR000174; -
DR InterPro; IPR000276; -
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PRINTS; PR00427; INTRLEUKIN8R.
DR PRINTS; PR00573; INTRLEUKIN8BR.
DR PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G-PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Chemotaxis.
FT DOMAIN 1 48 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 49 75 1 (POTENTIAL).
FT DOMAIN 76 84 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 85 105 2 (POTENTIAL).
FT DOMAIN 106 120 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 121 142 3 (POTENTIAL).
FT DOMAIN 143 163 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 164 183 4 (POTENTIAL).
FT DOMAIN 184 208 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 209 231 5 (POTENTIAL).
FT DOMAIN 232 251 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 252 273 6 (POTENTIAL).
FT DOMAIN 274 294 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 295 315 7 (POTENTIAL).
FT DOMAIN 316 360 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 22 22 N-LINKED (GLCNAC. .) (POTENTIAL).
FT DISULFID 119 196 BY STMILARITY.
SQ SEQUENCE 360 AA; 40759 MW; 564F04A8BCC0A197 CRC64;
Query Match 45.0%; Score 58; DB 1; Length 360;
Best Local Similarity 42.9%; Pred. No. 0.29;
Matches 9; Conservative 6; Mismatches 6; Indels 0; Gaps 0;
Oy 6 KIICLVWGLSVIISSSTFVF 26
| | | | | : | | | | : |
Db 163 KFCICLSIWGLSLLALPVLFF 183
RESULT 11
YHDY_BACSU
ID YHDY_BACSU STANDARD; PRT: 371 AA.
AC 007594;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE HYPOTHETICAL 42.5 KDA PROTEIN IN CITR-SSPB INTERGENIC REGION.
GN YHDY.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=168;
RA Noback M.A., Terpstra P., Holsappel S., Venema G., Bron S.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
CC -!- SIMILARITY: BELONGS TO THE UPF0003 FAMILY.
CC
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DR EMBL; Y14082; CAA74509.1; -
 DR EMBL; Z99109; CABI2803.1; -
 DR Subtilist; BG13031; yhdy.
 DR InterPro; IPR001880; -
 DR Pfam; PF00924; UPF0003; 1.
 DR PROSITE; PS01246; UPF0003; 1.
 KW Hypothetical protein; Transmembrane.
 FT TRANSMEM 9 29 POTENTIAL.
 FT TRANSMEM 58 78 POTENTIAL.
 FT TRANSMEM 98 118 POTENTIAL.
 FT TRANSMEM 133 153 POTENTIAL.
 FT TRANSMEM 159 179 POTENTIAL.
 FT TRANSMEM 183 203 POTENTIAL.
 FT TRANSMEM 330 350 POTENTIAL.
 SQ SEQUENCE 371 AA; 42537 MW; ABE76B77EBC2D9B7 CRC64;

Query Match 45.0%; Score 58; DB 1; Length 371;
 Best Local Similarity 43.5%; Pred. No. 0.29;
 Matches 10; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

QY 4 RSKICLVVWGLSVIISSTFVF 26

DR 96 RSLVALLCWGLCNTATSSFF 118

RESULT 12

ID IL8B_RABIT STANDARD; PRT; 358 AA.
 AC P35344;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE HIGH AFFINITY INTERLEUKIN-8 RECEPTOR B (IL-8R B) (CXCR-2) (GRO/MGSA RECEPTOR)
 GN IL8RB OR CXCR2.
 OS Oryctolagus cuniculus (Rabbit).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ALBINO; TISSUE=Blood;
 RX MEDLINE=94230294; PubMed=8175642;
 RA Prado G.N., Thomas K.M., Suzuki H., Larosa G.J., Wilkinson N.C.,
 RA Folco E., Navarro J.;
 RT Molecular characterization of a novel rabbit interleukin-8 receptor isotype.";

RL J. Biol. Chem. 269:12391-12394(1994).
 CC -!- FUNCTION: RECEPTOR TO INTERLEUKIN-8, WHICH IS A POWERFUL
 CC NEUTROPHILS CHEMOTACTIC FACTOR. BINDING OF IL-8 TO THE RECEPTOR
 CC CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA A
 CC G-PROTEIN THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND
 CC MESSENGER SYSTEM. THE AFFINITY OF THIS RECEPTOR IS IL-8 >> NAP-2 >
 CC MSGA (GRO).
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -!- TISSUE SPECIFICITY: EXPRESSED PREFERENTIALLY IN NEUTROPHILS.
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----

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DR EMBL; L24445; AAA31378.1; -
 DR PIR; A53752; A53752.
 DR GCRDb; GCR 0861; -
 DR InterPro; IPR000057; -
 DR InterPro; IPR000174; -
 DR InterPro; IPR000276; -
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PRINTS; PR00427; INTRLEUKIN8R.
 DR PRINTS; PR00573; INTRLEUKIN8R.
 DR PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS02662; G-PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 Chemotaxis.
 FT DOMAIN 1 46 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 47 73 1 (POTENTIAL).
 FT DOMAIN 74 82 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 83 103 2 (POTENTIAL).
 FT DOMAIN 104 118 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 119 140 3 (POTENTIAL).
 FT DOMAIN 141 161 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 162 181 4 (POTENTIAL).
 FT DOMAIN 182 206 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 207 229 5 (POTENTIAL).
 FT DOMAIN 230 249 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 250 271 6 (POTENTIAL).
 FT DOMAIN 272 292 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 293 313 7 (POTENTIAL).
 FT DOMAIN 314 358 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 8 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 20 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT DISULFID 117 BY SIMILARITY.
 SQ SEQUENCE 358 AA; 40632 MW; 6899716944D6126A CRC64;

Query Match 44.2%; Score 57; DB 1; Length 358;
 Best Local Similarity 47.6%; Pred. No. 0.4;
 Matches 10; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 6 KIIICLVVWGLSVIISSTFVF 26

DR 161 KFIICLVVWGLSVIISSTFVF 181

RESULT 13

ID BONZ_CERAE STANDARD; PRT; 342 AA.
 AC O18983;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE G PROTEIN-COUPLED RECEPTOR BONZO.
 GN BONZO.
 OS Cercopithecus aethiops (Green monkey) (Grivet).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
 CC Cercopithecinae; Cercopithecus.
 OX NCBI_TaxID=9534;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97373958; PubMed=9230441;
 RA Deng H.K., Unutmaz D., Kewalramani V.N., Littman D.R.;
 RT "Expression cloning of new receptors used by simian and human
 RT immunodeficiency viruses.";
 RL Nature 388:296-300(1997).

CC -!- FUNCTION: ORPHAN RECEPTOR. COULD BE A CHEMOKINE RECEPTOR. USED AS
 CC A CORCEPTOR BY SIYS AND BY STRAINS OF HIV-2 AND M-TROPIC HIV-1.
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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DR	ENBL; AFI24380; AAD31419.1; -	
DR	InterPro; IPR000276; -	
DR	InterPro; IPR002235; -	
DR	Pfam; PF00001; 7tm.1; 1.	
DR	PRINTS; PR00237; GPCRHHODOPSN.	
DR	PRINTS; PR01105; BONZOORPHANR.	
DR	PROSITE; PS00237; G_PROTEIN_RECEP_FL_1; 1.	
DR	PROSITE; PS0262; G_PROTEIN_RECEP_FL_2; 1.	
KW	G-protein coupled receptor; Transmembrane; Glycoprotein.	
FT	DOMAIN 1	33
FT	TRANSMEM	34
FT	FT DOMAIN	61
FT	TRANSMEM	70
FT	FT DOMAIN	91
FT	TRANSMEM	105
FT	FT DOMAIN	127
FT	TRANSMEM	145
FT	FT DOMAIN	166
FT	TRANSMEM	189
FT	FT DOMAIN	217
FT	TRANSMEM	233
FT	FT DOMAIN	261
FT	TRANSMEM	277
FT	FT DOMAIN	295
FT	CARBOHYD	17
FT	DISULFID	103
FT	SEQUENCE	343 AA
DR	ENBL; AFI24380; AAD31419.1; -	
DR	InterPro; IPR000276; -	
DR	InterPro; IPR002235; -	
DR	Pfam; PF00001; 7tm.1; 1.	
DR	PRINTS; PR00237; GPCRHHODOPSN.	
DR	PRINTS; PR01105; BONZOORPHANR.	
DR	PROSITE; PS00237; G_PROTEIN_RECEP_FL_1; 1.	
DR	PROSITE; PS0262; G_PROTEIN_RECEP_FL_2; 1.	
KW	G-protein coupled receptor; Transmembrane; Glycoprotein.	
FT	DOMAIN 1	33
FT	TRANSMEM	34
FT	FT DOMAIN	61
FT	TRANSMEM	70
FT	FT DOMAIN	91
FT	TRANSMEM	105
FT	FT DOMAIN	127
FT	TRANSMEM	144
FT	FT DOMAIN	165
FT	TRANSMEM	188
FT	FT DOMAIN	216
FT	TRANSMEM	232
FT	FT DOMAIN	250
FT	TRANSMEM	276
FT	FT DOMAIN	294
FT	TRANSMEM	343
FT	CARBOHYD	17
FT	DISULFID	103
FT	SEQUENCE	343 AA
DR	ENBL; AFI24380; AAD31419.1; -	
DR	InterPro; IPR000276; -	
DR	InterPro; IPR002235; -	
DR	Pfam; PF00001; 7tm.1; 1.	
DR	PRINTS; PR00237; GPCRHHODOPSN.	
DR	PRINTS; PR01105; BONZOORPHANR.	
DR	PROSITE; PS00237; G_PROTEIN_RECEP_FL_1; 1.	
DR	PROSITE; PS0262; G_PROTEIN_RECEP_FL_2; 1.	
KW	G-protein coupled receptor; Transmembrane; Glycoprotein.	
FT	DOMAIN 1	33
FT	TRANSMEM	34
FT	FT DOMAIN	61
FT	TRANSMEM	70
FT	FT DOMAIN	91
FT	TRANSMEM	105
FT	FT DOMAIN	126
FT	TRANSMEM	144
FT	FT DOMAIN	165
FT	TRANSMEM	188
FT	FT DOMAIN	216
FT	TRANSMEM	232
FT	FT DOMAIN	250
FT	TRANSMEM	276
FT	FT DOMAIN	294
FT	TRANSMEM	343
FT	CARBOHYD	17
FT	DISULFID	103
FT	SEQUENCE	343 AA
DR	ENBL; AFI24380; AAD31419.1; -	
DR	InterPro; IPR000276; -	
DR	InterPro; IPR002235; -	
DR	Pfam; PF00001; 7tm.1; 1.	
DR	PRINTS; PR00237; GPCRHHODOPSN.	
DR	PRINTS; PR01105; BONZOORPHANR.	
DR	PROSITE; PS00237; G_PROTEIN_RECEP_FL_1; 1.	
DR	PROSITE; PS0262; G_PROTEIN_RECEP_FL_2; 1.	
KW	G-protein coupled receptor; Transmembrane; Glycoprotein.	
FT	DOMAIN 1	33
FT	TRANSMEM	34
FT	FT DOMAIN	61
FT	TRANSMEM	70
FT	FT DOMAIN	91
FT	TRANSMEM	105
FT	FT DOMAIN	126
FT	TRANSMEM	144
FT	FT DOMAIN	165
FT	TRANSMEM	188
FT	FT DOMAIN	216
FT	TRANSMEM	232
FT	FT DOMAIN	250
FT	TRANSMEM	276
FT	FT DOMAIN	294
FT	TRANSMEM	343
FT	CARBOHYD	17
FT	DISULFID	103
FT	SEQUENCE	343 AA
DR	ENBL; AFI24380; AAD31419.1; -	
DR	InterPro; IPR000276; -	
DR	InterPro; IPR002235; -	
DR	Pfam; PF00001; 7tm.1; 1.	
DR	PRINTS; PR00237; GPCRHHODOPSN.	
DR	PRINTS; PR0	

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Query Match      42.6%; Score 55; DB 1; Length 343;
Best Local Similarity 33.3%; Pred. NO. 0.74;
Matches 7; Conservative 9; Mismatches 5; Indels 0; Gaps 0;

QY      6 KIICLVVWGLSVIISSTFFVF 26
          |:::|:::|:::|:::|:::
DB     150 KVICLLIHWISLLVSLPQIIY 170

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Search completed: May 23, 2001, 15:36:18
Job time: 649 sec

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	90	69.8		367	11	Q9R1V0	Q9rlv0 mus musculus
2	63	48.8		174	6	Q9TU48	Q9tu48 bos taurus
3	63	48.8		174	6	Q9TQ57	Q9tqs7 bos taurus
4	60	46.5		367	11	Q9TJI9	Q9tji9 rattus norv
5	56	43.4		148	6	Q9T32	Q9tj32 bos sp. c5a
6	55	42.6		343	6	Q9XT45	Q9xt45 macaca mula
7	55	42.6		343	6	Q9N020	Q9n020 cercocebus
8	55	42.6		415	4	O15185	O15185 homo sapien
9	54	41.9		367	11	O88410	O88410 mus musculus
10	54	41.9		367	11	Q9QW6	Q9qwn6 mus musculus
11	53	41.1		368	13	O42444	O42444 oncorhynch
12	53	41.1		395	4	O94765	O94765 homo sapien
13	53	41.1		502	4	Q9Y5Y4	Q9y5y4 homo sapien
14	53	41.1		770	3	Q9P491	Q9p491. trichoderma
15	53	41.1		901	11	O88860	O88860 mus musculus
16	52	40.3		848	11	Q62889	Q62889 rattus norv
17	51	39.5		254	6	Q9N1D0	Q9n1d0 bos taurus
18	50.5	39.1		419	13	Q9IA91	Q9ia91 morone saxa
19	50	38.8		261	11	O70439	O70439 mus musculus

```
Q9TU48
ID Q9TU48 PRELIMINARY; PRT; 174 AA.
AC Q9TU48;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE INTERLEUKIN 8 RECEPTOR-LIKE PROTEIN (FRAGMENT).
GN IL8R.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Grosse W.M., Kappes S.M., Laegreid W.W., Keele J.W.,
RA Chitko-McKown C.G., Heaton M.P.;
RT "Single Nucleotide Polymorphism (SNP) Discovery and Linkage Mapping of
RT Bovine Nucleotide Genes.";
RL Mann. Genome 10:1062-1069(1999).
DR EMBL; AF140650; AAF07867.1; -
DR INTERPRO; IPR000174; -
DR INTERPRO; IPR000276; -
DR PFAM; PF00001; 7tm_1; 1.
DR PRINTS; PRO0237; GPCRHHODPSN.
DR PRINTS; PRO0427; INTRLEUKIN8R.
KW Receptor.
FT NON_TER 1
FT NON_TER 174
SQ SEQUENCE 174 AA; 20107 MW; D20E223B0EFE836 CRC64;

Query Match 48.8%; Score 63; DB 6; Length 174;
Best Local Similarity 52.4%; Pred. No. 0.13;
Matches 11; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 6 KIICLVWGLSVIISSSTVFV 26
| | | | : | | | | : | : |
Db 11 KFCICGIALSVILALPIFIF 31

RESULT 3
Q9TOS7 PRELIMINARY; PRT; 174 AA.
ID Q9TOS7;
AC Q9TOS7;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE INTERLEUKIN 8 RECEPTOR-LIKE PROTEIN (FRAGMENT).
GN IL8R.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Grosse W.M., Kappes S.M., Laegreid W.W., Keele J.W.,
RA Chitko-McKown C.G., Heaton M.P.;
RT "Single Nucleotide Polymorphism (SNP) Discovery and Linkage Mapping of
RT Bovine Nucleotide Genes.";
RL Mann. Genome 10:1062-1069(1999).
DR EMBL; AF140652; AAF07869.1; -
DR EMBL; AF140648; AAF07865.1; -
DR EMBL; AF140649; AAF07866.1; -
DR EMBL; AF140651; AAF07868.1; -
DR INTERPRO; IPR000174; -
DR INTERPRO; IPR000276; -
DR PFAM; PF00001; 7tm_1; 1.
DR PRINTS; PRO0237; GPCRHHODPSN.
DR PRINTS; PRO0427; INTRLEUKIN8R.
KW Receptor.
FT NON_TER 1
FT NON_TER 174
SQ SEQUENCE 174 AA; 20107 MW; D20E223B0EFE836 CRC64;

Query Match 48.8%; Score 63; DB 6; Length 174;
Best Local Similarity 52.4%; Pred. No. 0.13;
Matches 11; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 6 KIICLVWGLSVIISSSTVFV 26
| | | | : | | | | : | : |
Db 11 KFCICGIALSVILALPIFIF 31

RESULT 3
Q9TOS7 PRELIMINARY; PRT; 174 AA.
ID Q9TOS7;
AC Q9TOS7;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE INTERLEUKIN 8 RECEPTOR-LIKE PROTEIN (FRAGMENT).
GN IL8R.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Grosse W.M., Kappes S.M., Laegreid W.W., Keele J.W.,
RA Chitko-McKown C.G., Heaton M.P.;
RT "Single Nucleotide Polymorphism (SNP) Discovery and Linkage Mapping of
RT Bovine Nucleotide Genes.";
RL Mann. Genome 10:1062-1069(1999).
DR EMBL; AF140652; AAF07869.1; -
DR EMBL; AF140648; AAF07865.1; -
DR EMBL; AF140649; AAF07866.1; -
DR EMBL; AF140651; AAF07868.1; -
DR INTERPRO; IPR000174; -
DR INTERPRO; IPR000276; -
DR PFAM; PF00001; 7tm_1; 1.
DR PRINTS; PRO0237; GPCRHHODPSN.
DR PRINTS; PRO0427; INTRLEUKIN8R.
KW Receptor.
FT NON_TER 1
FT NON_TER 174
SQ SEQUENCE 174 AA; 20107 MW; D20E223B0EFE836 CRC64;
```

```
FT NON_TER 174
SQ SEQUENCE 174 AA; 20116 MW; D21C877CEC5BAFC6 CRC64;

Query Match 48.8%; Score 63; DB 6; Length 174;
Best Local Similarity 52.4%; Pred. No. 0.13;
Matches 11; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 6 KIICLVWGLSVIISSSTVFV 26
| | | | : | | | | : | : |
Db 11 KFCICGIALSVILALPIFIF 31

RESULT 4
Q9JIU9 PRELIMINARY; PRT; 367 AA.
ID Q9JIU9;
AC Q9JIU9;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE CHEMOKINE RECEPTOR CXCR3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-20286573; PubMed=10825390;
RA Wang X., Li X., Schmidt D.B., Foley J.J., Barone F.C., Ames R.S.,
RA Sarau H.M.;
RT "Identification and molecular characterization of rat CXCR3: receptor
RT expression and interferon-inducible protein-10 binding are increased
RT in focal stroke.";
RL Mol. Pharmacol. 57:1190-1198(2000).
DR EMBL; AF223642; AAF76982.1; -
KW Receptor.
SQ SEQUENCE 367 AA; 40934 MW; F67C0362EDDBFCB7 CRC64;

Query Match 46.5%; Score 60; DB 11; Length 367;
Best Local Similarity 43.5%; Pred. No. 0.65;
Matches 10; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 4 RSKIIICLVWGLSVIISSSTVFV 26
| | | | : | | | | : | : |
Db 166 RVALTCIVWGLCVLFLPDFIF 188

RESULT 5
Q9TS32 PRELIMINARY; PRT; 148 AA.
ID Q9TS32;
AC Q9TS32;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE C5A RECEPTOR.
OS Bos sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=29061;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-93111969; PubMed=1472004;
RA Perret J.J., Raspe E., Vassart G., Parmentier M.;
RT "Cloning and functional expression of the canine anaphylatoxin C5a
RT receptor. Evidence for high interspecies variability.";
RL Biochem. J. 288:911-917(1992).
DR INTERPRO; IPR000276; -
DR INTERPRO; IPR000496; -
DR INTERPRO; IPR000826; -
DR INTERPRO; IPR001274; -
DR INTERPRO; IPR002234; -
```

DR PFAM; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PRINTS; PR00425; BRADYKININR.
 DR PRINTS; PR00426; C5ANPHYLTXNR.
 DR PRINTS; PR00526; FMETLEUPHER.
 DR PRINTS; PR01104; ANPHYLATXNR.
 DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
 SQ SEQUENCE 148 AA; 16542 MW; 5EC5457F246562CE CRC64;

Query Match 43.4%; Score 56; DB 6; Length 148;
 Best Local Similarity 40.0%; Pred. No. 1.1;
 Matches 8; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

OY 7 IICLVVWGLSVIISSTFVF 26
 : | | | | : : : : :
 Db 73 VACAVAGLALLLTIPSFVF 92

RESULT 6
 O9XT45
 ID O9XT45 PRELIMINARY; PRT; 343 AA.
 AC O9XT45;
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
 DE CHEMOKINE RECEPTOR BONZO.
 GN STRL33.

OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
 OC Cercopitheinae; Macaca.
 OX NCBI_TaxID=9544;
 RN [1]
 RP SEQUENCE FROM N.A.

RA Margulies B.J., Hauer D.A., Clements J.E.;
 RT "Identification of Thirteen Rhesus Macaque Chemokine Receptors."
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF124380; AAD31419.1; -
 DR INTERPRO; IPR000248; -
 DR INTERPRO; IPR000276; -
 DR INTERPRO; IPR000355; -
 DR INTERPRO; IPR001277; -
 DR INTERPRO; IPR002235; -

DR PFAM; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PRINTS; PR00241; ANGIOTENSINR.
 DR PRINTS; PR00645; LCRIORPHANR.
 DR PRINTS; PR00657; CCHEMOKINER.
 DR PRINTS; PR01105; BONZOORPHANR.
 DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
 KW Receptor.
 SQ SEQUENCE 343 AA; 39423 MW; 48DB2544949EB83F CRC64;

Query Match 42.6%; Score 55; DB 6; Length 343;
 Best Local Similarity 33.3%; Pred. No. 3.2;
 Matches 7; Conservative 9; Mismatches 5; Indels 0; Gaps 0;

OY 6 KIICLVVWGLSVIISSTFVF 26
 : | | | | : : : : :
 Db 150 KVICLLIWIISLVSLPQIIY 170

RESULT 7
 O9N0Z0
 ID O9N0Z0 PRELIMINARY; PRT; 343 AA.
 AC O9N0Z0;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE STRL33.

OS Cercocebus torquatus atys (Red-crowned mangabey) (Sooty mangabey).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
 OC Cercopitheinae; Cercocebus.
 OX NCBI_TaxID=9531;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-20261727; PubMed-10799581;
 RA Pohlmann S., Lee B., Meister S., Krumbiegel M., Leslie G., Doms R.W.,
 RA Kirchhoff F.;
 RT "Simian immunodeficiency virus utilizes human and sooty mangabey but
 RT not rhesus macaque STRL33 for efficient entry."
 RL J. Virol. 74:5075-5082(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Pohlmann S., Lee B., Meister S., Krumbiegel M., Leslie G., Doms R.W.,
 RA Kirchhoff F.;
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF237559; AAF68392.1; -
 SQ SEQUENCE 343 AA; 39588 MW; A75B7A0751C13455 CRC64;

Query Match 42.6%; Score 55; DB 6; Length 343;
 Best Local Similarity 33.3%; Pred. No. 3.2;
 Matches 7; Conservative 9; Mismatches 5; Indels 0; Gaps 0;

OY 6 KIICLVVWGLSVIISSTFVF 26
 : | | | | : : : : :
 Db 150 KVICLLIWIISLVSLPQIIY 170

RESULT 8
 O15185
 ID O15185 PRELIMINARY; PRT; 415 AA.
 AC O15185;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
 DE G PROTEIN-COUPLED RECEPTOR CKR-L2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Gutierrez J., Varona R., Zaballós A., Lind P., Marquez G.;
 RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; Z79783; CAB02143.1; -
 DR INTERPRO; IPR000276; -
 DR PFAM; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
 SQ SEQUENCE 415 AA; 45608 MW; DE474B2084BC299B CRC64;

Query Match 42.6%; Score 55; DB 4; Length 415;
 Best Local Similarity 39.1%; Pred. No. 3.8;
 Matches 9; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

OY 4 RSKICLVVWGLSVIISSTFVF 26
 : | | | | : : : : :
 Db 214 RVTLCVWGLCLLFLPDPFIF 236

RESULT 9
 O88410
 ID O88410 PRELIMINARY; PRT; 367 AA.
 AC O88410;
 DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
 DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
 DE CHEMOKINE RECEPTOR CXCR3.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE=98318636; PubMed=9653165;
 RA Soto H., Wang W., Strieter R.M., Copeland N.G., Gilbert D.J.,
 RA Jenkins N.A., Hedrick J., Zlotnik A.;
 RT "The CC chemokine 6CKine binds the CXC chemokine receptor CXCR3.";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:8205-8210(1998).
 DR EMBL: AF045146; AAC40163.1; -;
 DR INTERPRO: IPR000276; -;
 DR PFAM: PF000001; 7tm1.1;
 DR PRINTS: PR00237; GPCRHHODOPSN.
 DR PROSITE: PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
 SQ SEQUENCE 367 AA; 41016 MW; 029FBB778E3CD4EA CRC64;

Query Match 41.9%; Score 54; DB 11; Length 367;

Best Local Similarity 34.8%; Pred. No. 4.7;
 Matches 8; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

OY 4 RSKIIICLVVWGLSVIISSTFFV 26

Db 166 RVALTCIVVWGLCLLFPDFIY 188

RESULT 10

O9QWN6 PRELIMINARY; PRT; 367 AA.

AC O9QWN6;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
 DE INTERFERON-INDUCIBLE PROTEIN 10 RECEPTOR.
 GN MCXCR3.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=BLOOD;
 RA Tanaru M., Tomimaga Y., Yatsunami K., Narumi S.;
 RT "Cloning of the murine interferon-inducible protein 10 (ip-10)
 RT receptor and its specific expression in lymphoid organs.";
 RL Biochem. Biophys. Res. Commun. 251:41-48(1998).
 DR EMBL: AB003174; BAA34045.1; -;
 DR INTERPRO: IPR000174; -;
 DR INTERPRO: IPR000248; -;
 DR INTERPRO: IPR000276; -;
 DR INTERPRO: IPR000355; -;
 DR INTERPRO: IPR001277; -;
 DR PFAM: PF000001; 7tm1.1;
 DR PRINTS: PR00237; GPCRHHODOPSN.
 DR PRINTS: PR00241; ANGIOTENSINR.
 DR PRINTS: PR00427; INTRLEUKINR.
 DR PRINTS: PR00645; LCRIORPHANR.
 DR PRINTS: PR00657; CCHEMOKINER.
 DR PROSITE: PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
 KW Receptor.
 SQ SEQUENCE 367 AA; 41017 MW; EF0348A8358AD951 CRC64;

Query Match 41.9%; Score 54; DB 11; Length 367;

Best Local Similarity 34.8%; Pred. No. 4.7;
 Matches 8; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

OY 4 RSKIIICLVVWGLSVIISSTFFV 26

Db 166 RVALTCIVVWGLCLLFPDFIY 188

RESULT 11

O42444

ID O42444 PRELIMINARY; PRT; 368 AA.

AC O42444;
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
 DE INTERLEUKIN-8-LIKE RECEPTOR.
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 OX NCBI_TaxID=8022;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zou J., Daniels G.D., Cunningham C., Secombes C.J.;
 RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ003159; CAA05917.1; -;
 DR INTERPRO: IPR000276; -;
 DR PFAM: PF00001; 7tm1.1;
 DR PRINTS: PR00237; GPCRHHODOPSN.
 DR PROSITE: PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
 SQ SEQUENCE 368 AA; 41523 MW; BE28E2D4C47E821A CRC64;

Query Match 41.1%; Score 53; DB 13; Length 368;

Best Local Similarity 40.9%; Pred. No. 6.6;
 Matches 9; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

OY 5 SKIICLVVWGLSVIISSTFFV 26

Db 165 SKFVCACVWLLAVLLALPEFMF 186

RESULT 12

O94765

ID O94765 PRELIMINARY; PRT; 395 AA.

AC O94765;
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
 DE CRTH2.
 GN DLIR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=B19; TISSUE=BLOOD;
 RX MEDLINE=99138803; PubMed=9973380;
 RA Nagata K., Tanaka K., Ogawa K., Kemmotsu K., Imai T., Yoshie O.,
 RA Abe H., Tada K., Nakamura M., Sugamura K., Takano S.;
 RT "Selective expression of a novel surface molecule by human Th2 cells
 RT in vivo.";
 RL J. Immunol. 162:1278-1286(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=PLACENTA;
 RA Methner A., Schroeder S.;
 RT "Tissue expression and chromosomal organization of a novel G protein-
 RT coupled receptor.";
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB008535; CAB17235.1; -;
 DR EMBL: AF144308; AAD34539.1; -;
 DR INTERPRO: IPR000276; -;
 DR INTERPRO: IPR000826; -;
 DR INTERPRO: IPR001179; -;
 DR INTERPRO: IPR002234; -;
 DR PFAM: PF00001; 7tm1.1;
 DR PRINTS: PR00237; GPCRHHODOPSN.
 DR PRINTS: PR00526; FMTELEUPHER.
 DR PRINTS: PR01104; ANPHYLATOXNR.
 DR PROSITE: PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.


```
DR PROSITE; PS00453; FKBP_PPIASE_1; UNKNOWN_1.
KW Receptor.
SQ SEQUENCE 395 AA; 43239 MW; 9DBB53B2008C1D1 CRC64;

Query Match
Best Local Similarity 41.1%; Score 53; DB 4; Length 395;
Matches 10; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 TLPRSKIICLVVWGLSVIISSSTFFVF 26
   : : : : : : : : : : : : : :
Db 144 TVAAAHKVCVLWALVAVLNTVPYFVF 169

RESULT 13
QY9Y5Y4
ID QY9Y5Y4 PRELIMINARY; PRT; 502 AA.
AC QY9Y5Y4;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE ORPHAN G PROTEIN-COUPLED RECEPTOR GPR44.
GN GPR44.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99156852; PubMed=10036181;
RA Marchese A., Sawadargo M., Nguyen T., Cheng R., Heng H.H., Nowak T.,
RA Im D.S., Lynch K.R., George S.R., O'dowd B.F.;
RT "Discovery of three novel orphan G-protein-coupled receptors.";
RL Genomics 56:12-21(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA O'dowd B.F.;
RL Submitted (JAN-1999) to the EMBL/GenBank/DBDJ databases.
DR EMBL; AF118265; AAD21055.1; -
DR INTERPRO; IPR000276; -
DR INTERPRO; IPR000826; -
DR INTERPRO; IPR001179; -
DR INTERPRO; IPR002234; -
DR PFAM; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PRINTS; PR00526; FMETLEUPHER.
DR PRINTS; PR01104; AMPHYLATONXR.
DR PROSITE; PS00237; G-PROTEIN-RECEPTOR; UNKNOWN_1.
DR PROSITE; PS00453; FKBP_PPIASE_1; UNKNOWN_1.
KW Receptor.
SQ SEQUENCE 502 AA; 54759 MW; 841F8A5A16CD9BAC CRC64;

Query Match
Best Local Similarity 41.1%; Score 53; DB 4; Length 502;
Matches 10; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 TLPRSKIICLVVWGLSVIISSSTFFVF 26
   : : : : : : : : : : : : : :
Db 221 TVAAAHKVCVLWALVAVLNTVPYFVF 246

RESULT 14
QY9P491
ID QY9P491 PRELIMINARY; PRT; 770 AA.
AC QY9P491;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE GLUCAN 1,3-BETA-GLUCOSIDASE GLUC78 PRECURSOR (EC 3.2.1.58).
OS Trichoderma atroviride.
OC Eukaryota; Fungi; Ascomycota; anamorphic Ascomycota; Trichoderma.
OX NCBI_TaxID=63577;

RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=P1;
RA Donzelli B.G.G., Lorito M., Scala F., Harman G.E.;
RT "Cloning, sequence and structure of a gene encoding an antifungal
glucan 1,3-beta-glucosidase from trichoderma atroviride (T. harzianum)
with a spliced regulatory sequence.";
RL Submitted (APR-2000) to the EMBL/GenBank/DBDJ databases.
DR EMBL; AF253421; AAF80600.1; -
KW Signal; Hydrolase; Glycosidase.
FT SIGNAL 1 40 POTENTIAL.
SQ SEQUENCE 770 AA; 81896 MW; 85148BB3B0A33D78 CRC64;

Query Match
Best Local Similarity 41.1%; Score 53; DB 3; Length 770;
Matches 8; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 9 CLVWVGLSVIISSSTFFVF 26
   : : : : : : : : : : : : : :
Db 679 CAGTGWIRVVNSNTFIY 696

RESULT 15
O88860
ID O88860 PRELIMINARY; PRT; 901 AA.
AC O88860;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE CHLORIDE CHANNEL CACC.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Romio L., Musante L., Cinti R., Moran O., Seri M., Galletta L.J.V.;
RT "Characterization of a murine gene homologous to the bovine CaCC
chloride channel.";
RL Submitted (MAR-1998) to the EMBL/GenBank/DBDJ databases.
DR EMBL; AF052746; AAC35003.1; -
DR INTERPRO; IPR002035; -
SQ SEQUENCE 901 AA; 100038 MW; 13DF068BF3337AAB CRC64;

Query Match
Best Local Similarity 41.1%; Score 53; DB 11; Length 901;
Matches 8; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 8 ICLVWVGLSVIISS 21
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Db 885 ICMTWGLTVIFNS 898

Search completed: May 23, 2001, 15:35:15
Job time: 621 sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 23, 2001, 15:28:29 ; Search time 184.73 Seconds
(without alignments)
9.283 Million cell updates/sec

Title: US-08-887-977-10_COPY_177_206

Perfect score: 164

Sequence: 1 NQKYNTQGSVCEPKYQTVSEPIRWKLML 30

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 390729 seqs, 57163235 residues

Total number of hits satisfying chosen parameters: 390729

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	164	100.0	365	19 W48086	Human dendritic ce
2	158	96.3	365	21 Y97077	Primate (human) ch
3	57	34.8	1757	20 W84351	Murine ubiquitin-p
4	50	30.5	547	21 Y79188	Haematopoietic ste
5	49	29.9	260	21 G42023	Arabidopsis thalia
6	49	28.9	395	21 G42022	Arabidopsis thalia
7	46.5	28.4	68	7 P60749	Sequence encoded b
8	46.5	28.4	353	12 R12365	HTLV-1 P40x antige
9	46.5	28.4	353	18 W25225	Tax mutant m319 pr
10	46	28.0	2050	20 W90117	Human mature von W
11	46	28.0	2050	20 W73499	Von Willebrand fac

12	46	28.0	2050	21 Y67241	Human von Willebra
13	46	28.0	2813	7 P60462	Sequence of human
14	45	27.4	52	19 W48752	T-cell surface ant
15	45	27.4	136	21 Y92363	G protein-coupled
16	45	27.4	406	20 Y32757	Endo-xylogalacturo
17	45	27.4	831	21 B01248	Human CD97 recepto
18	45	27.4	835	19 W48756	T-cell surface ant
19	45	27.4	835	20 Y41090	Human CD97 protein
20	45	27.4	835	21 B15728	Human CD97 protein
21	45	27.4	1621	18 W31228	Human immunodefici
22	44.5	27.1	88	21 G02929	Human secreted pro
23	44.5	27.1	361	20 Y28810	nn296.2 secreted p
24	44.5	27.1	450	20 Y30788	Guinea pig HKNG1 o
25	44.5	27.1	466	20 Y30787	Protein encoded by
26	44	26.8	84	20 Y30432	Mature nematode ex
27	44	26.8	84	21 B15317	A. caninum nematod
28	44	26.8	91	17 R91701	AcanAPC2. Ancylos
29	44	26.8	91	20 Y30393	Nematode extracted
30	44	26.8	91	20 Y30454	Nematode extracted
31	44	26.8	91	21 B15346	A. caninum nematod
32	44	26.8	151	20 Y07016	Breast cancer asso
33	44	26.8	217	20 Y01087	Mammalian disabled
34	44	26.8	482	17 W08085	Macrophage membran
35	44	26.8	505	14 R41941	prk gene LptK-2 pr
36	44	26.8	505	16 R85929	Protein tyrosine-k
37	44	26.8	1148	20 Y07087	Renal cancer assoc
38	43.5	26.5	1438	21 B18270	Plasmodium falcipa
39	43	26.2	131	21 G10847	Arabidopsis thalia
40	43	26.2	131	21 G45068	Arabidopsis thalia
41	43	26.2	143	18 Y11243	Streptococcus pneu
42	43	26.2	143	19 W38644	Streptococcus pneu
43	43	26.2	193	21 G33614	Arabidopsis thalia
44	43	26.2	199	21 G33613	Arabidopsis thalia
45	43	26.2	246	21 G10846	Arabidopsis thalia

ALIGNMENTS

RESULT 1

W48086

ID W48086 standard; Protein; 365 AA.

XX AC W48086;

XX DT 11-JUN-1998 (first entry)

XX DE Human dendritic cell chemokine receptor.

XX DE Human; thymus expressed chemokine; TECK; MIP-3alpha; MIP-3beta;

XX KW receptor; dendritic cell; macrophage; inflammation; asthma.

XX OS Homo sapiens.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT Misc-difference 193 /note= "encoded by CAN"

XX FT W09801557-A2.

XX PN 15-JAN-1998.

XX PD 02-JUL-1997; 97WO-US10819.

XX PR 04-JUN-1997; 97US-0048593.

XX PR 05-JUL-1996; 96US-0675814.

XX PR 11-OCT-1996; 96US-0028329.

XX PA (SCHE) SCHERING CORP.

XX XX Gish KC, Schall TJ, Vicari A, Wang W, Zlotnik A;

XX XX WPI; 1998-101054/09.

Y79188
ID Y79188 standard; Protein; 547 AA.
XX
AC Y79188;
XX
DT 19-JUN-2000 (first entry)
XX
XX Haematopoietic stem cell specific protein.
DE
DE Haematopoietic stem cell; immune system disorder;
KW leukaemia; antileukaemic; immunomodulator; therapy; mouse.
KW
XX Mus musculus.
XX
XX WO200011168-A2.
XX
XX 02-MAR-2000.
PD
XX 20-AUG-1999; 99WO-US19052.
PF
XX 21-AUG-1998; 98US-0138132.
XX
XX (UYPR-) UNIV PRINCETON.
PA
XX Lemischka I, Moore K;
XX
XX WPI; 2000-237650/20.
DR
XX N-PSDB; 294129.
XX
XX Hematopoietic stem cell signaling proteins modulating replication and
PT differentiation for treating immune system disorders and leukaemia -
PT
PS Claim 21; Page 240-242; 256pp; English.
XX
XX The present sequence is that of a mouse haematopoietic stem cell
CC (HSC) specific protein. It is an example of claimed HSC-specific
CC proteins (see Y79176-93) predicted from novel isolated HSC-specific
CC nucleic acids (see Z94077-131). The HSCs are especially primitive
CC HSCs (PHSCs) such as umbilical cord cells, bone marrow cells and
CC foetal liver cells. The encoded proteins are growth factors,
CC transcription factors, splicing factors, capping factors, transport
CC proteins, translation factors or replication factors that modulate
CC HSC activity, especially differentiation or replication. The
CC invention provides claimed methods: for identifying PHSC-specific
CC nucleic acids; for generating a stem cell/progenitor cell from
CC PHSCs; for identifying the presence of a PHSC in a sample; for
CC identifying the presence in a sample of a compound that modulates
CC HSC activity; for using such a compound to treat an immune system
CC condition, especially leukaemia; for introducing exogenous nucleic
CC acid into a HSC; and for ex vivo expansion of HSCs. Also claimed
CC are vectors, host cells, and an antibody that specifically binds a
CC an HSC-specific protein.
XX
SQ Sequence 547 AA;

Query Match 30.5%; Score 50; DB 21; Length 547;
Best Local Similarity 50.0%; Pred. No. 22;
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

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Db 312 eyeaggaekcqpky 325

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ID G42023 standard; Protein; 260 AA.
XX
AC G42023;
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DT 18-OCT-2000 (first entry)
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DE Arabidopsis thaliana protein fragment SEQ ID NO: 52357.
XX Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
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XX 25-FEB-2000; 2000EP-0301439.
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XX 25-FEB-1999; 99US-0121825.
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Query Match 29.9%; Score 49; DB 21; Length 260;

Best Local Similarity 41.7%; Pred No. 13;

Matches 10; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

Qy 1 NOKYNTQGSVDCEPKYQTVSEPIR 24

Db 228 nnnvqqgsgmqpcyqnnppnr 251

RESULT 6

G42022

ID G42022 standard; Protein; 395 AA.

XX

AC G42022;

XX

XX 18-OCT-2000 (first entry)

XX

XX Arabidopsis thaliana protein fragment SEQ ID NO: 52356.

XX Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.

XX

OS Arabidopsis thaliana.

XX PN EP1033405-A2.
XX XX
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XX PF 06-SEP-2000.
XX PF 25-FEB-2000; 2000EP-0301439.
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PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 06-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.

PR 16-SEP-1999; 99US-0154039.
 PR 20-SEP-1999; 99US-0154779.
 PR 22-SEP-1999; 99US-0155139.
 PR 23-SEP-1999; 99US-0155486.
 PR 24-SEP-1999; 99US-0155659.
 PR 28-SEP-1999; 99US-0156458.
 PR 29-SEP-1999; 99US-0156596.
 PR 04-OCT-1999; 99US-0157117.
 PR 05-OCT-1999; 99US-0157753.
 PR 06-OCT-1999; 99US-0157865.
 PR 07-OCT-1999; 99US-0158029.
 PR 08-OCT-1999; 99US-0158232.
 PR 12-OCT-1999; 99US-0158369.
 PR 13-OCT-1999; 99US-0159293.
 PR 13-OCT-1999; 99US-0159294.
 PR 13-OCT-1999; 99US-0159295.
 PR 14-OCT-1999; 99US-0159329.
 PR 14-OCT-1999; 99US-0159330.
 PR 14-OCT-1999; 99US-0159331.
 PR 14-OCT-1999; 99US-0159637.
 PR 14-OCT-1999; 99US-0159638.
 PR 18-OCT-1999; 99US-0159584.
 PR 21-OCT-1999; 99US-0160741.
 PR 21-OCT-1999; 99US-0160767.
 PR 21-OCT-1999; 99US-0160768.
 PR 21-OCT-1999; 99US-0160770.
 PR 21-OCT-1999; 99US-0160814.
 PR 21-OCT-1999; 99US-0160815.
 PR 22-OCT-1999; 99US-0160980.
 PR 22-OCT-1999; 99US-0160981.
 PR 22-OCT-1999; 99US-0160989.
 PR 25-OCT-1999; 99US-0161404.
 PR 25-OCT-1999; 99US-0161405.
 PR 25-OCT-1999; 99US-0161406.
 PR 26-OCT-1999; 99US-0161359.
 PR 26-OCT-1999; 99US-0161360.
 PR 26-OCT-1999; 99US-0161361.
 PR 28-OCT-1999; 99US-0161920.
 PR 28-OCT-1999; 99US-0161992.
 PR 28-OCT-1999; 99US-0161993.
 PR 29-OCT-1999; 99US-0162142.

Query Match 29.9%; Score 49; DB 21; Length 395;
 Best Local Similarity 41.7%; Pred. No. 21;
 Matches 10; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

QY 1 NQYNTQSGSDVCEPKYQTVSEPIR 24
 | | | | | : | : | | | | |
 Db 363 nnnqqgsgmqdpgyqnnppnr 386

RESULT 7
 P60749
 ID P60749 standard; Protein: 68 AA.
 AC P60749;
 XX
 XX

23-AUG-1991 (first entry)

DE Sequence encoded by the X-region of viruses in the HTLV family, esp.
 DE HTLV-I and HTLV-II.

KW Adult T-cell leukaemia; X region; immunoassay; HTLV; retrovirus;
 KW epitope; anti-X region protein antibody.

OS Human T-lymphotropic viruses.

XX WO8601834-A.

XX

XX 27-MAR-1986.

XX

XX 19-SEP-1985; 85WO-0904763.

XX

PR 19-SEP-1984; 84US-0652775.
 XX
 PA (REGC) UNIV OF CALIFORNIA.
 PA (SLAM/) SLAMON D J.
 XX
 PI Slamon DJ, Chen IS, Cline MJ;
 XX
 DR WPI; 1986-094087/14.
 XX
 XX New retroviral polypeptide(s), fragments antisera and antibodies
 PT - useful for detection of retroviruses in HTLV family, e.g.
 PT causing adult T-cell leukaemia
 XX
 PS Claim 22; Page 27; 33pp; English.

CC The inventors claim a polypeptide having a mol. wt. of about 35kd-
 CC 42kd and having at least one of the SQ in P60743-P60746. In
 CC P60743-P60746, X in the SQ corresp. to an AA such that the SQ is
 CC substantially the same as a polypeptide expressed by an HTLV, esp.
 CC HTLV-I or HTLV-II (see P60747-P60749). Also claimed is a
 CC polypeptide having a mol. wt. of not greater than about 42kd and
 CC having an AA SQ of at least 12 AAs found within at least one of
 CC the polypeptide SQ in P60743-P60746. Polypeptides encoded for in
 CC the region described as px-iv in the X SQ of HTLV-I and the region
 CC described as px-c in the X SQ of HTLV-II are characterized by being
 CC respectively about 40kd and 37kd. Detection of antibodies to these
 CC proteins in serum may be used to determine whether exposure to an HTLV
 CC virus has occurred.

XX Sequence 68 AA;

Query Match 28.4%; Score 46.5; DB 7; Length 68;
 Best Local Similarity 57.1%; Pred. No. 6.4;
 Matches 12; Conservative 1; Mismatches 7; Indels 1; Gaps 1;

QY 8 GSDVCEPKYQTVSEPIRWKLL 28
 | | | | | : | : | | | | |
 Db 39 gsvvcmylyq-lspptwpll 58

RESULT 8

R12365
 ID R12365 standard; Protein: 353 AA.
 XX
 AC R12365;
 XX

DT 19-AUG-1991 (first entry)

XX HTLV-1 P40x antigenic polypeptide.

XX Adult T-cell leukaemia; tropical spastic paraparesis.

XX Human t-cell leukaemia virus.

XX WO9107510-A.

XX 30-MAY-1991.

XX 14-NOV-1990; 90WO-US06647.

XX 17-NOV-1989; 89US-0438666.

XX (AMGE-) AMGEN INC.

XX Hare DL, Kieft GL, Lau EP, Renick MA, Yancik SA;

XX WPI; 1991-178118/24.

XX N-PSDB; Q12066.

XX DNA encoding HTLV-1 antigenic polypeptide(s) - used in immunoassay
 XX to detect HTLV-1 virus in serum or plasma.

PS Claim 24; Fig 3; 64pp; English.

XX The gene product may be used to raise Abs, useful in immunoassay for
 CC HTLV-1. Using Abs raised to env, tax and gag genes together
 CC maximises sensitivity to the virus. The antigens may be expressed
 CC from a transformed esp. E.coli.

XX Sequence 353 AA;

Query Match 28.4%; Score 46.5; DB 12; Length 353;
 Best Local Similarity 57.1%; Pred. No. 45;
 Matches 12; Conservative 1; Mismatches 7; Indels 1; Gaps 1;

QY 8 GSDVCEPKYQTVSEPIRWKLL 28
 ||||| ||||| ||||| |||||
 Db 149 gsvvcmylyq-ispptwpll 168

RESULT 9

ID W25225 standard; protein; 353 AA.

XX AC W25225;

XX DT 13-MAR-1998 (first entry)

XX DE Tax mutant m319 protein.

XX KW Tax mutant m319; NFkappaB; NFkB2 precursor; inhibition; cancer;
 XX inflammation; rheumatism; Immunoglobulin.

XX OS Synthetic.

XX PN JP09187283-A.

XX PD 22-JUL-1997.

XX PF 12-JAN-1996; 96JP-0021891.

XX PR 12-JAN-1996; 96JP-0021891.

XX PA (SHIO) SHIONOGI & CO LTD.

XX DR WPI; 1997-419401/39.

XX A cell constitutionally expressing NFkappaB - used to screen for
 PT agents inhibiting NFkappaB or the NFkB2 precursor

XX Claim 4; Fig 1; 22pp; Japanese.

XX A transfected cell strain has been developed which constitutively
 CC expresses NFkappaB. A method has been developed for screening a
 CC substance specifically inhibiting the activity of NFkappaB protein or
 CC of NFkB2 precursor by using the above cell strain. The present sequence
 CC represents a Tax mutant m319 protein sequence. The cells are used for
 CC screening for agents that can inhibit the gene activating effect of
 CC NFkappaB. This may be useful in the treatment of such conditions as
 CC cancer, inflammation and rheumatism.

XX Sequence 353 AA;

Query Match 28.4%; Score 46.5; DB 18; Length 353;
 Best Local Similarity 57.1%; Pred. No. 45;
 Matches 12; Conservative 1; Mismatches 7; Indels 1; Gaps 1;

QY 8 GSDVCEPKYQTVSEPIRWKLL 28
 ||||| ||||| ||||| |||||
 Db 149 gsvvcmylyq-ispptwpll 168

RESULT 10

W90117
 ID W90117 standard; Protein; 2050 AA.
 XX W90117;
 AC W90117;
 DT 12-APR-1999 (first entry)
 XX Human mature von Willebrand Factor.
 XX von Willebrand Factor; vWF; human; GPIb binding domain;
 KW antiagregant; platelet aggregation; cerebrovascular disorder;
 KW cardiovascular disorder; myocardial infarction; angina;
 KW thrombolytic; platelet adhesion; therapy.
 XX Homo sapiens.
 OS
 XX
 XX Key Location/Qualifiers
 FT Domain 504..728
 FT /note= "GPIb binding domain"
 FT Disulfide-bond 509..695
 XX US5849702-A.
 XX PD 15-DEC-1998.
 XX 05-JUN-1995; 95US-0464962.
 XX 03-SEP-1991; 91US-0753815.
 XX 02-MAR-1990; 90US-0487767.
 XX 01-MAR-1991; 91WO-US01416.
 XX 22-JUN-1993; 93US-0080690.
 XX 30-NOV-1994; 94US-0347594.
 XX 05-JUN-1995; 95US-0464962.
 XX (BIOT-) BIO-TECHNOLOGY GENERAL CORP.
 XX Garfinkel L, Richter T;
 XX WPI; 1999-069781/06.
 XX N-PSDB; V74156.
 XX Composition for inhibiting blood platelet aggregation - containing
 PT polypeptide comprising von Willebrand factor GPIb binding domain
 XX Example 1; Fig 12A-H; 50pp; English.
 XX This is the translated sequence of mature human von Willebrand
 CC Factor (vWF), as encoded by an isolated endothelial cDNA clone
 CC (see V74156). The invention provides non-glycosylated, biologically
 CC active polypeptides (see W90119-20) which comprise the vWF GPIb
 CC binding domain. Expression plasmids encoding these polypeptides
 CC and methods of production using transformed bacterial cells are
 CC also provided. The polypeptides are used in claimed methods for
 CC inhibiting platelet aggregation, for treating cerebrovascular
 CC disorders, for treating cardiovascular disorders, especially acute
 CC myocardial infarction or angina, for inhibiting platelet aggregation
 CC before, during or after angioplasty, thrombolytic treatment or
 CC coronary bypass surgery, for maintaining blood vessel patency
 CC before, during or after coronary bypass surgery, for inhibiting
 CC thrombosis, optionally associated with an inflammatory response,
 CC for inhibiting platelet adhesion to damaged vascular surfaces, for
 CC preventing platelet adhesion to prosthetic materials or devices,
 CC for inhibiting re-occlusion after angioplasty or thrombolysis, for
 CC preventing vaso-occlusive crises in sickle-cell anaemia, for
 CC thrombolytic treatment of thrombi-containing platelet-rich
 CC aggregates, for preventing platelet activation and thrombus
 CC formation due to high shear forces in a subject with stenosed or
 CC partially obstructed arteries, or for preventing thrombin-induced
 CC platelet activation.
 XX Sequence 2050 AA;

Query Match 28.0%; Score 46; DB 20; Length 2050;
 Best Local Similarity 41.2%; Pred. No. 4.4e+02;
 Matches 7; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 7 QGSDVCEPKYQTVSEPI 23

Db 1551 qnadqccpeycvcdpv 1567

RESULT 11

ID W73499 standard; Protein; 2050 AA.

XX AC W73499;

DT 26-FEB-1999 (first entry)

XX DE Von Willebrand factor.

XX KW Von Willebrand factor; GPIb binding domain; inhibitor; re-occlusion;
 KW platelet aggregation; cerebrovascular disorder; cardiovascular disorder;
 KW angioplasty; thrombi-containing platelet-rich aggregate; thrombosis;
 KW therapy.

XX OS Homo sapiens.

XX US5849536-A.

XX PD 15-DEC-1998.

XX PF 30-NOV-1994; 94US-0347594.

XX PR 01-MAR-1991; 91WO-US01416.

XX PR 02-MAR-1990; 90US-0487767.

XX PR 03-SEP-1991; 91US-0753815.

XX PR 22-JUN-1993; 93US-0080690.

XX PR 30-NOV-1994; 94US-0347594.

XX (BIOT-) BIO-TECHNOLOGY GENERAL CORP.

XX PA Garfinkel L, Richter T;

XX PI WPI; 1999-069733/06.

XX DR N-PSDB; V08901.

XX PT Polypeptide comprising von Willebrand factor GPIb binding domain -

XX PS useful as platelet aggregation inhibitor

XX PS Disclosure; Fig 12; 62pp; English.

XX CC This sequence represents the mature human Von Willebrand factor protein.
 CC GPIb binding domain of this sequence represents the protein of the
 CC invention. The protein is used for inhibiting platelet aggregation,
 CC especially for treating cerebrovascular disorders. It is also used for
 CC treating cardiovascular disorders, especially acute myocardial infarction
 CC or angina. The protein is also used for inhibiting platelet aggregation
 CC before, during or after angioplasty, thrombolytic treatment or coronary
 CC bypass surgery, for maintaining blood vessel potency before, during or
 CC after coronary bypass surgery. It can also be used for inhibiting
 CC thrombosis, optionally associated with an inflammatory response, for
 CC inhibiting platelet adhesion to damaged vascular surfaces, for preventing
 CC platelet adhesion to prosthetic materials or devices, for inhibiting
 CC re-occlusion after angioplasty or thrombolysis, or for thrombolytic
 CC treatment of thrombi-containing platelet-rich aggregates.

XX SQ Sequence 2050 AA;

Query Match 28.0%; Score 46; DB 20; Length 2050;
 Best Local Similarity 41.2%; Pred. No. 4.4e+02;
 Matches 7; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 7 QGSDVCEPKYQTVSEPI 23

Db 1551 qnadqccpeycvcdpv 1567

RESULT 12

ID Y67241 standard; Protein; 2050 AA.

XX AC Y67241;

XX DT 27-MAR-2000 (first entry)

XX DE Human von Willebrand Factor (vWF) amino acid sequence.

XX KW Von Willebrand Factor; vWF; GPIb binding domain; arteriosclerosis;
 KW platelet adhesion inhibitor; stenosis; cerebrovascular injury; human;
 KW thrombosis; cardiovascular injury.

XX OS Homo sapiens.

XX PN US6008193-A.

XX PD 28-DEC-1999.

XX PF 05-JUN-1995; 95US-0463682.

XX PR 30-NOV-1994; 94US-0347594.

XX PR 03-SEP-1991; 91US-0753815.

XX PR 22-JUN-1993; 93US-0080690.

XX PR 02-MAR-1990; 90US-0487767.

XX PR 01-MAR-1991; 91WO-US01416.

XX (BIOT-) BIO-TECHNOLOGY GEN CORP.

XX PI Richter T, Garfinkel L;

XX DR WPI; 2000-096379/08.

XX DR N-PSDB; 256177.

XX PT Preventing arteriosclerosis and stenosis using polypeptides derived
 XX PT from the human von Willebrand factor GPIb binding domain -

XX PS Claim 1; Fig 12; 65pp; English.

XX CC This is the amino acid sequence of human von Willebrand factor (vWF).
 CC The invention relates to methods of treating arteriosclerosis and
 CC stenosis using polypeptides derived from the human vWF GPIb binding
 CC domain. vWF is a large plasma protein which is synthesised in the
 CC endothelial cells of the blood vessels, and also by megakaryocytes which
 CC are the precursors of platelets. The treatment methods involve the
 CC administration of a polypeptide (see Y67242 or Y67243). These
 CC polypeptides contain a fragment of the vWF GPIb binding domain amino acid
 CC sequence. The polypeptides inhibit platelet adhesion and aggregation,
 CC therefore the methods may be used for preventing arteriosclerosis and
 CC stenosis (as a result of smooth muscle proliferation following vascular
 CC injury). The polypeptides may also be used for treating other
 CC cerebrovascular and cardiovascular injuries and thrombosis.

XX SQ Sequence 2050 AA;

Query Match 28.0%; Score 46; DB 21; Length 2050;
 Best Local Similarity 41.2%; Pred. No. 4.4e+02;
 Matches 7; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 7 QGSDVCEPKYQTVSEPI 23

Db 1551 qnadqccpeycvcdpv 1567

RESULT 13

P60462

ID P60462 standard; Protein; 2813 AA.

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XX AC P60462;
XX 25-JUN-1991 (first entry)
XX DE Sequence of human von Willebrand Factor (VWF) precursor.
XX KW Chronic renal failure; therapy; factor VIII C.
XX OS Homo sapiens.
XX PN W08606096-A.
XX PD 23-OCT-1986.
XX PF 10-APR-1986; 86WO-US00760.
XX PR 11-APR-1985; 85US-0722108.
XX PA (CHIL-) CHILDRENS MED CENT.
XX PA (GINS/) GINSBURG D.
XX PI Ginsburg D, Orkin SH, Kaufman RJ;
XX DR WPI; 1986-291663/44.
XX DR N-PSDB; N60404.
XX PT Pure Von Willebrand Factor - produced using an expression vector
XX including a DNA sequence encoding functional VWF protein
XX PS Disclosure; Table 2, Pages 18-36A; 54pp; English.
XX CC cDNA clones pWH33, pWH5 and pWH6 which span 9 kb pairs of DNA and
XX encompass the entire protein coding region of VWF, were selected to
XX construct full length cDNA (N60404). The pure VWF produced is useful
XX in the treatment of von Willebrand's disease (VWD) and the patients
XX with chronic renal failure whose abnormal bleeding times are
XX corrected by crude cryoprecipitate. Pure VWF can also be used to
XX carry, stabilise and improve the therapeutic efficacy of factor
XX VIII:C.
XX SQ Sequence 2813 AA;

Query Match 28.08; Score 46; DB 7; Length 2813;
Best Local Similarity 41.28; Pred. No. 6.3e+02;
Matches 7; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 7 QGSDVCEPKYQTVSEPI 23
   | | | | | | | |
Db 2314 qnadqccpeycvcdpv 2330

RESULT 14
W48752
ID W48752 standard; Peptide; 52 AA.
XX AC W48752;
XX 14-SEP-1998 (first entry)
XX DE T-cell surface antigen CD97 EGF-like repeat 2.
XX KW T-cell surface antigen; CD97; human; inflammation; angiogenesis;
XX KW atherosclerosis; antagonist; antibody; human.
XX OS Homo sapiens.
XX PN W09817796-A2.
XX PD 30-APR-1998.
XX PF 24-OCT-1997; 97WO-US19772.

```

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XX 25-OCT-1996; 96US-0027871.
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX PI Kelly K;
XX WP1; 1998-261492/23.
XX PT New soluble CD97 alpha subunit isoform(s) - used to develop
XX products for the detection and treatment of inflammation,
XX atherosclerosis and angiogenesis
XX PS Claim 1; Page 88; 101pp; English.
XX CC This peptide comprises EGF-like repeat 2 found in alpha subunits
XX of human T-cell surface antigen CD97 (see W48756). Novel soluble
XX CD97 alpha subunits of the invention contain different combinations
XX of 5 EGF-like repeats (see W48751-55). They are selected from:
XX alpha1, which contains EGF-like repeats 1-5; alpha2, which contains
XX EGF-like repeats 1, 2, 3 and 5; and alpha3, which contains EGF-like
XX repeats 1, 2 and 5. The alpha subunit of CD97 is localised
XX extracellularly on T-cells. Upon activation, expression of the
XX alpha subunit is dramatically increased and shed into the external
XX medium. The alpha subunit plays a role in angiogenesis,
XX inflammation and atherosclerosis. Detection and inhibition of the
XX alpha subunit using CD97 alpha polypeptides, nucleic acids,
XX antibodies and antagonists provides diagnostic and therapeutic
XX methods for these disease states.
XX SQ Sequence 52 AA;

Query Match 27.48; Score 45; DB 19; Length 52;
Best Local Similarity 52.68; Pred. No. 7.9;
Matches 10; Conservative 3; Mismatches 4; Indels 2; Gaps 1;

QY 4 YNTQGS--DVCEPKYQTVS 20
   |||:| | | | | |
Db 20 wntegsydcvcpypvps 38

RESULT 15
Y92363
ID Y92363 standard; Protein; 136 AA.
XX AC Y92363;
XX 10-AUG-2000 (first entry)
XX DE G protein-coupled receptor protein 3.
XX KW GCRP-3; G protein-coupled receptor protein; antipsoriatic; antirheumatic;
XX KW CD97; immunosuppressive; antiasthmatic; antianemic; antiarteriosclerotic;
XX KW antithyroid; cytostatic; hepatotropic; dermatological; anti-inflammatory;
XX KW antitumor; thyromimetic; haemostatic; virucide; hepatotropic; osteopathic;
XX KW antiparasitic; immunostimulant.
XX OS Homo sapiens.
XX FH Key
XX FT Peptide 1..25 Location/Qualifiers
XX FT Domain 22..37 /label= signal_peptide
XX FT Domain 35..56 /label= EGF-like
XX FT Modified-site 41..52 /label= EGF-like
XX FT Modified-site /note= "Asx hydroxylation site"
XX FT Modified-site 64 /note= "potential phosphorylation site"
XX FT Modified-site 67 /note= "potential glycosylation site"

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FT Modified-site 80 /note= "potential phosphorylation site"
FT Modified-site 86 /note= "potential phosphorylation site"
FT Modified-site 124 /note= "potential phosphorylation site"
FT Modified-site 124 /note= "potential phosphorylation site"
XX
XX PN W0200020590-A2.
XX
XX PD 13-APR-2000.
XX
XX PF 06-OCT-1999; 99WO-US23317.
XX
XX PR 06-OCT-1998; 98US-0167219.
XX PR 06-OCT-1998; 98US-0172211.
XX PR 11-MAY-1999; 99US-0133585.
XX
XX PA (INCY-) INCYTE PHARM INC.
XX
XX PI Tang YT, Yue H, Lal P, Bandman O, Au-Oung J, Reddy R, Corley NC;
XX PI Guegler KJ, Gorgone GA, Baughn MR, Azimzai Y;
XX
XX DR WPI: 2000-328934/28.
XX DR N-PSDB; A09349.
XX
XX PT Novel human G-protein coupled receptor proteins used in the diagnosis,
XX PT treatment and prevention of nervous system disorders,
XX PT autoimmune/inflammatory disorders, and cell proliferative disorders
XX PT such as cancer
XX
XX PS Claim 1; Page 70; 84pp; English.
XX
XX CC This sequence shows human G-protein coupled receptor protein (GCRP) 3,
XX CC which has similarity with human CD97. The GCRP polypeptides,
XX CC polynucleotides, antibodies, antagonists and agonists may be administered
XX CC to human patients for the diagnosis, treatment and prevention of nervous
XX CC system disorders (e.g. epilepsy, stroke, neoplasms, Alzheimer's disease),
XX CC autoimmune or inflammatory disorders, complications of cancer,
XX CC haemodialysis and extracorporeal circulation, and cell proliferative
XX CC disorders. They are also used to treat or prevent disorders associated
XX CC with decreased or increased expression or activity of GCRP.
XX
XX SQ Sequence 136 AA;

Query Match 27.4%; Score 45; DB 21; Length 136;
Best Local Similarity 52.6%; Pred. No. 25;
Matches 10; Conservative 3; Mismatches 4; Indels 2; Gaps 1;

QY 4 YNTQGS--DVCEPKYQTVS 20
   :||:| | | | | | | |
Db 42 wntegsydcvcspgypvs 60

Search completed: May 23, 2001, 15:28:31
Job time: 408 sec

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QY 7 QGSDVCEPKYQTVSEPI 23
| : | | : | : | :
:

Db 1551 QNADCCPEYECVDPV 1567

RESULT 2

US-08-242-677-2
; Sequence 2, Application US/08242677
; Patent No. 5677143
; GENERAL INFORMATION:
; APPLICANT: Gaynor, Richard B
; APPLICANT: Wu, Foon W.
; TITLE OF INVENTION: Cellular Nucleic Acid Binding Protein
; TITLE OF INVENTION: and Uses Thereof in regulating Gene Expression and in the
; TITLE OF INVENTION: Treatment of AIDS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/242,677
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mayfield, Denise L.
; REGISTRATION NUMBER: 33,732
; REFERENCE/DOCKET NUMBER: UTSD:401
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713-787-1400
; TELEFAX: 713-789-2679
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1621 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-242-677-2

Query Match 27.4%; Score 45; DB 1; Length 1621;
Best Local Similarity 40.7%; Pred. No. 1.7e+02;
Matches 11; Conservative 4; Mismatches 8; Indels 4; Gaps 1;

QY 2 QKYN----TQSDVCEPKYQTVSEPIR 24
:||: |||: || | |||
Db 901 KKYHFLIPTGSEILEPLPAVQMPIR 927

RESULT 3

US-08-465-380-59
; Sequence 59, Application US/08465380
; Patent No. 5863894
; GENERAL INFORMATION:
; APPLICANT: George P. Vlasuk, Patric H. Stanssens,
; APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys,
; APPLICANT: Yves R. Laroche, Laurent S. Jespers,
; APPLICANT: Yannick G.J. Gansemans, Matthew Moyle,
; APPLICANT: Peter W. Bergum
; TITLE OF INVENTION: NEMATOIDE-EXTRACTED ANTICOAGULANT
; TITLE OF INVENTION: PROTEIN
; NUMBER OF SEQUENCES: 356
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles

; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: Storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,380
; FILING DATE: June 5, 1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/326,110
; FILING DATE: October 18, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BIGGS, SUZANNE L.
; REGISTRATION NUMBER: 30,158
; REFERENCE/DOCKET NUMBER: 213/268
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 84 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Ancylostoma caninum
US-08-465-380-59

Query Match 26.8%; Score 44; DB 2; Length 84;
Best Local Similarity 43.5%; Pred. No. 6.6;
Matches 10; Conservative 4; Mismatches 7; Indels 2; Gaps 1;

QY 1 NOKYNTQGSVDVCEP--KYQTVSE 21
:|||: || | || | || | ||
Db 9 NERYDCSGSKECDKCKKYDGVVE 31

RESULT 4

US-08-486-397-59
; Sequence 59, Application US/08486397
; Patent No. 5866542
; GENERAL INFORMATION:
; APPLICANT: George P. Vlasuk, Patric H. Stanssens,
; APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys,
; APPLICANT: Yves R. Laroche, Laurent S. Jespers,
; APPLICANT: Yannick G.J. Gansemans, Matthew Moyle,
; APPLICANT: Peter W. Bergum
; TITLE OF INVENTION: NEMATOIDE-EXTRACTED ANTICOAGULANT
; TITLE OF INVENTION: PROTEIN
; NUMBER OF SEQUENCES: 357
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: Storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,397


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; ORGANISM: Ancylostoma caninum
US-08-634-641-59

Query Match          26.8%; Score 44; DB 2; Length 84;
Best Local Similarity 43.5%; Pred. No. 6.6;
Matches 10; Conservative 4; Mismatches 7; Indels 2; Gaps 1;

QY 1 NOKYNTQSDVCEP--KYQTWSE 21
   I::: I I I I
Db 9 NEKYDCSGSKCKCKYDGVVE 31

RESULT 8
US-09-249-471-59
; Sequence 59, Application US/09249471
; Patent No. 6040441
; GENERAL INFORMATION:
; APPLICANT: Vlasuk, George Phillip
; APPLICANT: Stanssens, Patrick Eric Hugo
; APPLICANT: Messens, Joris Hilda Lieven
; APPLICANT: Lauwereys, Marc Josef
; APPLICANT: Laroche, Yves Rene
; APPLICANT: Jespers, Laurent Stephane
; APPLICANT: Gansemans, Yannick Georges Jozef
; APPLICANT: Moyle, Matthew
; APPLICANT: Berghum, Peter W.
; TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE
; NUMBER OF SEQUENCES: 356
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; PRIOR APPLICATION NUMBER: US/09/249,471
; FILING DATE:
; APPLICATION DATA:
; APPLICATION NUMBER: 08/809,455
; FILING DATE: April 17, 1997
; APPLICATION NUMBER: PCT/US95/13231
; FILING DATE: October 17, 1995
; APPLICATION NUMBER: 08/486,399
; FILING DATE: June 5, 1995
; APPLICATION NUMBER: 08/486,397
; FILING DATE: June 5, 1995
; APPLICATION NUMBER: 08/465,380
; FILING DATE: June 5, 1995
; APPLICATION NUMBER: 08/461,965
; FILING DATE: June 5, 1995
; APPLICATION NUMBER: 08/326,110
; FILING DATE: October 18, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BIGGS, SUZANNE L.
; REGISTRATION NUMBER: 30,158
; REFERENCE/DOCKET NUMBER: 216/270
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 84 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:

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; ORGANISM: Ancylostoma caninum
US-08-634-641-59

Query Match          26.8%; Score 44; DB 2; Length 84;
Best Local Similarity 43.5%; Pred. No. 6.6;
Matches 10; Conservative 4; Mismatches 7; Indels 2; Gaps 1;

QY 1 NOKYNTQSDVCEP--KYQTWSE 21
   I::: I I I I
Db 9 NEKYDCSGSKCKCKYDGVVE 31

RESULT 7
US-08-634-641-59
; Sequence 59, Application US/08634641
; Patent No. 5955294
; GENERAL INFORMATION:
; APPLICANT: Vlasuk, George P. Vlasuk
; APPLICANT: Stanssens, Patrick Eric Hugo
; APPLICANT: Messens, Joris Hilda Lieven
; APPLICANT: Lauwereys, Marc Josef
; APPLICANT: Laroche, Yves Rene
; APPLICANT: Jespers, Laurent Stephane
; APPLICANT: Gansemans, Yannick Georges Jozef
; APPLICANT: Moyle, Matthew
; APPLICANT: Berghum, Peter W.
; TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT
; NUMBER OF SEQUENCES: 356
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/634,641
; FILING DATE: April 19, 1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/13231
; FILING DATE: October 17, 1995
; APPLICATION NUMBER: 08/486,399
; FILING DATE: June 5, 1995
; APPLICATION NUMBER: 08/486,397
; FILING DATE: June 5, 1995
; APPLICATION NUMBER: 08/465,380
; FILING DATE: June 5, 1995
; APPLICATION NUMBER: 08/461,965
; FILING DATE: June 5, 1995
; APPLICATION NUMBER: 08/326,110
; FILING DATE: October 18, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BIGGS, SUZANNE L.
; REGISTRATION NUMBER: 30,158
; REFERENCE/DOCKET NUMBER: 219/136
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 84 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:

```


; LENGTH: 84 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Ancylostoma caninum
US-09-249-471-59

Query Match 26.8%; Score 44; DB 3; Length 84;
Best Local Similarity 43.5%; Pred. No. 6.6;
Matches 10; Conservative 4; Mismatches 7; Indels 2; Gaps 1;

Qy 1 NOKYNTQSDVCEP--KYQTVSE 21
I::: || |:
Db 9 NEKYDSGSKCEDKCKRYDGVVE 31

RESULT 9
US-09-249-472-59
; Sequence 59, Application US/09249472
; Patent No. 6046318
; GENERAL INFORMATION:
; APPLICANT: Vlasuk, George Phillip
; APPLICANT: Stanssens, Patrick Eric Hugo
; APPLICANT: Messens, Joris Hilda Lieven
; APPLICANT: Lauwereys, Marc Josef
; APPLICANT: Laroche, Yves Rene
; APPLICANT: Jespers, Laurent Stephane
; APPLICANT: Gansmans, Yannick Georges Jozef
; APPLICANT: Moyle, Matthew
; APPLICANT: Berghum, Peter W.
; TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE
; TITLE OF INVENTION: INHIBITORS AND ANTICOAGULANT
; NUMBER OF SEQUENCES: 356
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/249,472
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/809,455
; FILING DATE: April 17, 1997
; APPLICATION NUMBER: PCT/US95/13231
; FILING DATE: October 17, 1995
; APPLICATION NUMBER: 08/486,399
; FILING DATE: June 5, 1995
; APPLICATION NUMBER: 08/486,397
; FILING DATE: June 5, 1995
; APPLICATION NUMBER: 08/465,380
; FILING DATE: June 5, 1995
; APPLICATION NUMBER: 08/461,965
; FILING DATE: June 5, 1995
; APPLICATION NUMBER: 08/326,110
; FILING DATE: October 18, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BIGGS, SUZANNE L.
; REGISTRATION NUMBER: 30,158
; REFERENCE/DOCKET NUMBER: 216/270
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 84 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Ancylostoma caninum
US-09-249-472-59

Query Match 26.8%; Score 44; DB 3; Length 84;
Best Local Similarity 43.5%; Pred. No. 6.6;
Matches 10; Conservative 4; Mismatches 7; Indels 2; Gaps 1;

Qy 1 NOKYNTQSDVCEP--KYQTVSE 21
I::: || |:
Db 9 NEKYDSGSKCEDKCKRYDGVVE 31

RESULT 10
US-09-249-451-59
; Sequence 59, Application US/09249451
; Patent No. 6087487
; GENERAL INFORMATION:
; APPLICANT: Vlasuk, George Phillip
; APPLICANT: Stanssens, Patrick Eric Hugo
; APPLICANT: Messens, Joris Hilda Lieven
; APPLICANT: Lauwereys, Marc Josef
; APPLICANT: Laroche, Yves Rene
; APPLICANT: Jespers, Laurent Stephane
; APPLICANT: Gansmans, Yannick Georges Jozef
; APPLICANT: Moyle, Matthew
; APPLICANT: Berghum, Peter W.
; TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE
; TITLE OF INVENTION: INHIBITORS AND ANTICOAGULANT
; NUMBER OF SEQUENCES: 356
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/249,451
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/809,455
; FILING DATE: April 17, 1997
; APPLICATION NUMBER: PCT/US95/13231
; FILING DATE: October 17, 1995
; APPLICATION NUMBER: 08/486,399
; FILING DATE: June 5, 1995
; APPLICATION NUMBER: 08/486,397
; FILING DATE: June 5, 1995
; APPLICATION NUMBER: 08/465,380
; FILING DATE: June 5, 1995
; APPLICATION NUMBER: 08/461,965
; FILING DATE: June 5, 1995
; APPLICATION NUMBER: 08/326,110
; FILING DATE: October 18, 1994

CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/249,461
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/809,455
FILING DATE: April 17, 1997
APPLICATION NUMBER: PCT/US95/13231
FILING DATE: October 17, 1995
APPLICATION NUMBER: 08/486,399
FILING DATE: June 5, 1995

APPLICATION NUMBER: 08/486,397
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/465,380
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/326,110
FILING DATE: October 18, 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 216/270
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 84 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Ancylostoma caninum
US-09-249-461-59

Query Match 26.8%; Score 44; DB 3; Length 84;
Best Local Similarity 43.5%; Pred. No. 6.6;
Matches 10; Conservative 4; Mismatches 7; Indels 2; Gaps 1;

QY 1 NOKYNTGSDVCEP--KYQTVSE 21
I::: || |
Db 9 NEKYDSCGSKCKKCKYDGVVEE 31

RESULT 13
US-09-249-448-59
Sequence 59, Application US/09249448
Patent No. 6121435
GENERAL INFORMATION:
APPLICANT: Vlasuk, George Phillip
APPLICANT: Stanstons, Patrick Eric Hugo
APPLICANT: Messens, Joris Hilda Lieven
APPLICANT: Lauwereys, Marc Josef
APPLICANT: Laroche, Yves Rene
APPLICANT: Jespers, Laurent Stephane
APPLICANT: Gansemans, Yannick Georges Jozef
APPLICANT: Moyle, Matthew
APPLICANT: Begum, Peter W.
TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE
TITLE OF INVENTION: INHIBITORS AND ANTICOAGULANT
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 356
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/249,448
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/809,455

FILING DATE: April 17, 1997
APPLICATION NUMBER: PCT/US95/13231
FILING DATE: October 17, 1995
APPLICATION NUMBER: 08/486,399
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/486,397
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/465,380
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/326,110
FILING DATE: October 18, 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 216/270
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 84 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Ancylostoma caninum
US-09-249-448-59

Query Match 26.8%; Score 44; DB 4; Length 84;
Best Local Similarity 43.5%; Pred. No. 6.6;
Matches 10; Conservative 4; Mismatches 7; Indels 2; Gaps 1;

QY 1 NOKYNTGSDVCEP--KYQTVSE 21
I::: || |
Db 9 NEKYDSCGSKCKKCKYDGVVEE 31

RESULT 14
US-08-465-380-128
Sequence 128, Application US/08465380
Patent No. 5863894
GENERAL INFORMATION:
APPLICANT: George P. Vlasuk, Patric H. Stanstons,
APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys,
APPLICANT: Yves R. Laroche, Laurent S. Jespers,
APPLICANT: Yannick G.J. Gansemans, Matthew Moyle,
APPLICANT: Peter W. Begum
TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 356
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,380
FILING DATE: June 5, 1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/326,110
 FILING DATE: October 18, 1994
 ATTORNEY/AGENT INFORMATION:
 NAME: BIGGS, SUZANNE L.
 REGISTRATION NUMBER: 30,158
 REFERENCE/DOCKET NUMBER: 213/268
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELEX: 67-3510
 INFORMATION FOR SEQ ID NO: 128:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 91 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 ORIGINAL SOURCE:
 ORGANISM: Ancylostoma caninum
 US-08-485-380-128

Query Match 26.8%; Score 44; DB 2; Length 91;
 Best Local Similarity 43.5%; Pred. No. 7.3;
 Matches 10; Conservative 4; Mismatches 7; Indels 2; Gaps 1;

QY 1 NOKYNTQGSVDVCEP--KYQTVSE 21
 I::: I I I I
 Db 16 NEKYDSCGSKCKCKYDGVVE 38

RESULT 15
 US-08-480-478-50
 Sequence 50, Application US/08480478
 Patent No. 5864009
 GENERAL INFORMATION:
 APPLICANT: GEORGE P. VLASUK; PATRICK ERIC
 APPLICANT: HUGO STANSSENS; JORIS HILDA
 APPLICANT: LIEVEN MESSENS; MARC JOZEF
 APPLICANT: LAUMEREYS; YVES RENE LAROCHE;
 APPLICANT: LAURENT STEPHANE JESPER; and
 APPLICANT: YANNICK GEORGES JOZEF
 APPLICANT: GANSEMAN
 TITLE OF INVENTION: NEMATODE-EXTRACTED ANTI-
 TITLE OF INVENTION: COAGULANT PROTEIN
 NUMBER OF SEQUENCES: 86
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lyon & Lyon
 STREET: 633 West Fifth Street
 STREET: Suite 4700
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 MEDIUM TYPE: storage
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: FastSEQ Version 1.5
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/480,478
 FILING DATE: 06-JUN-1995
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/326,110
 FILING DATE: 18 OCTOBER 1994
 ATTORNEY/AGENT INFORMATION:
 NAME: BIGGS, SUZANNE L.
 REGISTRATION NUMBER: 30,158
 REFERENCE/DOCKET NUMBER: 208/290
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440

TELEX: 67-3510
 INFORMATION FOR SEQ ID NO: 50:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 91 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 US-08-480-478-50
 Query Match 26.8%; Score 44; DB 2; Length 91;
 Best Local Similarity 43.5%; Pred. No. 7.3;
 Matches 10; Conservative 4; Mismatches 7; Indels 2; Gaps 1;
 QY 1 NOKYNTQGSVDVCEP--KYQTVSE 21
 I::: I I I I
 Db 16 NEKYDSCGSKCKCKYDGVVE 38
 Search completed: May 23, 2001, 15:30:07
 Job time: 414 sec



GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 23, 2001, 15:32:01 ; Search time 110.15 seconds
(without alignments)
18.717 Million cell updates/sec

Title: US-08-887-977-10_COPY_177_206
Perfect score: 164
Sequence: 1 NOKYNTQSDVCEPKYQTVSEPIRWKLLML 30

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 198801 seqs, 68722935 residues

Total number of hits satisfying chosen parameters: 198801

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_67:**

1: piri:**

2: pir2:**

3: pir3:**

4: pir4:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	164	100.0	369	JC5068	G protein-coupled
2	57	34.8	1737	TL4318	ubiquitin-protein
3	52	31.7	98	B64360	hypothetical prote
4	50	30.5	453	T21528	hypothetical prote
5	48	29.3	357	A72220	conserved hypotet
6	48	29.3	500	S61591	hypothetical prote
7	48	29.3	1257	I58383	retinoblastoma bin
8	47	28.7	424	T08979	hypothetical prote
9	47	28.7	1116	S77213	NBS-directed DNA p
10	46.5	28.4	263	T02227	NBS-LRR type resis
11	46.5	28.4	353	G61547	trans-activating t
12	46.5	28.4	358	TNLCJH1	trans-activating t
13	46.5	28.4	358	TNLCJH1	trans-activating t
14	46.5	28.4	633	S49788	probable membrane
15	46	28.0	443	D64477	cobyrinic acid a,c
16	46	28.0	678	T05821	hypothetical prote
17	46	28.0	1139	B54962	sterol regulatory
18	46	28.0	2813	VWBU	von Willebrand fac
19	45.5	27.7	338	JGECT	thiosulfate-bindin
20	45	27.4	387	S64082	probable membrane
21	45	27.4	742	I37225	leucocyte antigen
22	45	27.4	867	GNLJMP	pol polyprotein (c
23	45	27.4	1621	S62356	TRP-185 protein -
24	44.5	27.1	196	T47140	hypothetical prote
25	44.5	27.1	239	T20255	hypothetical prote
26	44.5	27.1	950	T23975	hypothetical prote
27	44	26.8	316	A57356	lacyl-carrier-prot
28	44	26.8	372	S74859	hypothetical prote
29	44	26.8	373	T35452	probable solute bi

30	44	26.8	492	2	T43859	uroporphyrinogen I
31	44	26.8	505	2	I38396	protein-tyrosine k
32	44	26.8	510	2	F82523	hypothetical prote
33	44	26.8	687	2	A41905	ferric vibriobacti
34	44	26.8	747	2	B47093	cellulase (EC 3.2.
35	44	26.8	1009	2	T18533	CryIAC toxin-bindi
36	44	26.8	1148	2	T09073	splicing factor Si
37	44	26.8	3051	2	S42373	hypothetical prote
38	43.5	26.5	437	2	S60957	transcription modu
39	43.5	26.5	721	2	A44133	phenylalanine ammo
40	43.5	26.5	1438	2	B71610	WD40 WEB-1 homolog
41	43	26.2	80	2	H82194	conserved hypotet
42	43	26.2	200	2	T42678	hypothetical prote
43	43	26.2	241	2	H81536	hypothetical prote
44	43	26.2	246	2	T48338	arabinosacalactan pr
45	43	26.2	254	2	T12688	hypothetical prote

ALIGNMENTS

RESULT 1

JC5068
G protein-coupled receptor CKR-L3 - human
C:Species: Homo sapiens (man)
C:Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 21-Jul-2000
C:Accession: JC5068
R:Zaballos, A.; Varona, R.; Gutierrez, J.; Lind, P.; Marquez, G.
Biochem. Biophys. Res. Commun. 227, 846-853, 1996
A:Title: Molecular cloning and RNA expression of two new human chemokine receptor-lik
A:Reference number: JC5067; MUID:97040707
A:Accession: JC5068
A:Molecule type: DNA
A:Residues: 1-369 <ZAB>
A:CROSS-references: EMBL:Z79784; NID:gl668737; PIDN:CAB02144.1; PID:gl668738
C:Comment: This protein belongs to the family of alpha chemokine receptors.
C:Genetics:
A:Gene: GDB:CMKBR6; SFRSL22: GPR29; CCR6: CKR-L3; GPR-CY4
A:CROSS-references: GDB:5370639; OMIM:601835
A:Map position: 6q27-6q27
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; transmembrane protein
F:42-68/Domain: transmembrane #status predicted <TM1>
F:79-99/Domain: transmembrane #status predicted <TM2>
F:115-136/Domain: transmembrane #status predicted <TM3>
F:160-180/Domain: transmembrane #status predicted <TM4>
F:212-233/Domain: transmembrane #status predicted <TM5>
F:250-271/Domain: transmembrane #status predicted <TM6>
F:292-315/Domain: transmembrane #status predicted <TM7>

Query Match 100.0%; Score 164; DB 2; Length 369;
Best Local Similarity 100.0%; Pred. No. 1.2e-16;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NOKYNTQSDVCEPKYQTVSEPIRWKLLML 30
|||||
Db 181 NOKYNTQSDVCEPKYQTVSEPIRWKLLML 210

RESULT 2

TL4318
ubiquitin-protein ligase E3-alpha - mouse
N:Alternate names: N-recogin E3-alpha
C:Species: Mus musculus (house mouse)
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C:Accession: TL4318
R:Kwon, Y.T.; Reiss, Y.; Fried, V.A.; Hershko, A.; Yoon, J.K.; Gonda, D.K.; Sangan, P
Proc. Natl. Acad. Sci. U.S.A. 95, 7898-7903, 1998
A:Title: The mouse and human genes encoding the recognition component of the N-end ru
A:Reference number: 217977; MUID:98318583
A:Accession: TL4318
A:Status: preliminary; translated from GB/EMBL/DBJ

Query Match	30.5%	Score 50;	DB 2;	Length 453;
Best Local Similarity	37.5%	Pred. No. 13;		
Matches	9;	Conservative	5;	Mismatches 10;
Indels	0;	Gaps	0;	

Query Match	29.3%	Score 48;	DB 1;	Length 1257;
Best Local Similarity	35.3%;	Pred. No. 74;		
Matches 12;	Conservative	6;	Mismatches	8;
			Indels	8;
			Gaps	1;

102227
NBS-LRR type resistance protein - rice (fragment)
C:Species: Oryza sativa (rice)
C:Date: 05-Mar-1999 #sequence_revision 05-Mar-1999
C:Accession: T02227

C:Genetics:

A:Gene: tat

C:Superfamily: leukemia virus trans-activating transcription regulator

C:Keywords: transcription regulation

Query Match 28.4%; Score 46.5; DB 1; Length 358;

Best Local Similarity 57.1%; Pred. No. 33;

Matches 12; Conservative 1; Mismatches 7; Indels 1;

QY 8 GSDVCEPKYQTVPSEIRWKL 28
||| || : | | | | |
Db 154 GSVCMYLQ-LSPPIWPLL 173

RESULT 13

TNLJCN

trans-activating transcription regulator -human T-cell lymphotropic v

N:Alternate names: pX protein; x-lor protein

C:Species: human T-cell lymphotropic virus type 1, HTLV-1

A>Note: host Homo sapiens (man)

C>Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 02-Jul-

C:Accession: E28136

R:Malik, K.T.A.; Even, J.; Karpas, A.

J. Gen. Virol. 69, 1695-1710, 1988

A>Title: Molecular cloning and complete nucleotide sequence of an adul

bbers of the ATLIV/HTLV-I subgroup.

A:Reference number: A92797; MUID:88274338

A:Accession: E28136

A:Molecule type: DNA

A:Residues: 1-358 <MAL>

A:Cross-references: GB:D13784; GB:D00294; NID:g221866

A>Note: This ORF is not annotated in GenBank entry HTPVCAR

C:Genetics:

A:Gene: tat

A:Introns: 1/3

C:Superfamily: leukemia virus trans-activating transcription regulator

C:Keywords: transcription regulation

Query Match 28.4%; Score 46.5; DB 1; Length 358;

Best Local Similarity 57.1%; Pred. No. 33;

Matches 12; Conservative 1; Mismatches 7; Indels 1;

QY 8 GSDVCEPKYQTVPSEIRWKL 28
||| || : | | | | |
Db 154 GSVCMYLQ-LSPPIWPLL 173

RESULT 14

S49788

probable membrane protein YIL092w - yeast (Saccharomyces cerevisiae)

N:Alternate names: hypothetical protein YI910.04

C:Species: Saccharomyces cerevisiae

C>Date: 13-Jan-1995 #sequence_revision 10-Feb-1995 #text_change 04-Mar-

C:Accession: S49788

R:Connot, R.; Churcher, C.

submitted to the EMBL Data Library, November 1994

A:Reference number: S49786

A:Accession: S49786

A:Molecule type: DNA

A:Residues: 1-633 <CON>

A:Cross-references: GB:Z47047; EMBL:Z46728; NID:g603997; PID:g763254;

C:Genetics:

A:Gene: MIPS:YIL092w

A:Map position: 9L

C:Superfamily: Saccharomyces cerevisiae probable membrane protein YIL0

C:Keywords: transmembrane protein

F:99-115/Domain: transmembrane #status predicted <TM>

Query Match 28.4%; Score 46.5; DB 2; Length 633;

Best Local Similarity 50.0%; Pred. No. 60;

```

Query Match      28.0%; Score 46; DB 2; Length 443;
Best Local Similarity 37.5%; Pred. No. 48;
Matches 9; Conservative 5; Mismatches 6; Indels 4; Gaps 1;

QY 1 NQKYNQ-----GSDVCEPKYQTVS 20
      :| | | | | | | | | | | | | |
Db 29 SKKYNVQCYKVGPDYIDPTYHTIA 52

```

Search completed: May 23, 2001, 15:32:01
Job time: 508 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 23, 2001, 15:36:18 ; Search time 62.39 Seconds
(without alignments)
16.472 Million cell updates/sec

Title: US-08-887-977-10_COPY_177_206

Perfect score: 164

Sequence: 1 NQYNTQGSVDCEPKYQTVSEPIRWKLLML 30

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 3425486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	164	100.0	374	1	CRK6_HUMAN
2	110	67.1	367	1	CRK6_MOUSE
3	52	31.7	98	1	Y481_METJA
4	51.5	31.4	815	1	RPCR_HUMAN
5	50	30.5	453	1	YUOP_CAEEL
6	49	29.9	1277	1	NPCL_FIG
7	48	29.3	500	1	YDAK_YEAST
8	46.5	28.4	358	1	RBB1_HUMAN
9	46.5	28.4	358	1	TAT_HTLIA
10	46.5	28.4	358	1	TAT_HTLIC
11	46.5	28.4	633	1	YIJ2_YEAST
12	46	28.0	443	1	COBB_METJA
13	46	28.0	1139	1	SRE2_CRIGR
14	46	28.0	2813	1	VWF_HUMAN
15	45.5	27.7	122	1	IPSG_MUSLU
16	45.5	27.7	168	1	ARPL_CAEEL
17	45.5	27.7	338	1	CYSP_ECOLI
18	45.5	27.7	338	1	CYSP_SALTJ
19	45	27.4	387	1	YGH5_YEAST
20	45	27.4	835	1	CD97_HUMAN
21	45	27.4	867	1	POL_MPMV
22	44.5	27.1	950	1	YRM2_CAEEL
23	44	26.8	505	1	FRK_HUMAN
24	44	26.8	687	1	YVUA_VIBCH
25	44	26.8	747	1	GUND_CELFI
26	44	26.8	1009	1	AMPM_HELVI
27	44	26.8	3051	1	YXN3_CAEEL
28	43.5	26.5	437	1	WTM1_YEAST
29	43.5	26.5	721	1	PAL5_LYCES
30	43	26.2	285	1	GVC2_HALNI
31	43	26.2	285	1	GVC2_HALN2
32	43	26.2	566	1	XVLR_PSEPU
33	43	26.2	681	1	TRE_MANSE

34	43	26.2	867	1	POL_SRV1
35	43	26.2	901	1	SVV_LACCA
36	43	26.2	1691	1	POLN_HEVME
37	43	26.2	2183	1	RRPL_RINDR
38	42.5	25.9	453	1	GP39_HUMAN
39	42.5	25.9	1092	1	DPDQ_DRONE
40	42.5	25.9	1827	1	MAP2_HUMAN
41	42	25.6	116	1	MCS_HUMAN
42	42	25.6	513	1	COX1_HUMAN
43	42	25.6	514	1	COX1_PONPA
44	42	25.6	514	1	COX1_RHIUN
45	42	25.6	522	1	FBX7_HUMAN

ALIGNMENTS

RESULT	1
CRK6_HUMAN	
ID	CRK6_HUMAN STANDARD: PRT; 374 AA.
AC	P51684; Q92846; P78553;
DT	01-OCT-1996 (Rel. 34, Created)
DT	15-JUL-1998 (Rel. 36, Last sequence update)
DT	01-OCT-2000 (Rel. 40, Last annotation update)
DE	C-C CHEMOKINE RECEPTOR TYPE 6 (C-C CRK-6) (CCR-6) (LARC
DE	RECEPTOR) (GPR-CY4) (GPRCY4) (CHEMOKINE RECEPTOR-LIKE 3) (CRK-L3)
DE	(DRY6).
GN	CCR6 OR CMKBR6 OR STRL22 OR GPR29 OR CKRL3.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	NCBI_TaxID:9606;
RN	[1]
RP	SEQUENCE FROM N.A., AND FUNCTION.
RX	MEDLINE=97313465; PubMed=9169459;
RA	Baba M., Imai T., Nishimura M., Kakizaki M., Takagi S., Hieshima K.,
RA	Nomiyama H., Yoshie O.
RT	"Identification of CCR6, the specific receptor for a novel
RT	lymphocyte-directed CC chemokine LARC."
RL	J. Biol. Chem. 272:14893-14898(1997).
RN	[2]
RP	SEQUENCE FROM N.A.
RA	Lautens L.L., Modi W., Bonner T.I.;
RL	Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
RN	[3]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=97040707; PubMed=8886020;
RA	Zaballos A., Varona R., Gutierrez J., Lind P., Marquez G.;
RT	"Molecular cloning and RNA expression of two new human chemokine
RT	receptor-like genes."
RL	Biochem. Biophys. Res. Commun. 227:846-853(1996).
RN	[4]
RP	SEQUENCE FROM N.A.
RA	McCoy R., Perlmuter D.H.;
RL	Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
RN	[5]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=97224503; PubMed=9070937;
RA	Liao F., Lee H.-H., Farber J.M.;
RT	"Cloning of STRL22, a new human gene encoding a G-protein-coupled
RT	receptor related to chemokine receptors and located on chromosome
RT	6q27."
RL	Genomics 40:175-180(1997).
CC	-1- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-3-
CC	ALPHA/LARC AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE
CC	INTRACELLULAR CALCIUM IONS LEVELS.
CC	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC	-1- TISSUE SPECIFICITY: SPLEEN, LYMPH NODES, APPENDIX, AND FETAL
CC	LIVER. EXPRESSED IN LYMPHOCYTES, T CELLS AND B CELLS BUT NOT IN
CC	NATURAL KILLER CELLS, MONOCYTES, OR GRANULOCYTES.
CC	-1- INDUCTION: INTERLEUKIN-2.
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC	-1- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-6 IS THE INITIATOR.


```
RESULT 3
Y481_METJA STANDARD; PRT; 98 AA.
AC Q57906;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE HYPOTHETICAL PROTEIN MJ0481.
GN MJ0481.
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
OC Methanococcus.
OX NCBI_TaxID=2190;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=96337999; PubMed=8688087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
RA Kerlavage A.R., Dougherty B.A., Tomb J.F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
RA Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RA "Complete genome sequence of the methanogenic archaeon, Methanococcus
RT jannaschii".
RN Science 273:1058-1073(1996).
CC -----
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CC -----
CC EMBL: U67498; AAB98472.1; -
CC TIGR: MJ0481; -
CC KW Hypothetical protein.
SQ SEQUENCE 98 AA; 11218 MW; 6F31A08240C3CB3 CRC64;

Query Match 31.7%; Score 52; DB 1; Length 98;
Best Local Similarity 52.6%; Pred. No. 0.64; 7; Indels 0; Gaps 0;
Matches 10; Conservative 2; Mismatches 7;

QY 3 KYNTQGSQVCEPKYQTVSE 21
II :|||: ||||
Db 29 KYQNGSDITFEKPTVGE 47

RESULT 4
RPGR_HUMAN STANDARD; PRT; 815 AA.
AC Q92834; Q93039; O00737; O00702;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE X-LINKED RETINITIS PIGMENTOSA GTPASE REGULATOR.
GN RPGR OR RP3 OR XLRP3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96241570; PubMed=8673101;
RA Meindl A., Dry K., Herrmann K., Mansson F., Ciccodicola A.,
RA Edgar A., Carvalho M.R.S., Achatz H., Hellebrand H., Lennon A.,
RA Migliaccio C., Porter K., Zrenner E., Bird A., Jay M., Lorenz B.,
RA Wittwer B., D'Urso M., Meitinger T., Wright A.;
RT "A gene (RPGR) with homology to the RCC1 guanine nucleotide exchange
RT factor is mutated in X-linked retinitis pigmentosa (RP3).";
RL Nat. Genet. 13:35-42(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Retina;
RA Berger W.;
RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 1-509 FROM N.A., AND VARIANTS RP3 C-130; S-235 AND S-275.
RC TISSUE=Retina;
RX MEDLINE=96414315; PubMed=8817343;
RA Roepman R., van Duijnhoven G., Rosenberg T., Pinckers A.J.L.G.,
RA Bleeker-Wagemakers L.M., Bergen A.A.B., Post J., Beck A.,
RA Reinhardt R., Rogers H.-H., Cremers F., Berger W.;
RT "Positional cloning of the gene for X-linked retinitis pigmentosa 3:
RT homology with the guanine-nucleotide-exchange factor RCC1.";
RL Hum. Mol. Genet. 5:1035-1041(1996).
RN [4]
RP VARIANTS RP3.
RX MEDLINE=98153625; PubMed=9399904;
RA Buraczynska M., Wu W., Fujita R., Buraczynska K., Phelps E.,
RA Andreasson S., Bennett J., Birch D.G., Fishman G.A., Hoffman D.R.,
RA Inana G., Jacobson S.G., Musarella M.A., Sieving P.A., Swaroop A.;
RT "Spectrum of mutations in the RPGR gene that are identified in 20% of
RT families with X-linked retinitis pigmentosa.";
RL Am. J. Hum. Genet. 61:1287-1292(1997).
RN [5]
RP VARIANT RP3 VAL-60.
RX MEDLINE=99070804; PubMed=9855162;
RA Fishman G.A., Grover S., Jacobson S.G., Alexander K.R., Derlacki D.J.,
RA Wu W., Buraczynska M., Swaroop A.;
RT "X-linked retinitis pigmentosa in two families with a missense
RT mutation in the RPGR gene and putative change of glycine to valine at
RT codon 60.";
RL Ophthalmology 105:2286-2296(1998).
CC -!- FUNCTION: COULD BE GUANINE-NUCLEOTIDE RELEASING FACTOR.
CC -!- SUBCELLULAR LOCATION: POSSIBLY MEMBRANE-ANCHORED.
CC -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS: A LONG FORM (SHOWN HERE) AND A
CC SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING. THE SMALL FORM
CC LACKS PART OF REPEAT 7.
CC -!- TISSUE SPECIFICITY: HEART, BRAIN, PLACENTA, LUNG, LIVER, MUSCLE,
CC KIDNEY, PANCREAS AND FETAL RETINAL PIGMENT EPITHELIUM.
CC -!- DISEASE: DEFECTS IN RPGR ARE RESPONSIBLE FOR X-LINKED RETINITIS
CC PIGMENTOSA-3 (XLRP-3 OR RP3), A FORM OF CHOROIDO-RETINAL
CC DEGENERATION WHICH IS DISTINGUISHED FROM OTHER TYPES BY THE
CC PRESENCE IN HETEROZYGOUS WOMEN OF A TAPETAL-LIKE RETINAL REFLEX (A
CC BRILLIANT, SCINTILLATING, GOLDEN-HUED, PATCHY APPEARANCE MOST
CC STRIKING AROUND THE MACULA) BUT NO VISUAL DEFECT.
CC -!- SIMILARITY: CONTAINS 7 RCC1 REPEATS.
CC -!- DATABASE: NAME-Mutations of the RPGR gene;
CC NOTE=Retina International's Scientific Newsletter;
CC WWW="http://www.irpa.org/sci-news/rpgrmut.htm".
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CC -----
CC EMBL: U57629; AAC50481.1; -
CC DR EMBL: X97668; CAA66258.1; -
CC DR MIM: 312610; -
CC DR InterPro: IPR000408; -
CC DR Pfam: PF00415; RCC1_7.
CC DR PROSITE: PS00626; RCC1_2; 4.
CC DR PROSITE: PS50012; RCC1_3; 6.
CC KW Guanine-nucleotide releasing factor; Alternative splicing; Repeat;
FT Vision; Retinitis pigmentosa; Disease mutation.
FT REPEAT 11 52 RCC1 1.
FT REPEAT 53 104 RCC1 2.
```

FT REPEAT 106 157 RCC1 3.
FT REPEAT 158 207 RCC1 4.
FT REPEAT 208 260 RCC1 5.
FT REPEAT 262 312 RCC1 6.
FT REPEAT 314 366 RCC1 7.
FT VARSPLIC 354 415 MISSING (IN SHORT ISOFORM).
FT VARIANT 60 60 G -> V (IN RP3).
FT VARIANT 60 60 G -> N (IN RP3).
FT VARIANT 60 60 /FTId=VAR_008501.
FT VARIANT 60 60 /FTId=VAR_008502.
FT VARIANT 75 75 I -> V (IN RP3).
FT VARIANT 75 75 /FTId=VAR_008503.
FT VARIANT 98 98 H -> Q (IN RP3).
FT VARIANT 98 98 /FTId=VAR_008504.
FT VARIANT 130 130 F -> C (IN RP3).
FT VARIANT 130 130 /FTId=VAR_008505.
FT VARIANT 215 215 G -> V (IN RP3).
FT VARIANT 215 215 /FTId=VAR_008506.
FT VARIANT 235 235 P -> S (IN RP3).
FT VARIANT 235 235 /FTId=VAR_008507.
FT VARIANT 250 250 C -> R (IN RP3).
FT VARIANT 250 250 /FTId=VAR_008508.
FT VARIANT 262 262 A -> G (IN RP3).
FT VARIANT 262 262 /FTId=VAR_008509.
FT VARIANT 275 275 G -> S (IN RP3).
FT VARIANT 275 275 /FTId=VAR_008510.
FT VARIANT 425 425 R -> K (IN RP3).
FT VARIANT 425 425 /FTId=VAR_008511.
FT VARIANT 431 431 I -> V (IN RP3).
FT VARIANT 436 436 /FTId=VAR_008512.
FT VARIANT 566 566 G -> E (IN RP3).
FT VARIANT 566 566 /FTId=VAR_008513.
FT CONFLICT 1 3 MRE -> MAKLRSTTAL (IN REF. 3).
SQ SEQUENCE 815 AA; 90244 MW; 70D84EAD988348D1 CRC64;

Query Match 31.4%; Score 51.5; DB 1; Length 815;
Best Local Similarity 32.1%; Pred. No. 7;
Matches 9; Conservative 7; Mismatches 5; Indels 7; Gaps 1;

Qy 5 NTOQ-----SDVCEPKYQTVSEPIRW 25
I::I I::I I::I I::I I::I I::I I::I I::I I::I I::I
Db 167 NSEQIGLKNSVNCVPOQVTGKPVSW 194

RESULT 5
YUQP_CAEEL STANDARD; PRT; 453 AA.
AC Q19895;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE HYPOTHETICAL 52.9 KDA PROTEIN F28H7.8 IN CHROMOSOME V.
GN F28H7.8.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RC STRAIN=BRISTOL N2;
RP SEQUENCE FROM N.A.
RA Berks M.;
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE SEC14 CYTOSOLIC FACTOR FAMILY.
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CC -----
DR EMBL; 272508; CAA96639.1;
DR WormPep; F28H7.8; CE05757.
DR InterPro; IPR001251;
DR Pfam; PF00650; CRAL_TRIO; 1.
DR Hypothetical protein.
SQ SEQUENCE 453 AA; 52926 MW; CC07AF08D50FDE79 CRC64;

Query Match 30.5%; Score 50; DB 1; Length 453;
Best Local Similarity 37.5%; Pred. No. 6.3;
Matches 9; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

Qy 2 QKYNTQGSVDCEPKYQTVSEPIRW 25
I::I I::I I::I I::I I::I I::I I::I I::I I::I I::I
Db 20 EQVRLQVSDVIDPRYDTKNMLRW 43

RESULT 6

NPCL_PIG
ID NPCL_PIG STANDARD; PRT; 1277 AA.
AC P56941;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE NIEMANN-PICK C1 PROTEIN PRECURSOR.
GN NPCL.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Gevry N.Y., Lacroix D.A., Song J.H., Murphy B.D.;
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: INVOLVED IN THE INTRACELLULAR TRAFFICKING OF CHOLESTEROL
CC MAY BE CRUCIAL FOR MAINTAINING THE STRUCTURAL AND FUNCTIONAL
CC INTEGRITY OF NERVE TERMINALS (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. FOUND IN LATE
CC ENDOSOMES AND LYSSOMES (BY SIMILARITY).
CC -!- DOMAIN: A CYSTEINE-RICH N-TERMINAL DOMAIN AND A C-TERMINAL DOMAIN
CC CONTAINING A DI-LEUCINE MOTIF NECESSARY FOR LYSSOSOMAL TARGETING
CC ARE CRITICAL FOR MOBILIZATION OF CHOLESTEROL FROM LYSSOMES (BY
CC SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE PATCHED FAMILY.
CC -----
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CC -----
DR EMBL; AF169635; AAD47090.1;
DR PROSITE; P550156; SSD; 1.
KW Signal; Glycoprotein; Transmembrane; Lysosome.
FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 23 1277 NIEMANN-PICK C1 PROTEIN.
FT DOMAIN 249 259 POLY-PRO.
FT DOMAIN 1274 1277 DI-LEUCINE MOTIF.
FT TRANSMEM 271 291 POTENTIAL.
FT TRANSMEM 352 372 POTENTIAL.
FT TRANSMEM 623 643 POTENTIAL.
FT TRANSMEM 655 675 POTENTIAL.
FT TRANSMEM 685 705 POTENTIAL.
FT TRANSMEM 761 781 POTENTIAL.
FT TRANSMEM 834 854 POTENTIAL.
FT TRANSMEM 1099 1119 POTENTIAL.
FT TRANSMEM 1125 1145 POTENTIAL.
FT TRANSMEM 1196 1216 POTENTIAL.

```

Query Match          29.3%; Score 48; DB 1; Length 500;
Best Local Similarity 50.0%; Pred. No. 14;
Matches 8; Conservative 4; Mismatches 0; Gaps 0;

QY 11 VCEPKYQTVSEPIRWK 26
    ||| | : | : : | |||
DB 485 VCERKCEEVNDGLRWK 500

RESULT 8
RBB1_HUMAN
ID RBB1_HUMAN STANDARD; PRT; 1257 AA.
AC P29374;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE RETINOBLASTOMA BINDING PROTEIN 1 (RBBP-1).
GN RBBP1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxId=9606;
[1]
SEQUENCE FROM N.A.
MEDLINE=94020841; PubMed=8414517;
RATTAY A.R., Heilin K., Dembski M.S., Dyson N., Harlow E.,
RA Vuocolo G.A., Hanabik M.G., Haskell K.M., Oliff A., Defeo-Jones D.,
RA Jones R.E.;
RA "Characterization of the retinoblastoma binding proteins RBP1 and
RPB2";
RL Oncogene 8:3149-3156(1993).
[2]
SEQUENCE OF 855-1203 FROM N.A.
MEDLINE=91312450; PubMed=1857421;
RA Defeo-Jones D., Huang P.S., Jones R.E., Haskell K.M., Vuocolo G.A.,
RA Hanabik M.G., Huber H.E., Oliff A.;
RT "Cloning of cDNAs for cellular proteins that bind to the
retinoblastoma gene product.";
RL Nature 352:251-254(1991).
-1- FUNCTION: INTERACTS WITH THE VIRAL PROTEIN-BINDING DOMAIN OF THE
RETINOBLASTOMA PROTEIN.
-1- SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
-----
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-----
EMBL: S66427; AAB28543.1;
PIR: S16953; S16953.
MIM: 180201;
InterPro: IPR001606;
PFam: PF01388; ARID; 1.
KW Trans-acting factor; Nuclear protein.
FT CONFLICT 1178 1178 D -> S (IN REF. 2).
FT CONFLICT 1196 1201 IRKYYM -> SENIICL (IN REF. 2).
SEQUENCE 1257 AA; 142666 MW; F5C0AB6D6ED431DC CRC64;

Query Match          29.3%; Score 48; DB 1; Length 1257;
Best Local Similarity 35.3%; Pred. No. 36;
Matches 12; Conservative 6; Mismatches 8; Indels 8; Gaps 1;

QY 4 YNTQGSVD-----CEPKYQTVSEPIRWKLLM 29
    ||| | : | : : | |||
DB 9 YLAVGTVDVSAKYRGAFCEAIKTRKVLKRVLL 42

```


Search completed: May 23, 2001, 15:36:19
Job time: 650 sec

Result No.	Score	Query %		Length	DB	ID	Description.
		Match					
1	111	67.7	367	11	Q9R1V0	Q9rlv0 mus musculus	
2	57	34.8	1757	11	O70481	O70481 mus musculus	
3	51.5	31.4	646	4	Q9UMR1	Q9umr1 homo sapien	
4	50.5	30.8	683	6	Q9N1T4	Q9n1t4 canis famill	
5	50.5	30.8	616	6	Q9N1T5	Q9n1t5 canis famill	
6	50.5	30.8	918	6	Q9N1T3	Q9n1t3 canis famill	
7	50.5	30.8	1003	6	Q9N1T2	Q9n1t2 canis famill	
8	49.5	30.2	746	11	O88408	O88408 mus musculus	
9	49.5	30.2	1001	11	Q9R0X5	Q9r0x5 mus musculus	
10	49	29.9	395	10	Q9LKA5	Q9lka5 arabidopsis	
11	49	29.9	1276	6	Q9N0Q0	Q9n0q0 felis silve	
12	49	29.9	1277	11	Q9JLG3	Q9jlg3 cricetulus	
13	48.5	29.6	653	5	Q9VBW7	Q9vbw7 drosophila	
14	48	29.3	53	10	Q41315	Q41315 solarium car	
15	48	29.3	219	4	Q9UDK7	Q9udk7 homo sapien	
16	48	29.3	357	2	Q9X221	Q9x221 thermotoga	
17	48	29.3	545	11	Q9JIC0	Q9jic0 mus musculus	
18	47	28.7	375	10	Q9LTF5	Q9ltf5 arabidopsis	
19	47	28.7	424	10	Q9SZV6	Q9szv6 arabidopsis	

RESULT 2

REPK. *Canis familiaris* (Dog).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis..
 OX NCBI_TaxID=9615;
 RN [1]
 RN SEQUENCE FROM N.A. PubMed-10699176;
 RP MEDLINE-20164291; Acland G.M., Aguirre G.D.;
 RA Zeiss C.J., Ray K., Mapping of X-linked progressive retinal atrophy (XLPRA), the can
 RT RT homolog of retinitis pigmentosa 3 (RP3).;
 RN

30.88: score 50.5: DB 6: Length 1003:

DR PFAM; PF00415; RC

DR PFAM; PF00415; RCC1; 7.
DR PRINTS: PR00633: RCC1NSATION

DR PROSITE; PS00626; RCCL_2; UNKNOWN_4.
SQ SEQUENCE 1001 AA; 111855 MW; DE145FBFEAF0F8759 CRC64;

Query Match 30.2%; Score 49.5; DB 11; Length 1001;
Best Local Similarity 39.3%; Pred. No. 48;
Matches 11; Conservative 4; Mismatches 6; Indels 7; Gaps 1;

QY 5 NTQG-----SDVCEPKYQTVSEPIRW 25
I::I I::I I::I I::I I::I I::I I::I I::I
Db 167 NSEGIQIGLEDKSNVCIPHEVTGKPISW 194

RESULT 10
Q9LKA5 PRELIMINARY; PRT; 395 AA.
ID Q9LKA5
AC Q9LKA5
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
DE SIMILARITY TO DAG PROTEIN.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
OC Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RA Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S.;
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RA Nakamura Y.;
RT "Structural analysis of Arabidopsis thaliana chromosome 3. II.
RT Sequence features of the regions of 4,251,695 bp covered by ninety pl,
RT TAC and BAC clones.";
RL DNA Res. 7:217-221(2000).
DR EMBL; AP000370; BAA97063.1; -.
SQ SEQUENCE 395 AA; 42869 MW; D15E5CCC89E2A33C CRC64;

Query Match 29.9%; Score 49; DB 10; Length 395;
Best Local Similarity 41.7%; Pred. No. 21;
Matches 10; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

QY 1 NOKYNTQGSQSDVCEPKYQTVSEPIR 24
I::I I::I I::I I::I I::I I::I I::I I::I
Db 363 NNNYQQGGSGMQQPYQNNYPNR 386

RESULT 11
Q9N0Q0 PRELIMINARY; PRT; 1276 AA.
ID Q9N0Q0
AC Q9N0Q0
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
DE NIEMANN-PICK TYPE C1 DISEASE PROTEIN.
GN NPC1.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=KIDNEY;
RA Murakawa M., Freeman M.W.;
RT "Feline Niemann-Pick type C1 disease protein (NPC1).";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF258783; AAF72187.1; -.
SQ SEQUENCE 1276 AA; 141739 MW; CE9B7A0261691256 CRC64;

Query Match 29.9%; Score 49; DB 6; Length 1276;
Best Local Similarity 45.5%; Pred. No. 73;
Matches 10; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 9 SDVCEPKYQTVSEPIRWKLLML 30
I::I I::I I::I I::I I::I I::I I::I I::I
Db 244 SIVCGPRQPQPPVPVWRILGL 265

RESULT 12
Q9JLG3 PRELIMINARY; PRT; 1277 AA.
ID Q9JLG3
AC Q9JLG3
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
DE NIEMANN-PICK TYPE C1 PROTEIN.
GN NPC1.
OS Cricetulus griseus (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Cricetulus.
OX NCBI_TaxID=10029;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=OVARY;
RA Cruz J.C., Sugii S., Yu C., Chang T.-Y.;
RT "Role of Niemann-Pick Type C1 Protein in Intracellular Trafficking of
RT Low Density Lipoprotein-derived Cholesterol.";
RL J. Biol. Chem. 275:4013-4021(2000).
DR EMBL; AF182744; AAF31692.1; -.
SQ SEQUENCE 1277 AA; 142817 MW; 6B3D638094B4E156 CRC64;

Query Match 29.9%; Score 49; DB 11; Length 1277;
Best Local Similarity 45.5%; Pred. No. 73;
Matches 10; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 9 SDVCEPKYQTVSEPIRWKLLML 30
I::I I::I I::I I::I I::I I::I I::I I::I
Db 244 SIVCGPRQPQPPVPVWRILGL 265

RESULT 13
Q9VBW7 PRELIMINARY; PRT; 653 AA.
ID Q9VBW7
AC Q9VBW7
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TReMBLrel. 13, Last annotation update)
DE CG13661 PROTEIN.
GN CG13661.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Vandal M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J.J., Brokstein P., Brotter P.,

Query Match	29.38;	Score 48;	DB 10;	Length 53;
Best Local Similarity	52.98;	Pred. No. 3.7;		

Search completed: May 23, 2001, 15:35:16
Job time: 622 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 23, 2001, 15:28:31 ; Search time 184.73 Seconds
(without alignments)
7,117 Million cell updates/sec

Title: US-08-887-977-10_COPY_207_229

Perfect score: 123

Sequence: 1 GLELLFGFFIPLMFMYCYFTIV 23

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 390729 seqs, 57163235 residues

Total number of hits satisfying chosen parameters: 390729

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_0401.*
1: /SID56/gcgdata/geneseq/geneseq/AA1980.DAT.*
2: /SID56/gcgdata/geneseq/geneseq/AA1981.DAT.*
3: /SID56/gcgdata/geneseq/geneseq/AA1982.DAT.*
4: /SID56/gcgdata/geneseq/geneseq/AA1983.DAT.*
5: /SID56/gcgdata/geneseq/geneseq/AA1984.DAT.*
6: /SID56/gcgdata/geneseq/geneseq/AA1985.DAT.*
7: /SID56/gcgdata/geneseq/geneseq/AA1986.DAT.*
8: /SID56/gcgdata/geneseq/geneseq/AA1987.DAT.*
9: /SID56/gcgdata/geneseq/geneseq/AA1988.DAT.*
10: /SID56/gcgdata/geneseq/geneseq/AA1989.DAT.*
11: /SID56/gcgdata/geneseq/geneseq/AA1990.DAT.*
12: /SID56/gcgdata/geneseq/geneseq/AA1991.DAT.*
13: /SID56/gcgdata/geneseq/geneseq/AA1992.DAT.*
14: /SID56/gcgdata/geneseq/geneseq/AA1993.DAT.*
15: /SID56/gcgdata/geneseq/geneseq/AA1994.DAT.*
16: /SID56/gcgdata/geneseq/geneseq/AA1995.DAT.*
17: /SID56/gcgdata/geneseq/geneseq/AA1996.DAT.*
18: /SID56/gcgdata/geneseq/geneseq/AA1997.DAT.*
19: /SID56/gcgdata/geneseq/geneseq/AA1998.DAT.*
20: /SID56/gcgdata/geneseq/geneseq/AA1999.DAT.*
21: /SID56/gcgdata/geneseq/geneseq/AA2000.DAT.*
22: /SID56/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	123	100.0	365	19	W48086
2	123	100.0	365	21	Y97077
3	67	54.5	355	14	R33420
4	67	54.5	355	17	B09990
5	67	54.5	358	16	R80952
6	67	54.5	360	13	R28273
7	67	54.5	360	16	R80758
8	67	54.5	360	16	R80953
9	67	54.5	1064	16	R70124
10	66	53.7	302	19	W70001
11	66	53.7	351	20	Y23825
					Human dendritic ce
					Primate (human) ch
					Human IL-8 recepto
					Human IL-8 recepto
					Recombinant high a
					Sequence in a low
					Interleukin 8 rece
					Recombinant high a
					IL8-R type 2-GBP 1
					Rodent chemokine r
					A7 times membrane

12	66	53.7	359	15	R53747	Seven transmembran
13	66	53.7	359	19	W48728	Murine V31 seven t
14	66	53.7	359	21	B21691	Murine 7TM recepto
15	66	53.7	378	21	B21699	7TM receptor prote
16	66	53.7	474	21	B36479	Rat SNORF36 recept
17	65	52.8	342	19	W80806	STR133 protein seq
18	65	52.8	342	19	W54041	Human HBMBU14 prot
19	65	52.8	342	20	Y39366	Platelet factor-4
20	65	52.8	342	20	W97783	Human HIV/SIV rece
21	65	52.8	342	20	W97784	African green monk
22	65	52.8	342	20	W97785	Pig-tailed macaque
23	65	52.8	354	15	R53932	Interleukin 8 (IL-
24	65	52.8	355	13	R28272	Sequence in a high
25	65	52.8	355	16	R80950	Recombinant high a
26	65	52.8	357	21	B19605	Human CC chemokine
27	65	52.8	357	21	Y90615	Human G protein-co
28	65	52.8	357	21	Y90649	Human mutant G pro
29	65	52.8	369	19	W51405	Mouse protease-act
30	64	52.0	312	15	R48717	G-protein coupled
31	64	52.0	312	17	W02689	G-protein coupled
32	64	52.0	350	13	R27791	Interleukin-8 rece
33	64	52.0	350	16	R68811	Interleukin-8 rece
34	64	52.0	350	16	R80756	Interleukin 8 rece
35	64	52.0	350	16	R80951	Recombinant high a
36	64	52.0	350	17	B09989	Human IL-8 recepto
37	64	52.0	1060	16	R70123	IL8-R type 1-GBP 1
38	63	51.2	29	19	Y39999	Peptide effecting
39	63	51.2	209	21	B36414	Lung cancer associ
40	63	51.2	269	21	Y44466	Rhodopsin family t
41	63	51.2	269	21	Y44366	Seven transmembran
42	63	51.2	355	15	R52749	C-C chemokine rece
43	63	51.2	355	18	W26588	Human MIP-1 alpha/
44	63	51.2	355	18	W25751	Human MIP-lalpha/R
45	63	51.2	355	21	B20571	Human CC-chemokine

ALIGNMENTS

RESULT	1
W48086	W48086 standard; Protein; 365 AA.
ID	W48086 standard; Protein; 365 AA.
XX	
AC	W48086;
XX	
DT	11-JUN-1998 (first entry)
XX	
DE	Human dendritic cell chemokine receptor.
XX	
KW	Human; thymus expressed chemokine; TECK; MIP-3alpha; MIP-3beta;
XX	receptor; dendritic cell; macrophage; inflammation; asthma.
OS	Homo sapiens.
XX	
PH	Key Location/Qualifiers
FT	Misc-difference 193
FT	/note= "encoded by CAN"
XX	
PN	W09801557-A2.
PD	15-JAN-1998.
XX	
PF	02-JUL-1997; 97WO-US10819.
XX	
PR	04-JUN-1997; 97US-0048593.
PR	05-JUL-1996; 95US-0675814.
PR	11-OCT-1996; 96US-0028329.
XX	
PA	(SCHE) SCHERING CORP.
XX	
PI	Gish KC, Schall TJ, Vicari A, Wang W, Zlotnik A;
XX	
DR	WPI; 1998-101054/09.

QY 6 FGFFIPLMFIFCYTF 21
 ||| :||: | :||| |
 Db 213 fgfvplllmfcygf 228

RESULT 4
 B09990
 ID B09990 standard; Protein; 355 AA.
 AC B09990;
 XX
 DT 20-OCT-2000 (first entry)
 XX
 DE Human IL-8 receptor protein hIL8RB.

IL-8 receptor protein; hIL8RA; hIL8RB; human; interleukin-8; drug;
 treatment; inflammatory disease; anti-tumor.

OS Homo sapiens.
 XX
 XX JP08103276-A.
 PN
 XX
 XX 23-APR-1996.
 PD

XX 06-OCT-1994; 94JP-0242534.
 PF

XX 06-OCT-1994; 94JP-0242534.
 PR

XX (TAKE) TAKEDA CHEM IND LTD.
 FA

XX WPI; 1996-253878/26.
 DR

XX N-PSDB; A40128.
 DR

XX Recombinant human interleukin 8 receptor protein, - its prepn. and
 application.

Example 2; Fig 4; 22pp; Japanese.

This invention describes a novel expression vector which carries a DNA encoding human interleukin 8 receptor protein and is expressed by pAKKO1.11/hIL8RA or pAKKO1.11/hIL8RB. Also claimed are (I) CHO cell containing the above expression vector, (II) the preparation of a recombinant human interleukin 8 receptor protein in which the above CHO cell is cultured under a condition enabling the expression of a DNA coding human interleukin 8 receptor protein, (III) a CHO cell containing a recombinant human interleukin 8 receptor protein, (IV) a recombinant human interleukin 8 receptor protein isolated from a CHO cell containing the above recombinant human interleukin 8 receptor protein, its partial peptide or their salt, (V) the screening of human interleukin 8 receptor agonist or antagonist in which the above CHO cell or its cell membrane fraction is used or the above recombinant human interleukin 8 receptor protein, its partial peptide or their salt is used (VI) a kit for screening the human interleukin 8 receptor agonist or antagonist containing the above CHO cell or its cell membrane fraction or the above recombinant human interleukin 8 receptor protein, its partial peptide or their salt, (VII) a human interleukin 8 receptor agonist or antagonist prepared by using the above screening method or the above screening kit or its salt, (VIII) an activation promoter or a migration promoter of neutrophils containing the above agonist or its salt, and an activation inhibitor or a migration inhibitor containing the above antagonist or its salt. The agonist or the antagonist can be used in drug compositions for the prevention and treatment of inflammatory diseases and anti-tumor agents. The screening method can select an agonist or an antagonist advantageously. This sequence represents the human IL-8 receptor protein hIL8RB which is described in the method of the invention.

XX Sequence 355 AA;

Query Match 54.5%; Score 67; DB 17; Length 355;

Best Local Similarity 62.5%; Pred. No. 0.009;
 Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 6 FGFFIPLMFIFCYTF 21
 ||| :||: | :||| |
 Db 213 fgfvplllmfcygf 228

RESULT 5
 R80952
 ID R80952 standard; Protein; 358 AA.
 AC R80952;
 XX

DT 24-APR-1996 (first entry)
 XX

DE Recombinant high affinity Interleukin-8 receptor subtype B.

XX IL-8A; IL-8B; receptor; monoclonal antibody; inflammatory disorder;
 KW anaphylaxis; systemic lupus erythematosus; rheumatoid arthritis;
 KW systemic necrotizing vasculitis; psoriasis; asthma; allergy; ARDS;
 KW adult respiratory distress syndrome; neutrophil detection.

OS Oryctolagus cuniculus.

XX WO9525126-A1.
 PN

XX 21-SEP-1995.
 PD

XX 09-MAR-1995; 95WO-US03032.
 PF

XX 02-MAY-1994; 94US-0237937.
 PR

XX 15-MAR-1994; 94US-0210250.
 PR

XX (REFK) REPLIGEN CORP.
 PA

XX (UYBO-) UNIV BOSTON.

XX Greenfield EA, Larosa GJ, Navarro J, Thomas KM;
 PI

XX WPI; 1995-336945/43.
 PI

XX N-PSDB; Q99951.
 DR

XX Monoclonal antibody against recombinant IL-8 receptor polypeptide -
 useful for treating inflammatory disorders, for detecting
 neutrophil(s) and for isolating IL-8 receptor from liq.mixt.

Claim 6; Fig 3A-B; 74pp; English.

XX Monoclonal antibodies were raised against recombinant interleukin-8
 (IL-8) receptor subtypes A and B from both human and rabbit sources
 (R80950-53 encoded by Q99949-52). The A subtype receptor (IL-8RA) is
 a high affinity receptor and the B subtype receptor (IL-8RB) is a
 low affinity receptor. The monoclonal antibody (mAb) pref. binds to
 the IL-8 binding domain thus blocking its activation. The mAbs are
 useful for treating inflammatory disorders (see key words) and for
 detecting the presence of neutrophils in a biological sample. The
 mAbs are also useful in the isolation of IL-8 receptors from a mixture.

XX Sequence 358 AA;

Query Match 54.5%; Score 67; DB 16; Length 358;

Best Local Similarity 62.5%; Pred. No. 0.0091;
 Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 6 FGFFIPLMFIFCYTF 21
 ||| :||: | :||| |
 Db 216 fgfvplllmfcygf 231

RESULT 6
 R28273

ID R28273 standard; Protein; 360 AA.

XX

AC R28273;

XX

DT 04-APR-1993 (first entry)

XX

DE Sequence in a low affinity recombinant human interleukin-8 (IL-8) receptor polypeptide in 4AB.

XX

KW IL-8 receptor polypeptide; G-protein-coupled receptor.

XX

OS Homo sapiens.

XX

PN W09218641-A.

XX

PD 29-OCT-1992.

XX

PF 10-APR-1992; 92WO-US02977.

XX

PR 10-APR-1991; 91US-0685101.

XX

PR 09-JUL-1991; 91US-0726606.

XX

PR 09-DEC-1991; 91US-0803842.

XX

PA (REPK) REPLIGEN CORP.

XX

PA (UTBO-) UNIV BOSTON.

XX

PI Navarro J, Thomas KM, Witt DP;

XX

DR WPI; 1992-382123/46.

XX

DR N-PSDB; Q30012.

XX

PS Recombinant mammalian interleukin-8 receptor - used for screening

XX

PT interleukin-8 binding antagonists, used to treat inflammation

XX

PS Disclosure; Fig 2; 71pp; English.

XX

CC Rabbit high affinity IL-8 receptor gene was isolated from rabbit

XX

CC peritoneal neutrophils and used as a source of poly(A)+ RNA, to

XX

CC produce a rabbit neutrophil cDNA library. 250,000 recombinant

XX

CC plaques were screened for those which hybridized to an antisense

XX

CC oligonucleotide (Q30015). This probe was designed based on the

XX

CC sequence derived from the second transmembrane domain of G-protein-

XX

CC coupled receptors. After tertiary screening, six plaques were

XX

CC isolated. The insert of one of these plaques, termed F3R was of 2.5

XX

CC kb in size. This insert was sequenced. The protein deduced from

XX

CC the F3R clone demonstrates that it belongs to the family of

XX

CC G-protein-coupled receptors. The deduced protein sequence

DT

XX

DE 26-MAR-1996 (first entry)

XX

XX Interleukin 8 receptor B.

XX

KW Interleukin; IL-8; inflammation; psoriasis; dermatitis;

XX

KW rheumatoid arthritis; inflammatory bowel disease;

XX

KW chronic lung inflammation; treatment; antibody;

XX

KW affinity purification; detection.

XX

OS Homo sapiens.

XX

PN US5440021-A.

XX

PD 08-AUG-1995.

XX

PF 29-MAR-1991; 91US-0677211.

XX

PR 25-FEB-1994; 94US-0202056.

XX

PR 29-MAR-1991; 91US-0677211.

XX

PA (CHUN/) CHUNTHARAPAI A.

XX

PA (HEBE/) HEBERT C.

XX

PA (KIMK/) KIM K J.

XX

PA (LEEJ/) LEE J.

XX

PI Chuntharapai A, Hebert C, Kim KJ, Lee J;

XX

DR WPI; 1995-283151/37.

XX

DR N-PSDB; Q99008.

XX

XX New antibodies against interleukin 8 type B receptor - used to treat

XX

PT or prevent inflammation, also for detecting receptor expression and

XX

PT purific.

XX

PS Disclosure; Columns 53-56; 62pp; English.

XX

XX Antibodies directed against the interleukin-8 receptor B can be used

XX

CC to treat or prevent inflammation e.g. psoriasis, dermatitis,

XX

CC rheumatoid arthritis and particularly inflammatory bowel disease and

XX

CC chronic lung inflammation. When immobilised, these antibodies may

XX

CC be used to detect interleukin-8 receptor B expression in cells and

XX

CC tissues and for affinity purification of interleukin-8 receptor B

DT

XX

DE 26-MAR-1996 (first entry)

XX

XX Interleukin 8 receptor B.

XX

KW Interleukin; IL-8; inflammation; psoriasis; dermatitis;

XX

KW rheumatoid arthritis; inflammatory bowel disease;

XX

KW chronic lung inflammation; treatment; antibody;

XX

KW affinity purification; detection.

XX

OS Homo sapiens.

XX

PN US5440021-A.

XX

PD 08-AUG-1995.

XX

PF 29-MAR-1991; 91US-0677211.

XX

PR 25-FEB-1994; 94US-0202056.

XX

PR 29-MAR-1991; 91US-0677211.

XX

PA (CHUN/) CHUNTHARAPAI A.

XX

PA (HEBE/) HEBERT C.

XX

PA (KIMK/) KIM K J.

XX

PA (LEEJ/) LEE J.

XX

PI Chuntharapai A, Hebert C, Kim KJ, Lee J;

XX

DR WPI; 1995-283151/37.

XX

DR N-PSDB; Q99008.

XX

XX New antibodies against interleukin 8 type B receptor - used to treat

XX

PT or prevent inflammation, also for detecting receptor expression and

XX

PT purific.

XX

PS Disclosure; Columns 53-56; 62pp; English.

XX

XX Antibodies directed against the interleukin-8 receptor B can be used

XX

CC to treat or prevent inflammation e.g. psoriasis, dermatitis,

XX

CC rheumatoid arthritis and particularly inflammatory bowel disease and

XX

CC chronic lung inflammation. When immobilised, these antibodies may

XX

CC be used to detect interleukin-8 receptor B expression in cells and

XX

CC tissues and for affinity purification of interleukin-8 receptor B

Sequence 360 AA;

Query Match

54.5%; Score 67; DB 16; Length 360;

Best Local Similarity 62.5%; Pred. No. 0.0091;

Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 6 FGFFIPLMFIFCYTF 21

|||||:|||||

Db 218 fgfvpllmficygf 233

RESULT 8

R80953

ID R80953 standard; Protein; 360 AA.

XX

AC R80953;

XX

DT 24-APR-1996 (first entry)

XX

DE Recombinant high affinity interleukin-8 receptor subtype B.

XX

KW IL-8A; IL-8B; receptor; monoclonal antibody; inflammatory disorder;

XX

KW anaphylaxis; systemic lupus erythematosus; rheumatoid arthritis;

XX

KW systemic necrotising vasculitis; psoriasis; asthma; allergy; ARDS;

XX

XX adult respiratory distress syndrome; neutrophil detection.

XX

XX Homo sapiens.

XX

PN W09525126-A1.
 XX 21-SEP-1995.
 XX 09-MAR-1995; 95WO-US03032.
 XX 02-MAY-1994; 94US-0237937.
 PR 15-MAR-1994; 94US-0210250.
 XX (REPK) REPLIGEN CORP.
 PA (UYBO-) UNIV BOSTON.
 XX Greenfield EA, Larosa GJ, Navarro J, Thomas KM;
 PI Witt DT;
 XX WPI: 1995-336945/43.
 DR N-PSDB; Q99952.
 XX Monoclonal antibody against recombinant IL-8 receptor polypeptide -
 PT useful for treating inflammatory disorders, for detecting
 PT neutrophil(s) and for isolating IL-8 receptor from liq.mixt.
 XX Claim 5; Fig 4A-B; 74pp; English.
 XX Monoclonal antibodies were raised against recombinant interleukin-8
 CC (IL-8) receptor subtypes A and B from both human and rabbit sources
 CC (R80950-53 encoded by Q99949-52). The A subtype receptor (IL-8RA) is
 CC a high affinity receptor and the B subtype receptor (IL-8RB) is a
 CC low affinity receptor. The monoclonal antibody (mAb) pref. binds to
 CC the IL-8 binding domain thus blocking its activation. The mAbs are
 CC useful for treating inflammatory disorders (see key words) and for
 CC detecting the presence of neutrophils in a biological sample. The
 CC mAbs are also useful in the isolation of IL-8 receptors from a mixture.
 XX
 SQ Sequence 360 AA;
 Query Match 54.5%; Score 67; DB 16; Length 360;
 Best Local Similarity 62.5%; Pred. No. 0.0091;
 Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 OY 6 FGFFPLMFMEFYCYTF 21
 Db 218 fgfvpllmficygf 233
 RESULT 9
 ID R70124 standard; Protein; 1064 AA.
 XX R70124;
 XX 14-FEB-1996 (first entry)
 XX IL-8 R type 2-GPB 130 fusion protein.
 XX Hybrid peptide; malaria parasite; Plasmodium falciparum; fusion protein;
 KW red blood cell; cytokine receptor; glycoporphin binding peptide 130;
 KW GBP 130; GBPH; glycoporphin binding peptide homologue; glycoporphin A.
 XX Chimeric Homo sapiens.
 OS Chimeric Plasmodium falciparum.
 XX W09506737-A.
 PN 09-MAR-1995.
 XX 01-SEP-1994; 94WO-GB01900.
 XX 03-SEP-1993; 93GB-0018350.
 PR 23-AUG-1994; 94GB-0017021.
 XX (PREN/) PRENDERCAST K F.

XX Prendergast KF;
 PI WPI: 1995-115452/15.
 DR New hybrid peptide(s) for binding cytokine(s) - comprising a
 PT malaria parasite peptide capable of binding a red blood cell and
 PT a receptor peptide.
 XX Example A; Page 80-82; 93pp; English.
 XX Hybrid peptides for binding cytokines, comprising a malaria parasite
 CC (Plasmodium falciparum) peptide (capable of binding to a red blood
 CC cell (RBC)) and a receptor peptide are claimed. R70103-25 are examples
 CC of these hybrid peptides. R70124 is a fusion of interleukin 8 receptor
 CC type 2 and glycoporphin binding protein (GBP) 130. The use of cytokine
 CC receptors not normally found on RBCs means that the cytokine can bind
 CC harmlessly to the RBC without deleterious effect. The RBC protects the
 CC hybrid peptides from excretion from the kidney, and due to steric
 CC hindrance prevents the cytokines binding to a receptor in another cell.
 CC GBP 130 or GBPH (GBP homologue) are the pref. malaria parasite peptides
 CC used, others include EBA 175 (175 kDa erythrocyte binding antigen),
 CC PMMSA (pre major merozoite surface antigen) and the Duffy binding
 CC receptor molecule (eg. exhibited by Plasmodium vivax). These peptides
 CC bind to pref. glycoporphin A, B and C, sialo glycoproteins, found on
 CC the surface of RBCs. The hybrid peptides are thus used to lower
 CC the levels of free cytokines in the circulation to reduce pathological
 CC damage.
 XX Sequence 1064 AA;
 Query Match 54.5%; Score 67; DB 16; Length 1064;
 Best Local Similarity 62.5%; Pred. No. 0.027;
 Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 OY 6 FGFFPLMFMEFYCYTF 21
 Db 212 fgfvpllmficygf 227
 RESULT 10
 ID W70001 standard; Protein; 302 AA.
 XX W70001;
 XX 20-OCT-1998 (first entry)
 XX Rodent chemokine receptor 941D12 amino acid sequence.
 XX Chemokine; primate; human; rodent; chemokine receptor; asthma;
 KW inflammatory response; immune response; leukocyte migration; GPCR;
 KW leukocyte adhesion; chemoattractant; modulation; antiviral response;
 KW cellular morphology modification response; G-protein coupled receptor;
 KW phosphoinositide lipid turnover; abnormal proliferation; regeneration;
 atrophy; 941D12.
 XX Mus sp.
 OS W09832858-A2.
 PN 30-JUL-1998.
 XX 22-JAN-1998; 98WO-US00902.
 XX 23-JAN-1997; 97US-0036715.
 XX (SCHE) SCHERING CORP.
 PA Gorman DM, Hedrick JA, Mattson JD, Soto-trejo H;
 PI Zlotnik A;
 XX

DR WPI: 1998-427954/36.
XX N-PSDB: V43795.

PT Rodent and primate chemokines and chemokine receptors - useful
PT diagnostically and therapeutically to treat conditions associated
PT with abnormal physiology or development e.g. inflammatory conditions
XX
PS Claim 5; Pages 97-99; 105pp; English.

XX This represents a rodent chemokine receptor 941D12 amino acid sequence.
CC The invention provides novel primate and rodent chemokines and chemokine
CC receptors. The chemokines, receptors and binding compounds (optionally
CC antibodies/fragments specifically binding the chemokines) are useful
CC therapeutically to treat conditions associated with abnormal physiology
CC or development e.g. inflammatory conditions such as asthma. Chemokines
CC are important in immune and inflammatory responses in that they induce
CC leukocyte migration and adhesion. They are also chemoattractants for
CC several cells involved in inflammation and can induce other biological
CC responses e.g. modulation of second messenger levels (e.g. Ca⁺⁺);
CC cellular morphology modification responses, phosphoinositide lipid
CC turnover, possible antiviral responses etc. The chemokine receptors of
CC the invention exhibit structural properties of G-protein coupled
CC receptors (GPCR), although their ligands have not yet been identified.
CC The chemokine and chemokine receptor polypeptides are useful to produce
CC ligand-receptor complexes in vivo or in assay techniques. Assays may
CC also involve chemical antagonists which block complex production or
CC utilise competitive binding. Binding compounds identified (agonists or
CC antagonists) can be used to modulate the physiological responses in cells
CC (especially neurons, macrophages or lymphocytes) to treat e.g. abnormal
CC proliferation, regeneration, generation and atrophy. The polypeptides
CC are also used to produce antibodies useful diagnostically, for drug
CC screening or for polypeptide purification. The polynucleotides are useful
CC to produce probes for detecting the polypeptides, and to isolate the
CC polypeptides or related sequences, especially from other species. They
CC also allow transformation of cells for polypeptide production.

XX Sequence 302 AA;

Query Match 53.7%; Score 66; DB 19; Length 302;
Best Local Similarity 45.5%; Pred. No. 0.011;
Matches 10; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 2 LELFGFFIPLMFIMFYTFIV 23
:: |||:: || ||: |:
Db 203 iqmgtlglflpiltmilysgii 224

RESULT 11

ID Y23825 standard; Protein; 351 AA.

XX AC Y23825;

XX 15-SEP-1999 (first entry)

XX A7 times membrane penetrating type receptor protein ET60.

XX 7 times membrane-penetrating type receptor protein; ET60;
XX leukocyte function; control; drug.

XX Unidentified.

XX JP11155573-A.

XX 15-JUN-1999.

XX 27-NOV-1997; 97JP-0325823.

XX 27-NOV-1997; 97JP-0325823.

XX (ASAH) ASAHI KASEI KOGYO KK.

XX SQ

DR WPI: 1999-398070/34.
XX N-PSDB: X86032.

PT New 7 times membrane-penetrating type receptor protein ET60 - useful
PT for detecting drug controlling function of leukocyte
XX
XX Claim 1; Page 17-18; 20pp; Japanese.

XX The present sequence represents a 7 times membrane-penetrating type
CC receptor protein ET60. The 7 times membrane-penetrating type
CC receptor protein ET60 can be used for detecting a drug controlling
CC the function of leukocyte.

XX Sequence 351 AA;

Query Match 53.7%; Score 66; DB 20; Length 351;
Best Local Similarity 45.5%; Pred. No. 0.013;
Matches 10; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 2 LELFGFFIPLMFIMFYTFIV 23
:: |||:: || ||: |:
Db 203 iqmgtlglflpiltmilysgii 224

RESULT 12

R53747

ID R53747 standard; Protein; 359 AA.

XX AC R53747;

XX 03-FEB-1995 (first entry)

XX Seven transmembrane receptor (V31) partial sequence of mouse.

XX Primer: seven transmembrane receptor; receptor; amplification; PCR;
XX polymerase chain reaction.

XX Mus musculus.

XX WO9412635-A.

XX 09-JUN-1994.

XX 17-NOV-1993; 93WO-US11153.

XX 17-NOV-1992; 92US-0977452.

XX (ICOS-) ICOS CORP.

XX Godiska R, Gray PW, Schweickart VL;

XX WPI: 1994-200264/24.

XX N-PSDB; Q66164.

XX DNA encoding seven transmembrane receptors - used to develop
XX prods. for use as therapeutic or diagnostic agents for conditions
XX involving the receptors.

XX Example 5; Page 61-62; 100pp; English.

XX Two primers (Q66148, Q66149) were used to amplify human genomic DNA
CC purified from leukocytes. Approximately 1000 clones were isolated
CC after the initial amplification reaction and probed with sequences
CC specific for seven transmembrane receptors IL8R1, AT2R and R20.
CC Clones which did not hybridise were then chosen for sequence
CC analysis. Three new clones were identified that appeared to encode
CC seven transmembrane receptor segments. Two more primers (Q66151,
CC Q66152) were used to isolate a full length version of one of the
CC human V31 clone (See Q66153). A fragment of the human clone was used
CC to isolate a V31 genomic clone of the mouse from a library.

XX Sequence 359 AA;

XX SQ

Query Match 53.7%; Score 66; DB 15; Length 359;
Best Local Similarity 42.9%; Pred. No. 0.013; Mismatches 5; Indels 0; Gaps 0;

Matches 9; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 3 ELLFGFFIPLMFIFCYTFIV 23

Db 207 qmvfgflvpmlamsfcylili 227

RESULT 13

W48728
ID W48728 standard; Protein; 359 AA.

XX AC W48728;

XX DT 25-SEP-1998 (first entry)

XX DE Murine V31 seven transmembrane (7TM) receptor.

XX KW V28; placenta; seven transmembrane receptor; 7TM; signal transduction;

XX KW immunology; inflammation; V31; ss.

XX OS Mus sp.

XX PN US5759804-A.

XX PD 02-JUN-1998.

XX PF 17-NOV-1993; 93US-0153848.

XX PR 17-NOV-1992; 92US-0977452.

XX PA (ICOS-) ICOS CORP.

XX PI Godiska R, Gray PW, Schweickart VL;

XX DR WPI: 1998-332132/29.

XX DR N-PSDB; V18351.

XX PT DNA encoding V28 seven transmembrane receptor polypeptide - useful

XX PT for producing recombinant polypeptide and anti-V28 antibodies, and

XX PT in screening assays for V28 agonists and antagonists

XX PS Example 5; Columns 55-58; 56pp; English.

XX CC The present sequence represents the murine V31 seven transmembrane

XX CC (7TM) receptor which is encoded by the murine V31 genomic DNA (V18351)

XX CC isolated from a mouse genomic library. The invention claims for the

XX CC full length V28 genomic DNA sequence isolated from a human placenta

XX CC genomic library. V28 (W48722) and V31 proteins are seven transmembrane

XX CC (7TM) receptors which are probably involved in signal transduction.

XX CC The invention also claims that cells transformed with V28 DNA can be

XX CC used to produce the recombinant polypeptide, to produce anti-V28

XX CC antibodies or in screening assays for V28 agonists or antagonists. The

XX CC antibodies, agonists and antagonists could then be used to modulate

XX CC V28 receptor-ligand binding, for e.g. in immunological and/or

XX CC inflammatory events in vivo.

XX SQ Sequence 359 AA;

Query Match 53.7%; Score 66; DB 19; Length 359;
Best Local Similarity 42.9%; Pred. No. 0.013;

Matches 9; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 3 ELLFGFFIPLMFIFCYTFIV 23

Db 207 qmvfgflvpmlamsfcylili 227

RESULT 14

B21691

ID B21691 standard; Protein; 359 AA.

XX AC B21691;

XX DT 26-JAN-2001 (first entry)

XX DE Murine 7TM receptor V31cDNA clone protein.

XX KW Seven transmembrane receptor; 7TM; heptahelical; serpentine;

XX KW G-protein-coupled; V28; V31; V112; R20; R2; R12; RM3; gene therapy;

XX KW cancer.

XX OS Mus sp.

XX PN US6107475-A.

XX PD 22-AUG-2000.

XX PF 26-APR-1999; 99US-0299843.

XX PR 17-MAY-1994; 94US-0245242.

XX PR 01-JUN-1998; 98US-0088337.

XX PR 17-NOV-1992; 92US-0977452.

XX PR 17-NOV-1993; 93US-0153848.

XX PA (ICOS-) ICOS CORP.

XX PI Schweickart VL, Gray PW, Godiska R;

XX DR WPI: 2000-571335/53.

XX DR N-PSDB; A91711.

XX PT Polynucleotide encoding seven transmembrane receptors, antibody

XX PT specific to the receptor, agonist and antagonist of the receptor useful

XX PT for treating inflammation in a mammal

XX PS Example 4; Columns 57-60; 61pp; English.

XX CC The present sequence is a novel seven transmembrane (7TM) receptors

XX CC (also known as heptahelical, serpentine or G-protein-coupled receptors).

XX CC The coding sequence for the present sequence may be used for gene

XX CC therapy for diseases such as cancer.

XX SQ Sequence 359 AA;

Query Match 53.7%; Score 66; DB 21; Length 359;
Best Local Similarity 42.9%; Pred. No. 0.013;

Matches 9; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 3 ELLFGFFIPLMFIFCYTFIV 23

Db 207 qmvfgflvpmlamsfcylili 227

RESULT 15

B21699

ID B21699 standard; Protein; 378 AA.

XX AC B21699;

XX DT 26-JAN-2001 (first entry)

XX DE 7TM receptor protein.

XX KW Seven transmembrane receptor; 7TM; heptahelical; serpentine;

XX KW G-protein-coupled; V28; V31; V112; R20; R2; R12; RM3; gene therapy;

XX KW cancer.

XX OS Unidentified.

XX PN US6107475-A.

```

XX 22-AUG-2000.
PD
XX
XX PF 26-APR-1999; 99US-0299843.
XX
XX PR 17-MAY-1994; 94US-0245242.
XX
XX PR 01-JUN-1998; 98US-0088337.
XX
XX PR 17-NOV-1992; 92US-0977452.
XX
XX PR 17-NOV-1993; 93US-0153848.
XX
XX PA (ICOS-) ICOS CORP.
XX
XX PI Schweickart VL, Gray PW, Godiska R;
XX
XX DR WPI; 2000-571335/53.
XX
XX DR N-PSDB; A91745.
XX
XX PT Polynucleotide encoding seven transmembrane receptors, antibody
XX specific to the receptor, agonist and antagonist of the receptor useful
XX for treating inflammation in a mammal -
XX
XX PS Disclosure; Columns 111-112; 61pp; English.
XX
XX CC The present sequence is a novel seven transmembrane (7TM) receptors
XX (also known as heptahelical, serpentine or G-protein-coupled receptors).
XX CC The coding sequence for the present sequence may be used for gene
XX CC therapy for diseases such as cancer.
XX
XX SQ Sequence 378 AA;

Query Match 53.7%; Score 66; DB 21; Length 378;
Best Local Similarity 42.9%; Pred. No. 0.014;
Matches 9; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

Qy 3 ELLEGFPIPLMFIFCYTFIV 23
Db ::|||::|::|::|::|
227 qmvfgflvpmlamsfcylili 247

```

Search completed: May 23, 2001, 15:28:31
Job time: 408 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 23, 2001, 15:30:07 ; Search time 95.91 Seconds
(without alignments)
4.607 Million cell updates/sec

Title: US-08-887-977-10_COPY_207_229
Perfect score: 123
Sequence: 1 GLELLFGFTPLMFIFCYFTIV 23

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 185757 seqs, 19210857 residues

Total number of hits satisfying chosen parameters: 185757

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
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6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	67	54.5	115	4	US-08-513-974B-356
2	67	54.5	355	1	Sequence 356, App
3	67	54.5	355	1	Sequence 1, Appli
4	67	54.5	355	1	Sequence 8, Appli
5	67	54.5	355	2	Sequence 5, Appli
6	67	54.5	355	4	Sequence 8, Appli
7	67	54.5	355	5	Sequence 8, Appli
8	66	53.7	359	3	Sequence 24, Appl
9	66	53.7	359	3	Sequence 24, Appl
10	66	53.7	359	3	Sequence 24, Appl
11	66	53.7	359	3	Sequence 24, Appl
12	65	52.8	342	2	Sequence 2, Appli
13	65	52.8	342	1	Sequence 2, Appli
14	65	52.8	407	2	Sequence 3, Appli
15	64	52.0	312	1	Sequence 38, Appl
16	64	52.0	312	5	Sequence 38, Appl
17	64	52.0	350	1	Sequence 1, Appli
18	64	52.0	350	1	Sequence 2, Appli
19	64	52.0	350	1	Sequence 7, Appli
20	64	52.0	350	1	Sequence 1, Appli
21	64	52.0	350	1	Sequence 2, Appli
22	64	52.0	350	1	Sequence 1, Appli
23	64	52.0	350	2	Sequence 2, Appli
24	64	52.0	350	2	Sequence 1, Appli
25	64	52.0	350	2	Sequence 1, Appli
26	64	52.0	350	2	Sequence 2, Appli
27	64	52.0	350	2	Sequence 2, Appli

28	64	52.0	350	2	US-08-801-228-2	Sequence 2, Appli
29	64	52.0	350	3	US-09-104-296-2	Sequence 2, Appli
30	64	52.0	350	4	US-08-446-669-7	Sequence 7, Appli
31	64	52.0	350	5	PCT-US95-00476-7	Sequence 7, Appli
32	63	51.2	355	1	US-08-012-988A-2	Sequence 2, Appli
33	63	51.2	355	1	US-08-450-393A-5	Sequence 5, Appli
34	63	51.2	355	4	US-08-446-669-5	Sequence 5, Appli
35	63	51.2	355	5	PCT-US95-00476-5	Sequence 5, Appli
36	62	50.4	115	4	US-08-513-974B-351	Sequence 351, App
37	62	50.4	368	4	US-08-709-838-2	Sequence 2, Appli
38	62	50.4	368	4	US-08-829-839-2	Sequence 2, Appli
39	62	50.4	482	2	US-08-876-874-2	Sequence 2, Appli
40	61	49.6	358	1	US-08-153-848-19	Sequence 19, Appl
41	61	49.6	358	3	US-09-299-843A-19	Sequence 19, Appl
42	61	49.6	358	5	PCT-US93-11153-19	Sequence 19, Appl
43	61	49.6	361	2	US-08-902-294-2	Sequence 2, Appli
44	61	49.6	361	3	US-09-178-637-2	Sequence 2, Appli
45	61	49.6	378	1	US-08-383-750-2	Sequence 2, Appli

ALIGNMENTS

```

RESULT 1
US-08-513-974B-356
; Sequence 356, Application US/08513974B
; Patent No. 6114139
; GENERAL INFORMATION:
; APPLICANT: Hinuma, Shuji
; APPLICANT: Hosoya, Masaki
; APPLICANT: Fujii, Ryo
; APPLICANT: Ohtaki, Tetsuya
; APPLICANT: Fukusumi, Shoji
; APPLICANT: Ongi, Kazuhiko
; TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
; NUMBER OF SEQUENCES: 380
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
; STREET: 130 Water Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/513,974B
; FILING DATE: 14-SEP-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP95/01599
; FILING DATE: 10-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-093989
; FILING DATE: 19-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-057186
; FILING DATE: 16-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-007177
; FILING DATE: 20-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-326611
; FILING DATE: 28-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-270017
; FILING DATE: 02-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-236357

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;; FILING DATE: 30-SEP-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: JP 6-236356
;; FILING DATE: 30-SEP-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: JP 6-189274
;; FILING DATE: 11-AUG-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: JP 6-189273
;; FILING DATE: 11-AUG-1994
;; APPLICATION NUMBER: JP 6-189272
;; FILING DATE: 11-AUG-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Resnick, David S.
;; REGISTRATION NUMBER: 34,235
;; REFERENCE/DOCKET NUMBER: 45753
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 617-523-3400
;; TELEFAX: 617-523-6440
;; INFORMATION FOR SEQ ID NO: 356:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 115 amino acids
;; TYPE: amino acid
;; STRANDEDNESS:
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-08-513-974B-356

Query Match 54.5%; Score 67; DB 4; Length 115;
Best Local Similarity 62.5%; Pred. No. 0.0058;
Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 6 FGFPIPLMFIFCYTF 21
DB 74 FGLVPLLLIMLCYGF 89

RESULT 2
US-07-759-568-1
; Sequence 1, Application US/07759568
; Patent No. 5374506
; GENERAL INFORMATION:
; APPLICANT: Murphy, Philip M.
; TITLE OF INVENTION: Cloning of cDNA Encoding a Functional
; TITLE OF INVENTION: Human Interleukin-8 Receptor
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cushman, Darby & Cushman
; STREET: 1615 L Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036-5601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 19910913
; APPLICATION NUMBER: US/07/759,568
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Scott, Watson T.
; REGISTRATION NUMBER: 26581
; REFERENCE/DOCKET NUMBER: WTS/5683/91535/WBH
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3000
; TELEFAX: 202-822-0944
; TELEX: 6714627 cush
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-759-568-1

;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 355 amino acids
;; TYPE: AMINO ACID
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-07-759-568-1

Query Match 54.5%; Score 67; DB 1; Length 355;
Best Local Similarity 62.5%; Pred. No. 0.018;
Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 6 FGFPIPLMFIFCYTF 21
DB 213 FGFIVPLLLIMLCYGF 228

RESULT 3
US-08-450-393A-8
; Sequence 8, Application US/08450393A
; Patent No. 5707815
; GENERAL INFORMATION:
; APPLICANT: Charo, Israel
; APPLICANT: Coughlin, Shaun
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
; TITLE OF INVENTION: PROTEIN RECEPTORS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
; STREET: 5 Palo Alto Square
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,393A
; FILING DATE: May 25, 1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Cserr, Luann
; REGISTRATION NUMBER: 31,822
; REFERENCE/DOCKET NUMBER: UCAL-237/020US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5165
; TELEFAX: 415-8857-0663
; TELEX: 380816CooleyPA
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-450-393A-8

Query Match 54.5%; Score 67; DB 1; Length 355;
Best Local Similarity 62.5%; Pred. No. 0.018;
Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 6 FGFPIPLMFIFCYTF 21
DB 213 FGFIVPLLLIMLCYGF 228

RESULT 4
US-08-390-000A-5

; Sequence 5, Application US/083900000A
; Patent No. 5985383
; GENERAL INFORMATION:
; APPLICANT: Sealfon, Stuart C.
; TITLE OF INVENTION: Cloning and Expression of
; TITLE OF INVENTION: Gonadotropin-Releasing Hormone Receptor
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/390,000A
; FILING DATE: 17-FEB-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 6923-052
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-390-000A-5

Query Match 54.5%; Score 67; DB 2; Length 355;
Best Local Similarity 62.5%; Pred. No. 0.018;
Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 6 FGFFPLMFMYCYTF 21
Db 213 FGFIPLMLFCYGF 228

RESULT 5
US-08-446-669-8
; Sequence 8, Application US/08446669
; Patent No. 6132987
; GENERAL INFORMATION:
; APPLICANT: Charo, Israel
; APPLICANT: Coughlin, Shaun
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
; TITLE OF INVENTION: PROTEIN RECEPTORS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
; STREET: 5 Palo Alto Square
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,669

; FILING DATE: May 25, 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Neeley, Richard
; REGISTRATION NUMBER: 30,092
; REFERENCE/DOCKET NUMBER: UCAL-237/01US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5000
; TELEFAX: 415-857-0663
; TELEX: 380816COOLEYPA
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; US-08-446-669-8

Query Match 54.5%; Score 67; DB 4; Length 355;
Best Local Similarity 62.5%; Pred. No. 0.018;
Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 6 FGFFPLMFMYCYTF 21
Db 213 FGFIPLMLFCYGF 228

RESULT 6
PCT-US95-00476-8
; Sequence 8, Application PC/TUS9500476
; GENERAL INFORMATION:
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
; TITLE OF INVENTION: PROTEIN RECEPTORS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Robbins, Berliner & Carson
; STREET: 201 N. Figueroa Street, 5th Floor
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90012-2628
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/00476
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Berliner, Robert
; REGISTRATION NUMBER: 20,121
; REFERENCE/DOCKET NUMBER: 5555-291
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 310-977-1001
; TELEFAX: 310-977-1003
; TELEX:
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; PCT-US95-00476-8

Query Match 54.5%; Score 67; DB 5; Length 355;
Best Local Similarity 62.5%; Pred. No. 0.018;

Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 6 FGFFIPLMFICYTF 21
 ||| :||: |:||| |
 Db 213 FGFIPLMLFCYGF 228

RESULT 7

US-08-202-056-7
 ; Sequence 7, Application US/08202056
 ; Patent No. 5440021
 ; GENERAL INFORMATION:
 ; APPLICANT: Chuntharapai, Anan
 ; APPLICANT: Hebert, Caroline
 ; APPLICANT: Kim, Kyung Jin
 ; APPLICANT: Lee, James
 ; TITLE OF INVENTION: Antibodies to Human IL-8 Type B Receptor
 ; NUMBER OF SEQUENCES: 8
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genentech, Inc.
 ; STREET: 460 Point San Bruno Blvd
 ; CITY: South San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94080

COMPUTER READABLE FORM:
 MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk

COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: patin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/202,056
 FILING DATE: 25-FEB-1994

CLASSIFICATION: 436

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/677211

FILING DATE: 29-MAR-1991

ATTORNEY/AGENT INFORMATION:

NAME: Love, Richard B.

REGISTRATION NUMBER: 34,659

REFERENCE/DOCKET NUMBER: 706P3

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415/225-5530

TELEFAX: 415/952-9881

TELEX: 910/371-7168

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 360 amino acids

TYPE: amino acid

TOPOLOGY: linear

US-08-202-056-7

Query Match 54.5%; Score 67; DB 1; Length 360;

Best Local Similarity 62.5%; Pred. No. 0.016;

Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 6 FGFFIPLMFICYTF 21
 ||| :||: |:||| |
 Db 218 FGFIPLMLFCYGF 233

RESULT 8

US-08-153-848-24
 ; Sequence 24, Application US/08153848
 ; Patent No. 5759804
 ; GENERAL INFORMATION:
 ; APPLICANT: Godiska, Ronald
 ; APPLICANT: Gray, Patrick W.
 ; APPLICANT: Schweikart, Vicki L.
 ; TITLE OF INVENTION: No. 5759804el Seven Transmembrane Receptors
 ; NUMBER OF SEQUENCES: 64
 ; CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
 ADDRESSEE: Bicknell
 STREET: 6300 Sears Tower, 233 South Wacker Drive
 CITY: Chicago
 STATE: Illinois
 COUNTRY: USA

ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/153,848

FILING DATE:

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/977,452

FILING DATE: 17-NOV-1992

ATTORNEY/AGENT INFORMATION:

NAME: No. 5759804and, Greta E.

REGISTRATION NUMBER: 35,302

REFERENCE/DOCKET NUMBER: 31794

TELECOMMUNICATION INFORMATION:

TELEPHONE: (312) 474-6300

TELEFAX: (312) 474-0448

TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 24:

SEQUENCE CHARACTERISTICS:

LENGTH: 359 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-153-848-24

Query Match 53.7%; Score 66; DB 1; Length 359;

Best Local Similarity 42.9%; Pred. No. 0.025;

Matches 9; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 3 ELFGFFIPLMFICYTFIV 23
 :||| :||: |:||| |
 Db 207 QMVEGFLVPLMLAMSFYLI 227

RESULT 9

US-09-299-843A-24
 ; Sequence 24, Application US/09299843A
 ; Patent No. 6107475
 ; GENERAL INFORMATION:
 ; APPLICANT: Godiska, Ronald
 ; APPLICANT: Gray, Patrick W.
 ; APPLICANT: Schweikart, Vicki L.
 ; TITLE OF INVENTION: No. 6107475el Seven Transmembrane Receptors
 ; NUMBER OF SEQUENCES: 66
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
 ; ADDRESSEE: Borun
 ; STREET: 6300 Sears Tower, 233 South Wacker Drive
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: USA
 ; ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/299,843A

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 09/088,337
FILING DATE: 01-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/153,848
FILING DATE: 17-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Jill E. Uhl
REGISTRATION NUMBER: 43,213
REFERENCE/DOCKET NUMBER: 27866/32059B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX:
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 359 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-299-843A-24

Query Match 53.7%; Score 66; DB 3; Length 359;
Best Local Similarity 42.9%; Pred. No. 0.025;
Matches 9; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

Qy 3 ELLGFFFIPLMFICYTFIV 23
Db 207 QMVFGFLVPLMAMSCYLI 227

RESULT 10
PCT-US93-11153-24
Sequence 24, Application PC/TUS9311153
GENERAL INFORMATION:
APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schweikart, Vicki L.
TITLE OF INVENTION: Novel Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Bicknell
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/11153
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Noland, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31794
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 359 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-299-843A-24

LENGTH: 359 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US93-11153-24

Query Match 53.7%; Score 66; DB 5; Length 359;
Best Local Similarity 42.9%; Pred. No. 0.025;
Matches 9; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

Qy 3 ELLGFFFIPLMFICYTFIV 23
Db 207 QMVFGFLVPLMAMSCYLI 227

RESULT 11
US-09-299-843A-66
Sequence 66, Application US/09299843A
Patent No. 6107475
GENERAL INFORMATION:
APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schweikart, Vicki L.
TITLE OF INVENTION: No. 6107475el Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/299,843A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/088,337
FILING DATE: 01-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/153,848
FILING DATE: 17-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Jill E. Uhl
REGISTRATION NUMBER: 43,213
REFERENCE/DOCKET NUMBER: 27866/32059B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX:
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
LENGTH: 378 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-299-843A-66

Query Match 53.7%; Score 66; DB 3; Length 378;
Best Local Similarity 42.9%; Pred. No. 0.027;
Matches 9; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

ADDRESS: Cushman, Darby & Cushman
STREET: 1615 L Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20036-5601
COMPUTER READABLE FORM:

ATTORNEY/AGENT INFORMATION:
NAME: Sherwood, Pamela J
REGISTRATION NUMBER: 36, 677
REFERENCE/DOCKET NUMBER: UCAL/060PAT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-327-3400
TELEFAX: 650-327-3231
TELEX:

; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 407 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
US-08-742-440A-3

Query Match 52.8%; Score 65; DB 2; Length 407;
Best Local Similarity 55.6%; Pred. No. 0.04;
Matches 10; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 6 FGFFPLMFIFCYTFV 23
DB 284 FGFLPFIIFCYTTLI 301

RESULT 15

US-08-118-270-38
; Sequence 38, Application US/08118270
; Patent No. 5508384
; GENERAL INFORMATION:

; APPLICANT: Murphy, Randall B.

; APPLICANT: Schuster, David I.

; TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN

; TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF

; NUMBER OF SEQUENCES: 348

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BROWDY AND NEIMARK

; STREET: 419 Seventh Street, N.W., Suite 300

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20004

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/118,270

; FILING DATE: 09-SEP-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/943,236

; FILING DATE: 10-SEP-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Townsend, Kevin G.

; REGISTRATION NUMBER: 34,033

; REFERENCE/DOCKET NUMBER: MURPHY-2A

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-628-5197

; TELEFAX: 202-737-3528

; TELEX: 248633

; INFORMATION FOR SEQ ID NO: 38:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 312 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-118-270-38

Query Match 52.0%; Score 64; DB 1; Length 312;
Best Local Similarity 56.2%; Pred. No. 0.042;
Matches 9; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 6 FGFFPLMFIFCYTF 21
DB 170 FGFIPLIMLYCYGF 185

Search completed: May 23, 2001, 15:30:07
Job time: 414 sec

Result No.	Query			Length	DB	ID	Description
	Score	Match	%				
1	123	100.0	369	2	J55068	G protein-coupled	
2	67	54.5	358	2	A53752	interleukin-8 rece	
3	67	54.5	359	2	A48921	interleukin-8 rece	
4	67	54.5	360	2	A53611	interleukin-8 rece	
5	66	53.7	378	2	A55735	G protein-coupled	
6	65	52.8	354	2	A423669	interleukin-8 rece	
7	65	52.8	355	2	JQ1231	interleukin-8 rece	
8	64	52.0	350	2	A39445	interleukin-8 rece	
9	63	51.2	355	2	A45177	chemokine (C-C) re	
10	63	51.2	356	2	S42096	interleukin-8 rece	
11	62.5	50.8	376	2	A48197	opsin, ocular - A	
12	62	50.4	351	1	A46525	complement C3a ana	
13	62	50.4	352	1	S27357	complement C3a ana	
14	62	50.4	367	2	JE0349	interferon-inducib	
15	62	50.4	482	2	S65766	G protein-coupled	
16	61.5	50.0	376	2	B48197	opsin, lateral eye	
17	61	49.6	378	2	A45680	G protein-coupled	
18	61	49.6	378	2	B55735	lymphocyte-specifi	
19	59	48.0	350	1	A37963	complement C3a ana	
20	58	47.2	473	2	JC5835	anaphylatoxin C3a	
21	57	46.3	557	2	T16619	hypothetical prote	
22	56.5	45.9	360	2	A57160	chemokine (C-C) re	
23	56	45.5	354	2	I58186	probable G protein	
24	56	45.5	380	2	JC2434	kappa opioid recep	
25	56	45.5	380	2	JC2338	kappa opioid recep	
26	55	44.7	356	2	S29248	somatostatin recep	
27	55	44.7	356	2	I49340	MIP-1 alpha recept	
28	55	44.7	359	2	I49341	MIP-1 alpha recept	
29	55	44.7	360	2	G02064	G protein-coupled	

A;Molecule type: mRNA

A:Residues: 1-358 <PRA>
 A:Cross-references: GB:L24445; NID:g437661; PIDN:AAA31378.1; PID:g437662
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 54.5%; Score 67; DB 2; Length 358;
 Best Local Similarity 62.5%; Pred. No. 0.016;
 Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 6 FGFFIPLMFIMFCYTF 21
 ||| :|| :|:| |
 Db 216 FGFIPLLMFICVYF 231

RESULT 3

Interleukin-8 receptor type B - mouse
 N:Alternate names: G-protein coupled receptor Gpcrl6
 C:Species: Mus musculus (house mouse)
 C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 05-Nov-1999
 C:Accession: A48921; A53677; I49348; I55421; H48909; I53774
 R:Cerretti, D.P.; Nelson, N.; Kozlosky, C.J.; Morrissey, P.J.; Copeland, N.G.; Gilbert, Genomics 18, 410-413, 1993
 A:Title: The murine homologue of the human interleukin-8 receptor type B maps near the
 A:Reference number: A48921; MUID:94117014
 A:Accession: A48921
 A:Molecule type: DNA
 A:Residues: 1-359 <CER>
 A:Cross-references: GB:L23637; NID:g435093; PIDN:AAA39305.1; PID:g435094
 R:Suzuki, H.; Prado, G.N.; Wilkinson, N.; Navarro, J.
 J. Biol. Chem. 269, 18263-18266, 1994
 A:Title: The N terminus of interleukin-8 (IL-8) receptor confers high affinity binding to
 A:Reference number: A53677; MUID:94308043
 A:Accession: A53677
 A>Status: nucleic acid sequence not shown; not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 1-359 <SUZ>
 A:Cross-references: GB:L26549
 A:Note: sequence extracted from NCBI backbone (NCBIP:149812)
 R:Lee, J.; Cacalano, G.; Camerato, T.; Toy, K.; Moore, M.W.; Wood, W.I.
 J. Immunol. 155, 2158-2164, 1995
 A:Title: Chemokine binding and activities mediated by the mouse IL-8 receptor.
 A:Reference number: I49348; MUID:95363183
 A:Accession: I49348
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-359 <RES>
 A:Cross-references: EMBL:U31207; NID:g950174; PIDN:AAC52239.1; PID:g950175
 R:Bozic, C.R.; Gerard, N.P.; von Uexkull-Guldenband, C.; Kolakowski, L.F.
 J. Biol. Chem. 269, 29355-29358, 1994
 A:Title: The murine interleukin 8 type B receptor homologue and its ligands. Expression
 A:Reference number: I55421; MUID:95050766
 A:Accession: I55421
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-359 <RE2>
 A:Cross-references: PIDN:AAA62109.1; PID:g293666
 R:Wilkie, T.M.; Chen, Y.; Gilbert, D.J.; Moore, K.J.; Yu, L.; Simon, M.I.; Copeland, N.C.
 Genomics 16, 175-184, 1993
 A:Title: Identification, chromosomal location, and genome organization of mammalian G-pr
 A:Reference number: A48909; MUID:94116980
 A:Accession: H48909
 A>Status: preliminary; nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 145-258 <MIL>
 A:Cross-references: GB:L20337; NID:g438800; PIDN:AAA16853.1; PID:g438801
 R:Harada, A.; Kuno, K.; Nomura, H.; Mukaida, N.; Murakami, S.; Matsushima, K.
 Gene 142, 297-300, 1994
 A:Title: Cloning of a cDNA encoding a mouse homolog of the interleukin-8 receptor.
 A:Reference number: I53774; MUID:94252584
 A:Accession: I53774
 A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA
 A:Residues: 1-359 <RE3>
 A:Cross-references: GB:DL7630; NID:g493671; PIDN:BAA04536.1; PID:g493672
 C:Genetics:
 A:Gene: IL8rb
 A:Introns: #status absent
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: G protein-coupled receptor; glycoprotein; transmembrane protein
 F:49-74/Domain: transmembrane #status predicted <TM1>
 F:84-106/Domain: transmembrane #status predicted <TM2>
 F:120-141/Domain: transmembrane #status predicted <TM3>
 F:163-182/Domain: transmembrane #status predicted <TM4>
 F:213-234/Domain: transmembrane #status predicted <TM5>
 F:251-271/Domain: transmembrane #status predicted <TM6>
 F:308-328/Domain: transmembrane #status predicted <TM7>

Query Match 54.5%; Score 67; DB 2; Length 359;
 Best Local Similarity 62.5%; Pred. No. 0.016;
 Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 6 FGFFIPLMFIMFCYTF 21
 ||| :|| :|:| |
 Db 217 FGFIPLLMFICYGF 232

RESULT 4

Interleukin-8 receptor type B - human
 C:Species: Homo sapiens (man)
 C:Date: 07-Oct-1994 #sequence_revision 12-Apr-1996 #text_change 05-Nov-1999
 C:Accession: I37898; I38712; A53611; A39446
 R:Ahuja, S.K.; Shetty, A.; Tiffany, H.L.; Murphy, P.M.
 J. Biol. Chem. 269, 26381-26389, 1994
 A:Title: Comparison of the genomic organization and promoter function for human inter
 A:Reference number: I37898; MUID:95014476
 A:Accession: I37898
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-360 <RES>
 A:Cross-references: EMBL:U11869; NID:g511801; PIDN:AA560556.1; PID:g511803
 A:Accession: I38712
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-15 <RE2>
 A:Cross-references: EMBL:U11872; NID:g511808; PIDN:AAA64380.1; PID:g511809; EMBL:U118
 I1876; NID:g511816; PID:g511817; EMBL:U11877; NID:g511818; PID:g511819; EMBL:U11878;
 R:Spranger, H.; Lloyd, A.R.; Lautens, L.L.; Bonner, T.I.; Kelvin, D.J.
 J. Biol. Chem. 269, 11065-11072, 1994
 A:Title: Structure, genomic organization, and expression of the human interleukin-8 r
 A:Reference number: A53611; MUID:94209273
 A:Accession: A53611
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 6-360 <SPR>
 A:Cross-references: GB:M99412; GB:L19593
 R:Murphy, P.M.; Tiffany, H.L.
 Science 253, 1280-1283, 1991
 A:Title: Cloning of complementary DNA encoding a functional human interleukin-8 recep
 A:Reference number: A39446; MUID:91368200
 A:Accession: A39446
 A>Status: preliminary; nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 6-360 <MUR>
 A:Cross-references: GB:M73969
 C:Comment: This receptor, unlike IL8RA, binds several peptides besides interleukin-8,
 C:Genetics:
 A:Gene: GDB:IL8RB; IL8RA
 A:Cross-references: GDB:127868; OMIM:146928
 A:Map position: 2q35-2q35
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 54.5%; Score 67; DB 2; Length 360;
 Best Local Similarity 62.5%; Pred. No. 0.016;
 Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 6 FGFFIPLMFIMFCYTF 21
 ||| :|| :||| |

Db 218 FGFIPLMLFCYGF 233

RESULT 5

G protein-coupled receptor EB11 - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 24-Nov-1999
 C:Accession: A55735
 R:Schweickart, V.L.; Raport, C.J.; Godiska, R.; Byers, M.G.; Eddy Jr., R.L.; Shows, T.B.
 Genomics 23, 643-650, 1994
 A:Title: Cloning of human and mouse EB11, a lymphoid-specific G-protein-coupled receptor
 A:Reference number: A55735; MUID:95154835
 A:Accession: A55735
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-378 <SCH>
 A:Cross-references: GB:L31580; NID:g468340; PIDN:AAA74232.1; PID:g468341
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: G protein-coupled receptor

Query Match 53.7%; Score 66; DB 2; Length 378;
 Best Local Similarity 42.9%; Pred. No. 0.023;
 Matches 9; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 3 ELLFGFIPLMFIMFCYTFIV 23
 :||| :|| :||| |

Db 227 QMVFGLVPLMLAMSFYLLIII 247

RESULT 6

Az3669
 Interleukin-8 receptor, high affinity - rabbit
 N:Alternate names: fMLP receptor
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C:Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 05-Nov-1999
 C:Accession: A23669
 R:Thomas, K.M.; Pyun, H.Y.; Navarro, J.
 J. Biol. Chem. 265, 20061-20064, 1990
 A:Title: Molecular cloning of the fMet-Leu-Phe receptor from neutrophils.
 A:Reference number: A23669; MUID:91056034
 A:Accession: A23669
 A:Molecule type: mRNA
 A:Residues: 1-354 <THO>
 A:Cross-references: GB:M58021; GB:J05705; NID:gi65442; PIDN:AAA31377.1; PID:gi65443
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: G protein-coupled receptor; glycoprotein; membrane protein; neutrophil

Query Match 52.8%; Score 65; DB 2; Length 354;
 Best Local Similarity 62.5%; Pred. No. 0.03;
 Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 6 FGFFIPLMFIMFCYTF 21
 ||| :|| :||| |

Db 213 FGFIPLMLFCYGF 228

RESULT 7

Interleukin-8 receptor - rabbit
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 05-Nov-1999
 C:Accession: JQ1231; A46483
 R:Beckmann, M.P.; Munger, W.E.; Kozlosky, C.; VandenBos, T.; Price, V.; Lyman, S.; Gerard

Biochem. Biophys. Res. Commun. 179, 784-789, 1991
 A:Title: Molecular characterization of the interleukin-8 receptor.
 A:Reference number: JQ1231; MUID:91378994
 A:Accession: JQ1231

A:Molecule type: DNA

A:Residues: 1-355 <BEC>

A:Cross-references: GB:M74240; NID:gi65438; PIDN:AAA31375.1; PID:gi65439
 R:Lee, J.; Kuang, W.J.; Rice, G.C.; Wood, W.I.

J. Immunol. 148, 1261-1264, 1992

A:Title: Characterization of complementary DNA clones encoding the rabbit IL-8 receptor
 A:Reference number: A46483; MUID:92148149

A:Accession: A46483

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-355 <LEE>

A:Cross-references: GB:M82873; NID:gi65440; PIDN:AAA31376.1; PID:gi65441

A:Experimental source: neutrophils

A:Note: sequence extracted from NCBI backbone (NCBIN:81526, NCBI:81530)

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 52.8%; Score 65; DB 2; Length 355;
 Best Local Similarity 62.5%; Pred. No. 0.03;
 Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 6 FGFFIPLMFIMFCYTF 21
 ||| :|| :||| |

Db 214 FGFIPLMLFCYGF 229

RESULT 8

A39445
 Interleukin-8 receptor type A - human
 N:Alternate names: interleukin-8 receptor, high-affinity
 C:Species: Homo sapiens (man)
 C:Date: 22-Jan-1993 #sequence_revision 12-Apr-1996 #text_change 05-Nov-1999
 C:Accession: I37449; I38710; I38711; A39445
 R:Molliereau, C.; Muscatelli, F.; Mattei, M.G.; Vassart, G.; Parmentier, M.
 Genomics 16, 248-251, 1993
 A:Title: The high-affinity interleukin 8 receptor gene (IL8RA) maps to the 2q33-q36 r-

A:Reference number: I37449; MUID:93252387

A:Accession: I37449

A:Molecule type: DNA

A:Residues: 1-350 <RES>

A:Cross-references: EMBL:X65858; NID:g312046; PIDN:CAA46688.1; PID:g312047

R:Ahuja, S.K.; Shetty, A.; Tiffany, H.L.; Murphy, P.M.

J. Biol. Chem. 269, 26381-26389, 1994

A:Title: Comparison of the genomic organization and promoter function for human inter

A:Reference number: I37898; MUID:95014476

A:Accession: I38710

A:Molecule type: DNA

A:Residues: 1-350 <RE2>

A:Cross-references: EMBL:U11870; NID:g511804; PIDN:AAA64378.1; PID:g511805

A:Accession: I38711

A:Molecule type: mRNA

A:Residues: 1-16 <RE3>

A:Cross-references: EMBL:U11871; NID:g511806; PIDN:AAA64379.1; PID:g733002

R:Holmes, W.E.; Lee, J.; Kuang, W.J.; Rice, G.C.; Wood, W.I.

Science 253, 1278-1280, 1991

A:Title: Structure and functional expression of a human interleukin-8 receptor.

A:Reference number: A39445; MUID:91368199

A:Accession: A39445

A:Molecule type: mRNA

A:Residues: 1-275, 'T', 277-350 <HOL>

A:Cross-references: GB:M68932; NID:gi86369; PIDN:AAA59159.1; PID:gi86370

C:Genetics:

A:Gene: GDB:IL8RA

A:Cross-references: GDB:135039; OMIM:146929

A:Map position: 2q35-2q35

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor; glycoprotein; membrane protein

Query Match 52.0%; Score 64; DB 2; Length 350;
Best Local Similarity 62.5%; Pred. No. 0.042;
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 6 FGFFIPLMFMYCYTF 21
|||:|:| |:|:| |
Db 209 FGIYVPLFVMLFCYGF 224

RESULT 9

A45177
chemokine (C-C) receptor 1 - human
N:Alternate names: C-C CKR-1; macrophage inflammatory protein-1-alpha receptor
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 13-Aug-1999
C:Accession: A45177; I55671
R:Neote, K.; DiGregorio, D.; Mak, J.Y.; Horuk, R.; Schall, T.J.
Cell 72, 415-425, 1993
A:Title: Molecular cloning, functional expression, and signaling characteristics of a C-C chemokine receptor
A:Reference number: A45177; MUID:93161416
A:Accession: A45177
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-355 <NE>
A:Cross-references: GB:L10918; NID:g292416; PIDN:AAA36543.1; PID:g292417
A:Experimental source: HL60 cells
A:Note: sequence extracted from NCBI backbone (NCBIP:124876)
R:Gao, J.
J. Exp. Med. 177, 1421-1427, 1993
A:Title: Structure and functional expression of the human macrophage inflammatory protein 1 alpha
A:Reference number: I55671; MUID:93240122
A:Accession: I55671
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-355 <RES>
A:Cross-references: GB:L10918; NID:g292416; PIDN:AAA36543.1; PID:g292417
C:Genetics:

A:Gene: GDB:CMKBR1; CMKR-1
A:Cross-references: GDB:138446; OMIM:601159
A:Map position: 3p21-3p21
C:Superfamily: vertebrate rhodopsin
C:Keywords: disulfide bond; G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane
F:36-60/Domain: transmembrane #status predicted <TM1>
F:71-91/Domain: transmembrane #status predicted <TM2>
F:108-129/Domain: transmembrane #status predicted <TM3>
F:147-171/Domain: transmembrane #status predicted <TM4>
F:205-223/Domain: transmembrane #status predicted <TM5>
F:240-264/Domain: transmembrane #status predicted <TM6>
F:288-305/Domain: transmembrane #status predicted <TM7>
F:5/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:24-273,106-183/Disulfide bonds: #status predicted
F:345/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted

Query Match 51.2%; Score 63; DB 2; Length 355;
Best Local Similarity 57.9%; Pred. No. 0.059;
Matches 11; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 5 LFQFFIPLMFMYCYTFIV 23
|||:|:| |:|:| |
Db 205 LFGLVPLLVMIICYTGII 223

RESULT 10

S42096
interleukin-8 receptor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 26-Aug-1999
C:Accession: S42096
R:Gobl, A.E.; Wang, S.; Zhou, Y.; Oeberg, K.
submitted to the EMBL Data Library, February 1994
A:Description: Molecular cloning of the rat IL8 receptor.

A:Reference number: S42096
A:Accession: S42096
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-356 <GOB>
A:Cross-references: EMBL:X77797
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 51.2%; Score 63; DB 2; Length 356;
Best Local Similarity 56.2%; Pred. No. 0.059;
Matches 9; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 6 FGFFIPLMFMYCYTF 21
||:|:| |:|:| |
Db 217 YGFLPLLMFCYGF 232

RESULT 11

A48197
opsin, ocular - Atlantic horseshoe crab
C:Species: Limulus polyphemus (Atlantic horseshoe crab)
C:Date: 17-Jul-1994 #sequence_revision 17-Jul-1994 #text_change 13-Aug-1999
C:Accession: A48197
R:Smith, W.C.; Price, D.A.; Greenberg, R.M.; Battelle, B.A.
Proc. Natl. Acad. Sci. U.S.A. 90, 6150-6154, 1993
A:Title: Opsins from the lateral eyes and ocelli of the horseshoe crab, Limulus polyphemus
A:Reference number: A48197; MUID:93317641
A:Accession: A48197
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-376 <SMI>
A:Cross-references: EMBL:L03792; NID:g156644; PIDN:AAA28274.1; PID:g156645
C:Superfamily: vertebrate rhodopsin
C:Keywords: chromoprotein; G protein-coupled receptor; lipoprotein; photoreceptor; retinal
F:318/Binding site: retinal (Lys) (covalent) #status predicted

Query Match 50.8%; Score 62.5; DB 2; Length 376;
Best Local Similarity 47.8%; Pred. No. 0.073;
Matches 11; Conservative 7; Mismatches 2; Indels 3; Gaps 1;

QY 4 LLFG---FFIPLMFMYCYTFIV 23
::| |:|:| |:|:| |
Db 213 IIVGLAVYFLPLTMIICYTFIV 235

RESULT 12

A46525
complement C5a anaphylatoxin receptor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A46525
R:Gerard, C.; Bao, L.; Orozco, O.; Pearson, M.; Kunz, D.; Gerard, N.P.
J. Immunol. 149, 2600-2606, 1992
A:Title: Structural diversity in the extracellular faces of peptidergic G-protein-coupled receptors
A:Reference number: A46525; MUID:93017861
A:Accession: A46525
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-351 <GER>
A:Cross-references: GB:S46665; GB:L05630; NID:g257519; PIDN:AAB97774.1; PID:g257520
A:Experimental source: BALB/C
A:Note: sequence extracted from NCBI backbone (NCBIP:116075)
C:Function:
A:Description: mediates the inflammatory and chemotactic responses of polymorphonuclear leukocytes
C:Superfamily: vertebrate rhodopsin
C:Keywords: chemotaxis; G protein-coupled receptor; glycoprotein; inflammation; polymorphonuclear leukocyte
F:1-37/Domain: extracellular #status predicted <EX1>
F:38-61/Domain: transmembrane #status predicted <TM1>
F:62-71/Domain: intracellular #status predicted <IN1>

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OM protein - protein search, using sw model

Run on: May 23, 2001, 15:36:19 ; Search time 62.39 Seconds
(without alignments)
12.628 Million cell updates/sec

Title: US-08-887-977-10_COPY_207_229
Perfect score: 123
Sequence: 1 GLELLFGFFIPLMFIFCVTFIV 23

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	123	100.0	374	1 CRR6_HUMAN	P51684 homo sapien
2	103	83.7	367	1 CRR6_MOUSE	O54689 mus musculus
3	74	60.2	369	1 CRR9_MOUSE	Q9wtu7 mus musculus
4	67	54.5	353	1 IL8B_GORGO	Q28422 gorilla gor
5	67	54.5	353	1 IL8B_MACMU	Q28519 macaca mula
6	67	54.5	353	1 IL8B_PANTR	Q28807 pan troglod
7	67	54.5	358	1 IL8B_RABIT	P35344 oryctolagus
8	67	54.5	359	1 IL8B_MOUSE	P35343 mus musculus
9	67	54.5	360	1 IL8B_HUMAN	P25025 homo sapien
10	66	53.7	356	1 IL8B_CANFA	O97571 canis famli
11	66	53.7	378	1 CRR7_MOUSE	P47774 mus musculus
12	65	52.8	342	1 BONZ_CERAE	O18983 cercopithec
13	65	52.8	342	1 BONZ_HUMAN	O00574 homo sapien
14	65	52.8	342	1 BONZ_MACNE	O19024 macaca neme
15	65	52.8	343	1 BONZ_MACMU	Q9xt45 macaca mula
16	65	52.8	355	1 IL8A_RABIT	P21109 oryctolagus
17	65	52.8	357	1 CRR9_HUMAN	P51686 homo sapien
18	65	52.8	360	1 IL8B_BOVIN	Q28003 bos taurus
19	65	52.8	369	1 PAR3_MOUSE	O08675 mus musculus
20	64	52.0	350	1 IL8A_GORGO	P55919 gorilla gor
21	64	52.0	350	1 IL8A_HUMAN	P25024 homo sapien
22	64	52.0	350	1 IL8A_PANTR	P55920 pan troglod
23	63	51.2	355	1 CRR1_HUMAN	P32246 homo sapien
24	63	51.2	359	1 IL8B_RAT	P33407 rattus norv
25	62.5	50.8	376	1 OPS2_LIMPO	P35361 limulus pol
26	62	50.4	345	1 C5AR_CAVPO	O70129 cavia porce
27	62	50.4	347	1 C5AR_MOUSE	P30993 mus musculus
28	62	50.4	349	1 IL8A_RAT	P70612 rattus norv
29	62	50.4	352	1 C5AR_CANFA	P30992 canis famli
30	62	50.4	352	1 C5AR_RAT	P97520 rattus norv
31	62	50.4	355	1 CKR1_MACMU	P56482 macaca mula
32	62	50.4	367	1 CCR3_MOUSE	O88410 mus musculus
33	62	50.4	368	1 CCR3_HUMAN	P49682 homo sapien

ALIGNMENTS

RESULT	ID	CKR6_HUMAN	STANDARD	PRT	374 AA
34	AC	P51684	Q92846; P78553;		
35	DT	01-OCT-1996	(Rel. 34, Created)		
36	DT	15-JUL-1998	(Rel. 36, Last sequence update)		
37	DT	01-OCT-2000	(Rel. 40, Last annotation update)		
38	DE	C-C CHEMOKINE RECEPTOR TYPE 6 (C-C CKR-6) (CCR-6) (LARC			
39	DE	RECEPTOR) (GPR-CY4) (GPCV4) (CHEMOKINE RECEPTOR-LIKE 3) (CKR-L3)			
40	DE	(DRY6)			
41	GN	CCR6 OR CMKBR6 OR STRL22 OR GPR29 OR CKRL3.			
42	OS	Homo sapiens (Human)			
43	OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
44	OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
45	OX	NCBI_TaxID=9606;			
	RN	[1]			
	RP	SEQUENCE FROM N.A., AND FUNCTION.			
	RX	MEDLINE-97313465; PubMed-9169459;			
	RA	Baba M., Imai T., Nishimura M., Kakizaki M., Takagi S., Hieshima K.,			
	RA	Noniyama H., Yoshie O.;			
	RT	*Identification of CCR6, the specific receptor for a novel			
	RT	lymphocyte-directed CC chemokine LARC.;			
	RL	J-Biol.-Chem.-272:14893-14898(1997).			
	[2]				
	RN	SEQUENCE FROM N.A.			
	RP	Lautens L.L., Modi W., Bonner T.I.;			
	RL	Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.			
	[3]				
	RN	SEQUENCE FROM N.A.			
	RP	MEDLINE-97040707; PubMed-8886020;			
	RX	Zaballos A., Varona R., Gutierrez J., Lind P., Marquez G.;			
	RA	*Molecular cloning and RNA expression of two new human chemokine			
	RT	receptor-like genes.;			
	RL	Biochem. Biophys. Res. Commun. 227:846-853(1996).			
	[4]				
	RN	SEQUENCE FROM N.A.			
	RP	McCoy R., Perlmutter D.H.;			
	RA	Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.			
	[5]				
	RN	SEQUENCE FROM N.A.			
	RP	MEDLINE-97224503; PubMed-9070937;			
	RX	Liao F., Lee H.-H., Farber J.M.;			
	RA	*Cloning of STRL22, a new human gene encoding a G-protein-coupled			
	RT	receptor related to chemokine receptors and located on chromosome			
	RL	6q27.;			
	RL	Genomics 40:175-180(1997).			
	CC	-!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-3-			
	CC	ALPHA/LARC AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE			
	CC	INTRACELLULAR CALCIUM IONS LEVEL.			
	CC	-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.			
	CC	-!- TISSUE SPECIFICITY: SPLEEN, LYMPH NODES, APPENDIX, AND FETAL			
	CC	LIVER. EXPRESSED IN LYMPHOCYTES, T CELLS AND B CELLS BUT NOT IN			
	CC	NATURAL KILLER CELLS, MONOCYTES, OR GRANULOCYTES.			
	CC	-!- INDUCTION: INTERLEUKIN-2.			
	CC	-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.			
	CC	-!- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-6 IS THE INITIATOR.			

O88680 cavia porce
Q16581 homo sapien
P35360 limulus pol
P75240 pan troglod
Q92213 cavia porce
P32248 homo sapien
O16018 cambarellus
P79175 gorilla gor
P21730 homo sapien
O00254 homo sapien
O09047 mus musculus
O55137 rattus norv

34 62 50.4 475 1 C3AR_CAVPO
35 62 50.4 482 1 C3AR_HUMAN
36 61.5 50.0 376 1 OPSL_LIMPO
37 61 49.6 340 1 C5AR_PANTR
38 61 49.6 358 1 CRR3_CAVPO
39 61 49.6 378 1 CRR7_HUMAN
40 59 48.0 301 1 OPSD_CAMSC
41 59 48.0 340 1 C5AR_GORGO
42 59 48.0 350 1 C5AR_HUMAN
43 59 48.0 374 1 PAR3_MOUSE
44 59 48.0 477 1 C3AR_MOUSE
45 58 47.2 473 1 C3AR_RAT

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EMBL; U45984; AAB62714.1; -
 DR EMBL; 279784; CAB02144.1; ALT_INIT.
 DR EMBL; U60000; AAB06949.1; -
 DR EMBL; U68030; AAC51124.1; -
 DR EMBL; U68032; AAC51125.1; -
 DR HSSP; GCR1037; -
 DR GCRDB; GCR1037; -
 DR GCRDB; GCR1075; -
 DR GCRDB; GCR1906; -
 DR GCRDB; GCR1919; -
 DR GCRDB; GCR1941; -
 DR GCRDB; GCR2110; -
 DR MIM; 601835; -
 DR InterPro; IPR000276; -
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRHHODOPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECF_F1_1; 1.
 DR PROSITE; PS0262; G_PROTEIN_RECF_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 47 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 48 74 1 (POTENTIAL).
 FT DOMAIN 75 83 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 84 104 2 (POTENTIAL).
 FT DOMAIN 105 119 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 120 141 3 (POTENTIAL).
 FT DOMAIN 142 159 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 160 180 4 (POTENTIAL).
 FT DOMAIN 181 211 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 212 238 5 (POTENTIAL).
 FT DOMAIN 239 254 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 255 279 6 (POTENTIAL).
 FT DOMAIN 280 303 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 304 321 7 (POTENTIAL).
 FT DOMAIN 322 374 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 118 197 BY SIMILARITY.
 FT CARBOHYD 7 7 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 23 23 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CONFLICT 60 60 G -> A (IN REF. 4).
 FT CONFLICT 74 74 Y -> N (IN REF. 4).
 FT CONFLICT 86 86 L -> V (IN REF. 4).
 FT CONFLICT 164 164 S -> T (IN REF. 5).
 FT CONFLICT 182 182 T -> S (IN REF. 4).
 FT CONFLICT 192 192 Q -> L (IN REF. 4).
 FT CONFLICT 206 206 E -> V (IN REF. 4).
 FT CONFLICT 225 225 I -> F (IN REF. 4).
 FT CONFLICT 370 374 SSFTM -> VLVHVIIES (IN REF. 4).
 SQ SEQUENCE 374 AA; 42494 MW; D7F963534E990BC4 CRC64;

Query Match 100.0%; Score 123; DB 1; Length 374;
 Best Local Similarity 100.0%; Pred. No. 3.6e-09;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GLELLFGFFIPLMFMFCYTFIV 23
 |||||
 Db 216 GLELLFGFFIPLMFMFCYTFIV 238

RESULT 2
 ID CKR6_MOUSE STANDARD; PRT; 367 AA.
 AC O54689;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE C-C CHEMOKINE RECEPTOR TYPE 6 (C-C CKR-6) (CCR-6) (KY411).
 GN CCR6 OR CMKBR6.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Yanagihara S., Komura E., Yamaguchi Y.;
 RT "Mouse G protein-coupled receptor KY411.";
 RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99077268; PubMed=9862452;
 RA Varona R., Zaballós A., Gutierrez J., Martin P., Roncal F.,
 RA Albar J.P., Ardavin C., Marquez G.;
 RT "Molecular cloning, functional characterization and mRNA expression
 RT analysis of the murine chemokine receptor CCR6 and its specific ligand
 RT MIP-3alpha.";
 RL FEBS Lett. 440:188-194(1998).
 CC -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-3-
 CC ALPHA/LARC AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE
 CC INTRACELLULAR CALCIUM IONS LEVEL.
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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 EMBL; AB009369; BAA23776.1; -
 DR EMBL; AJ222714; CAA10956.1; -
 DR MGD; MGI:1333797; Cmkbr6.
 DR InterPro; IPR000276; -
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRHHODOPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECF_F1_1; 1.
 DR PROSITE; PS0262; G_PROTEIN_RECF_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 39 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 40 66 1 (POTENTIAL).
 FT DOMAIN 67 75 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 76 96 2 (POTENTIAL).
 FT DOMAIN 97 111 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 112 133 3 (POTENTIAL).
 FT DOMAIN 134 151 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 152 172 4 (POTENTIAL).
 FT DOMAIN 173 203 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 204 230 5 (POTENTIAL).
 FT DOMAIN 231 246 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 247 271 6 (POTENTIAL).
 FT DOMAIN 272 295 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 296 313 7 (POTENTIAL).
 FT DOMAIN 314 367 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 110 189 BY SIMILARITY.
 FT CARBOHYD 2 2 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 35 35 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 367 AA; 42102 MW; 6A309AF833B1117E CRC64;

Query Match 83.7%; Score 103; DB 1; Length 367;
 Best Local Similarity 73.9%; Pred. No. 1.3e-06;
 Matches 17; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Oy 1 GLELLFGFFIPLMFMFCYTFIV 23
 |||||
 Db 208 GLELLFGFFIPLMFMFCYTFIV 230

RESULT 3
 CKR9 MOUSE
 ID CKR9_MOUSE STANDARD; PRT; 369 AA.
 AC Q9WU7;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE C-C CHEMOKINE RECEPTOR TYPE 9 (C-C CKR-9) (CCR-9)
 DE (CHEMOKINE C-C RECEPTOR 10).
 GN CC9 OR CMKBR10.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Thymus;
 RX MEDLINE=99248139; PubMed=10229797;
 RA Zaballios A., Gutierrez J., Varona R., Ardavin C., Marquez G.;
 RT "Cutting edge: identification of the orphan chemokine receptor GPR-9-6
 as CC9, the receptor for the chemokine TECK.";
 RL J. Immunol. 162:5671-5675(1999).
 CC -1- FUNCTION: RECEPTOR FOR CHEMOKINE SCYA25/TECK. SUBSEQUENTLY
 CC LEVEL.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN THE THYMUS AND LOW IN
 CC LYMPH NODES AND SPLEEN.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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 CC
 DR EMBL: AJ132336; CAB43480.1;
 DR MGD; MGI:1341902; Cmkbr10.
 DR InterPro; IPR000174;
 DR InterPro; IPR000248;
 DR InterPro; IPR000276;
 DR InterPro; IPR000355;
 DR InterPro; IPR000496;
 DR InterPro; IPR001277;
 DR InterPro; IPR001718;
 DR Pfam; PF00001; 7tm1.1;
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PRINTS; PR00241; ANGIOTENSINR.
 DR PRINTS; PR00425; BRADYKININR.
 DR PRINTS; PR00427; INTRLEUKINR.
 DR PRINTS; PR00641; CHEMOKINER7.
 DR PRINTS; PR00645; LCRORPHANR.
 DR PRINTS; PR00657; CCEMOKINER.
 DR PROSITE; PS00237; G-PROTEIN RECEPTOR F1_1; 1.
 DR PROSITE; PS00262; G-PROTEIN RECEPTOR F1_2; 1.
 DR G-protein coupled receptor; Transmembrane; Glycoprotein.
 KW DOMAIN 1 49
 FT EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 1 49
 FT DOMAIN 50 76
 FT TRANSMEM 77 85
 FT DOMAIN 86 106
 FT TRANSMEM 107 120
 FT DOMAIN 121 142
 FT TRANSMEM 143 160
 FT DOMAIN 161 181
 FT TRANSMEM 182 210
 FT DOMAIN 211 238
 FT TRANSMEM 239 254
 FT DOMAIN 255 280
 FT TRANSMEM 281 304
 FT DOMAIN 305 322
 FT TRANSMEM 323 369
 FT CYTOPLASMIC (POTENTIAL).
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT BY SIMILARITY.
 SQ SEQUENCE 369 AA; 41913 MW; 6971F76F0A24B4AE CRC64;
 Query Match 60.2%; Score 74; DB 1; Length 369;
 Best Local Similarity 54.5%; Pred. No. 0.0071;
 Matches 12; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
 Oy 2 LELFGFFPLPMFICFYTFIV 23
 Db 217 LKVTGLGFLPFMVMFCTYIII 238
 RESULT 4
 IL8B_GORGO STANDARD; PRT; 353 AA.
 ID IL8B_GORGO
 AC Q28422;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE HIGH AFFINITY INTERLEUKIN-8 RECEPTOR B (IL-8R B) (CXCR-2) (FRAGMENT).
 GN IL8RB OR CXCR2.
 OS Gorilla gorilla gorilla (Lowland gorilla).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
 OX NCBI_TaxID=9595;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96175151; PubMed=9110929;
 RA Alvarez V., Coto E., Setien F., Gonzalez S., Gonzalez-Roces S.,
 RA Lopez-Larrea C.;
 RT "Characterization of interleukin-8 receptors in non-human primates.";
 RL Immunogenetics 43:261-267(1996).
 CC -1- FUNCTION: RECEPTOR TO INTERLEUKIN-8, WHICH IS A POWERFUL
 CC NEUTROPHILS CHEMOTACTIC FACTOR. BINDING OF IL-8 TO THE RECEPTOR
 CC CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA A
 CC G-PROTEIN THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND
 CC MESSENGER-SYSTEM. THIS RECEPTOR BINDS TO IL-8 WITH A HIGH AFFINITY
 CC AND TO GRO/MGSA AND NAP-2 ALSO WITH A HIGH AFFINITY.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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 CC
 DR EMBL; X91114; CAA62564.1;
 DR HSSP; P34996; 1DDO.
 DR InterPro; IPR000276;
 DR Pfam; PF00001; 7tm1.1;
 DR PROSITE; PS00237; G-PROTEIN RECEPTOR F1_1; 1.
 DR PROSITE; PS00262; G-PROTEIN RECEPTOR F1_2; 1.
 DR G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW NON_TER 1 45
 FT DOMAIN 46 72
 FT TRANSMEM 73 81
 FT DOMAIN 82 102
 FT TRANSMEM 103 117
 FT DOMAIN 118 139
 FT TRANSMEM 140 160
 FT DOMAIN 161 180
 FT TRANSMEM 181 205
 FT DOMAIN 206 228
 FT TRANSMEM 229 248
 FT TRANSMEM 249 270
 FT EXTRACELLULAR (POTENTIAL).
 FT CYTOPLASMIC (POTENTIAL).
 FT 2 (POTENTIAL).
 FT EXTRACELLULAR (POTENTIAL).
 FT 3 (POTENTIAL).
 FT CYTOPLASMIC (POTENTIAL).
 FT 4 (POTENTIAL).
 FT EXTRACELLULAR (POTENTIAL).
 FT 5 (POTENTIAL).
 FT CYTOPLASMIC (POTENTIAL).
 FT 6 (POTENTIAL).

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FT DOMAIN 271 291 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 292 312 7 (POTENTIAL).
FT DOMAIN 313 >353 CYTOPLASMIC (POTENTIAL).
FT DISULFID 116 193 BY SIMILARITY.
FT CARBOHYD 19 19 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT NON_TER 353 353
SQ SEQUENCE 353 AA; 39919 MW; 1FF04E31A7E825B4 CRC64;

Query Match 54.5%; Score 67; DB 1; Length 353;
Best Local Similarity 62.5%; Pred. No. 0.054;
Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 6 FGFFIPLMFICYTF 21
DB 215 FGFIPLLMFCYGF 230

RESULT 5
IL8B_MACMU
ID IL8B_MACMU STANDARD; PRT; 353 AA.
AC Q28519;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE HIGH AFFINITY INTERLEUKIN-8 RECEPTOR B (IL-8R B) (CXCR-2) (FRAGMENT).
GN IL8RB OR CXCR2
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96175151; PubMed=9110929;
RA Alvarez V., Coto E., Setien F., Gonzalez S., Gonzalez-Roces S.,
RA Lopez-Larrea C.;
RT "Characterization of interleukin-8 receptors in non-human primates.";
CC -!- FUNCTION: RECEPTOR TO INTERLEUKIN-8, WHICH IS A POWERFUL
CC CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA A
CC G-PROTEIN THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND
CC MESSENGER SYSTEM. THIS RECEPTOR BINDS TO IL-8 WITH A HIGH AFFINITY
CC AND TO GROM/MSA AND NAP-2 ALSO WITH A HIGH AFFINITY.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC
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CC
CC EMBL; X91116; CAA62565.1;
CC HSSP; P34996; 1DDD.
CC InterPro; IPR000276;
CC Pfam; PF00001; 7tm_1; 1.
CC PROSITE; PS00237; G_PROTEIN_RECEPTOR_F1_1; 1.
CC PROSITE; PS0262; G_PROTEIN_RECEPTOR_F1_2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein;
CC Chemotaxis.
FT NON_TER 1 1
FT DOMAIN <1 45 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 46 72 1 (POTENTIAL).
FT DOMAIN 73 81 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 82 102 2 (POTENTIAL).
FT DOMAIN 103 117 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 118 139 3 (POTENTIAL).
FT DOMAIN 140 160 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 161 180 4 (POTENTIAL).

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FT DOMAIN 181 205 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 206 228 5 (POTENTIAL).
FT DOMAIN 229 248 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 249 270 6 (POTENTIAL).
FT DOMAIN 271 291 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 292 312 7 (POTENTIAL).
FT DOMAIN 313 >353 CYTOPLASMIC (POTENTIAL).
FT DISULFID 116 193 BY SIMILARITY.
FT CARBOHYD 19 19 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT NON_TER 353 353
SQ SEQUENCE 353 AA; 39947 MW; EC8B38130657C713 CRC64;

Query Match 54.5%; Score 67; DB 1; Length 353;
Best Local Similarity 62.5%; Pred. No. 0.054;
Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 6 FGFFIPLMFICYTF 21
DB 215 FGFIPLLMFCYGF 230

RESULT 6
IL8B_PANTR
ID IL8B_PANTR STANDARD; PRT; 353 AA.
AC Q28607;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE HIGH AFFINITY INTERLEUKIN-8 RECEPTOR B (IL-8R B) (CXCR-2) (FRAGMENT).
GN IL8RB OR CXCR2
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96175151; PubMed=9110929;
RA Alvarez V., Coto E., Setien F., Gonzalez S., Gonzalez-Roces S.,
RA Lopez-Larrea C.;
RT "Characterization of interleukin-8 receptors in non-human primates.";
CC -!- FUNCTION: RECEPTOR TO INTERLEUKIN-8, WHICH IS A POWERFUL
CC CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA A
CC G-PROTEIN THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND
CC MESSENGER SYSTEM. THIS RECEPTOR BINDS TO IL-8 WITH A HIGH AFFINITY
CC AND TO GROM/MSA AND NAP-2 ALSO WITH A HIGH AFFINITY.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; X91113; CAA62563.1;
CC HSSP; P34996; 1DDD.
CC InterPro; IPR000276;
CC Pfam; PF00001; 7tm_1; 1.
CC PROSITE; PS00237; G_PROTEIN_RECEPTOR_F1_1; 1.
CC PROSITE; PS0262; G_PROTEIN_RECEPTOR_F1_2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein;
CC Chemotaxis.
FT NON_TER 1 1
FT DOMAIN <1 45 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 46 72 1 (POTENTIAL).
FT DOMAIN 73 81 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 82 102 2 (POTENTIAL).
FT DOMAIN 103 117 EXTRACELLULAR (POTENTIAL).

```

FT TRANSMEM 118 139 3 (POTENTIAL).
 FT DOMAIN 140 160 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 161 180 4 (POTENTIAL).
 FT DOMAIN 181 205 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 206 228 5 (POTENTIAL).
 FT DOMAIN 229 248 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 249 270 6 (POTENTIAL).
 FT DOMAIN 271 291 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 292 312 7 (POTENTIAL).
 FT DOMAIN 313 >353 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 116 193 BY SIMILARITY.
 FT CARBOHYD 19 19 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT NON_TER 353 353
 SQ SEQUENCE 353 AA; 39998 MW; E745ACD9EC10C1E2 CRC64;

Query Match 54.5%; Score 67; DB 1; Length 353;
 Best Local Similarity 62.5%; Pred. No. 0.054; 3; Indels 0; Gaps 0;
 Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 6 FGFIPLMFIMFCYTF 21
 ||| :||: |:||| |
 Db 215 FGFIPLLMFLFCYGF 230

RESULT 7
 IL8B_RABIT STANDARD; PRT; 358 AA.
 ID IL8B_RABIT
 AC P35344;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE HIGH AFFINITY INTERLEUKIN-8 RECEPTOR B (IL-8R B) (CXCR-2) (GRO/MGSA RECEPTOR).
 DE RECEPTOR.
 GN IL8RB OR CXCR2.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ALBINO; TISSUE=Blood;
 RX MEDLINE=94230294; PubMed=8175642;
 RA Prado G.N., Thomas K.M., Suzuki H., Larosa G.J., Wilkinson N.C.,
 RA Folco E., Navarro J.;
 RT Molecular characterization of a novel rabbit interleukin-8 receptor
 RT isotype.;
 RL J. Biol. Chem. 269:12391-12394(1994).
 CC -!- FUNCTION: RECEPTOR TO INTERLEUKIN-8, WHICH IS A POWERFUL
 CC NEUTROPHILS CHEMOTACTIC FACTOR. BINDING OF IL-8 TO THE RECEPTOR
 CC CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA A
 CC G-PROTEIN THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND
 CC MESSENGER SYSTEM. THE AFFINITY OF THIS RECEPTOR IS IL-8 >> NAP-2 >
 CC MSGA (GRO).
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -!- TISSUE SPECIFICITY: EXPRESSED PREFERENTIALLY IN NEUTROPHILS.
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC
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 CC
 CC EMBL: L24445; AAA31378.1; -
 CC PIR: A53752; A53752.
 CC GCRdb; GCR_0861; -
 CC InterPro; IPR000057; -
 CC InterPro; IPR000174; -
 CC InterPro; IPR000276; -
 CC Pfam; PF00001; 7tm_1; 1.

DR PRINTS; PR00237; GPCRHHODPSN.
 DR PRINTS; PR00427; INTRLEUKIN8R.
 DR PRINTS; PR00573; INTRLEUKIN8R.
 DR PROSITE; PS00237; G-PROTEIN_RECP_FL_1; 1.
 DR PROSITE; PS00262; G-PROTEIN_RECP_FL_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Chemotaxis.
 FT DOMAIN 1 46 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 47 73 1 (POTENTIAL).
 FT DOMAIN 74 82 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 83 103 2 (POTENTIAL).
 FT DOMAIN 104 118 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 119 140 3 (POTENTIAL).
 FT DOMAIN 141 161 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 162 181 4 (POTENTIAL).
 FT DOMAIN 182 206 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 207 229 5 (POTENTIAL).
 FT DOMAIN 230 249 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 250 271 6 (POTENTIAL).
 FT DOMAIN 272 292 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 293 313 7 (POTENTIAL).
 FT DOMAIN 314 358 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 8 8 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 20 20 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT DISULFID 117 194 BY SIMILARITY.
 SQ SEQUENCE 358 AA; 40632 MW; 6899716944D6126A CRC64;

Query Match 54.5%; Score 67; DB 1; Length 358;
 Best Local Similarity 62.5%; Pred. No. 0.055;
 Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 6 FGFIPLMFIMFCYTF 21
 ||| :||: |:||| |
 Db 216 FGFIPLLMFLFCYVF 231

RESULT 8
 IL8B_MOUSE STANDARD; PRT; 359 AA.
 ID IL8B_MOUSE
 AC P35343;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE HIGH AFFINITY INTERLEUKIN-8 RECEPTOR B (IL-8R B) (CXCR-2) (GRO/MGSA RECEPTOR).
 DE RECEPTOR.
 GN IL8RB OR CXCR2 OR CMKAR2 OR GPCR16.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94117014; PubMed=8288247;
 RA Cerretti D.P., Nelson N., Kozlosky C.J., Morrissey P.J.,
 RA Copeland N.G., Gilbert D.J., Jenkins N.A., Dosik J.K., Mock B.A.;
 RT "The murine homologue of the human interleukin-8 receptor type B maps
 RT near the lty-lsh-Bcg disease resistance locus.";
 RL Genomics 18:410-413(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/C;
 RX MEDLINE=95050766; PubMed=7961909;
 RA Bozic C.R., Gerard N.P., von Uexkull-Guldenband C.,
 RA Kolakowski L.F. Jr., Conklyn M.J., Breslow R., Showell H.J.,
 RA Gerard C.;
 RT "The murine interleukin 8 type B receptor homologue and its ligands.
 RT Expression and biological characterization.";
 RL J. Biol. Chem. 269:29355-29358(1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SV;
 RX MEDLINE=95363183; PubMed=7636264;

RA Lee J., Cacalano G., Camerato T., Toy K., Moore M.W., Wood W.I.;
 RT "Chemokine binding and activities mediated by the mouse IL-8
 RL J. Immunol. 155:2158-2164(1995).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94252584; PubMed=8194768;
 RA Harada A., Kuno K., Nomura H., Mukaida N., Murakami S., Matsushima K.;
 RT "Cloning of a cDNA encoding a mouse homolog of the interleukin-8
 RL receptor".
 RL Gene 142:297-300(1994).
 RN [5]
 RP SEQUENCE OF 145-258 FROM N.A.
 RX MEDLINE=94116980; PubMed=8288218;
 RA Wilkie T.M., Chen Y., Gilbert D.J., Moore K.J., Yu L., Simon M.I.,
 RT "Identification, chromosomal location, and genome organization of
 RL mammalian G-protein-coupled receptors".
 RL Genomics 18:175-184(1993).
 CC -1- FUNCTION: RECEPTOR TO INTERLEUKIN-8, WHICH IS A POWERFUL
 CC NEUTROPHILS CHEMOTACTIC FACTOR. BINDING OF IL-8 TO THE RECEPTOR
 CC CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA A
 CC G-PROTEIN THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND
 CC MESSENGER SYSTEM. THIS RECEPTOR BINDS TO IL-8 WITH A HIGH AFFINITY
 CC AND TO GRO/MGSA AND NAP-2 ALSO WITH A HIGH AFFINITY.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC
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 CC -----
 CC EMBL; L23637; AAA39305.1; -
 CC EMBL; L13239; AAA62109.1; -
 CC EMBL; U31207; AAC52239.1; -
 CC EMBL; D17630; BAA04536.1; -
 CC EMBL; L20337; AAA16853.1; -
 CC PIR; A53677; A53677.
 CC GCRdb; GCR_0550; -
 CC GCRdb; GCR_0812; -
 CC GCRdb; GCR_0838; -
 CC GCRdb; GCR_1027; -
 CC GCRdb; GCR_1670; -
 CC MGD; MGI:105303; Cmkar2.
 CC InterPro; IPR000057; -
 CC InterPro; IPR000174; -
 CC InterPro; IPR000276; -
 CC Pfam; PF00001; 7tm1.1; 1.
 CC PRINTS; PR00237; GPCRHHODPSN.
 CC PRINTS; PR00427; INTRLEUKIN8R.
 CC PRINTS; PR00573; INTRLEUKIN8R.
 CC PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.
 CC PROSITE; PS0262; G-PROTEIN_RECEP_F1_2; 1.
 CC G-protein coupled receptor; Transmembrane; Glycoprotein;
 CC Chemotaxis.
 KW DOMAIN 1 47 EXTRACELLULAR (POTENTIAL).
 KW TRANSMEM 48 74 1 (POTENTIAL).
 KW DOMAIN 75 83 CYTOPLASMIC (POTENTIAL).
 KW TRANSMEM 84 104 2 (POTENTIAL).
 KW DOMAIN 105 119 EXTRACELLULAR (POTENTIAL).
 KW TRANSMEM 120 141 3 (POTENTIAL).
 KW DOMAIN 142 162 CYTOPLASMIC (POTENTIAL).
 KW TRANSMEM 163 182 4 (POTENTIAL).
 KW DOMAIN 183 207 EXTRACELLULAR (POTENTIAL).
 KW TRANSMEM 208 230 5 (POTENTIAL).
 KW DOMAIN 231 250 CYTOPLASMIC (POTENTIAL).
 KW TRANSMEM 251 272 6 (POTENTIAL).
 KW DOMAIN 273 293 EXTRACELLULAR (POTENTIAL).
 KW

FT TRANSMEM 294 314 7 (POTENTIAL).
 FT DOMAIN 315 359 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 23 23 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT DISULFID 118 195 BY SIMILARITY.
 SQ SEQUENCE 359 AA; 40425 MW; 74BD166E9B679F88 CRC64;
 Query Match 54.5%; Score 67; DB 1; Length 359;
 Best Local Similarity 62.5%; Pred. No. 0.055;
 Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 QY 6 FGFFPLMFIMFYCYTF 21
 Db 217 FGFLVPLLLMLFCYGF 232
 RESULT 9
 IL8B_HUMAN
 ID IL8B_HUMAN STANDARD; PRT; 360 AA.
 AC P25025;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE HIGH AFFINITY INTERLEUKIN-8 RECEPTOR B (IL-8R B) (CXCR-2) (GRO/MGSA
 DE RECEPTOR) (IL-8 RECEPTOR TYPE 2) (CDW128B).
 GN IL8RB OR CXCR2.
 OS Homo sapiens (Human).
 OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91368200; PubMed=1891716;
 RA Murphy P.M., Tiffany H.L.;
 RT "Cloning of complementary DNA encoding a functional human
 RT interleukin-8 receptor".
 RL Science 253:1280-1283(1991).
 RN [2]
 RP SEQUENCE FROM N.A. AND CHARACTERIZATION.
 RX MEDLINE=91205012; PubMed=8384312;
 RA Carretti D.P., Kozlosky C.J., Vanden Bos T., Nelson N., Gearing D.P.,
 RA Beckmann M.P.;
 RT "Molecular characterization of receptors for human interleukin-8,
 RT GRO/melanoma growth-stimulatory activity and neutrophil activating
 RT peptide-2".
 RL Mol. Immunol. 30:359-367(1993).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94209273; PubMed=7512557;
 RA Sprenger H., Lloyd A.R., Lautens L.L., Bonner T.I., Kelvin D.J.;
 RT "Structure, genomic organization, and expression of the human
 RT interleukin-8 receptor B gene".
 RL J. Biol. Chem. 269:11065-11072(1994).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=95014476; PubMed=7929358;
 RA Ahuja S.K., Shetty A., Tiffany H.L., Murphy P.M.;
 RT "Comparison of the genomic organization and promoter function for
 RT human interleukin-8 receptors A and B".
 RL J. Biol. Chem. 269:26381-26389(1994).
 RN [5]
 RP CHARACTERIZATION
 RX MEDLINE=92355587; PubMed=1379593;
 RA Lee J., Horuk R., Rice G.C., Bennett G.L., Camerato T., Wood W.I.;
 RT "Characterization of two high affinity human interleukin-8
 RT receptors".
 RL J. Biol. Chem. 267:16283-16287(1992).
 CC -1- FUNCTION: RECEPTOR TO INTERLEUKIN-8, WHICH IS A POWERFUL
 CC NEUTROPHILS CHEMOTACTIC FACTOR. BINDING OF IL-8 TO THE RECEPTOR
 CC CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA A
 CC G-PROTEIN THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND
 CC MESSENGER SYSTEM. THIS RECEPTOR BINDS TO IL-8 WITH A HIGH AFFINITY

CC AND TO GRO/MGSA AND NAP-2 ALSO WITH A HIGH AFFINITY.
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -!- DATABASE: NAME=PROW; NOTE=CD guide Cdw128b entry;
 CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cdw128b.htm"
 CC
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 CC
 CC -----
 CC EMBL; M73969; AAA83148.1; -
 CC EMBL; M94582; AAA36108.1; -
 CC EMBL; M9412; AAC14460.1; -
 CC EMBL; L19593; AAB59437.1; -
 CC EMBL; U11869; AAB60656.1; -
 CC PIR; A39446; A39446.
 CC PIR; A53611; A53611.
 CC HSP; P34996; 1DD0.
 CC GCRdb; GCR_0077; -
 CC GCRdb; GCR_0610; -
 CC GCRdb; GCR_1001; -
 CC GCRdb; GCR_1339; -
 CC GCRdb; GCR_1831; -
 CC MIM; 146928; -
 CC InterPro; IPR000057; -
 CC InterPro; IPR000174; -
 CC InterPro; IPR000276; -
 CC Pfam; PF00001; 7tm_1; 1.
 CC PRINTS; PR00237; GPCRHHODOPSN.
 CC PRINTS; PR00427; INTRLEUKIN8R.
 CC PRINTS; PR00573; INTRLEUKIN8R.
 CC PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.
 CC PROSITE; PS00262; G-PROTEIN_RECEP_F1_2; 1.
 CC G-protein coupled receptor; Transmembrane; Glycoprotein;
 CC Chemotaxis.

FT DOMAIN 1 48 ----- EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 49 75 1 (POTENTIAL).
 FT DOMAIN 76 84 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 85 105 2 (POTENTIAL).
 FT DOMAIN 106 120 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 121 142 3 (POTENTIAL).
 FT DOMAIN 143 163 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 164 183 4 (POTENTIAL).
 FT DOMAIN 184 208 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 209 231 5 (POTENTIAL).
 FT DOMAIN 232 251 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 252 273 6 (POTENTIAL).
 FT DOMAIN 274 294 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 295 315 7 (POTENTIAL).
 FT DOMAIN 316 360 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 22 22 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT DISULFID 119 196 BY SIMILARITY.
 SQ SEQUENCE 360 AA; 40759 MW; 564F04A8BCC0A197 CRC64;

Query Match 54.5%; Score 67; DB 1; Length 360;
 Best Local Similarity 62.5%; Pred. No. 0.055;
 Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Oy 6 FGFFIPLMFICYTF 21
 ||| :|| :||| |
 Db 218 FGFTVPLLMFLCYGF 233

RESULT 10
 IL8B_CANFA STANDARD; PRT; 356 AA.
 AC 097571;
 DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE HIGH AFFINITY INTERLEUKIN-8 RECEPTOR B (IL-8R B) (CXCR-2) (GRO/MGSA
 DE RECEPTOR).
 GN IL8RB OR CXCR2.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BEAGLE;
 RA Chang Y.F., Novosel V., Chang C.F.;
 RT "The isolation and sequence of canine interleukin-8 receptor
 RT homolog";
 RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: RECEPTOR TO INTERLEUKIN-8, WHICH IS A POWERFUL
 CC NEUTROPHILS CHEMOTACTIC FACTOR. BINDING OF IL-8 TO THE RECEPTOR
 CC CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA A
 CC G-PROTEIN THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND
 CC MESSENGER SYSTEM. THE AFFINITY OF THIS RECEPTOR IS IL-8 >> NAP-2 >
 CC MGSA (GRO).
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC
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 CC or send an email to license@isb-sib.ch)
 CC
 CC -----
 CC EMBL; AF047047; AAC98968.1; -
 CC InterPro; IPR000057; -
 CC InterPro; IPR000174; -
 CC InterPro; IPR000276; -
 CC InterPro; IPR000355; -
 CC InterPro; IPR003277; -
 CC Pfam; PF00001; 7tm_1; 1.
 CC PRINTS; PR00237; GPCRHHODOPSN.
 CC PRINTS; PR00427; INTRLEUKIN8R.
 CC PRINTS; PR00573; INTRLEUKIN8R.
 CC PRINTS; PR00645; LCR1ORPHANR.
 CC PRINTS; PR00657; CCHEMOKINER.
 CC PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.
 CC PROSITE; PS00262; G-PROTEIN_RECEP_F1_2; 1.
 CC G-protein coupled receptor; Transmembrane; Glycoprotein;
 CC Chemotaxis.
 FT DOMAIN 1 46 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 47 73 1 (POTENTIAL).
 FT DOMAIN 74 82 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 83 103 2 (POTENTIAL).
 FT DOMAIN 104 118 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 119 140 3 (POTENTIAL).
 FT DOMAIN 141 161 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 162 181 4 (POTENTIAL).
 FT DOMAIN 182 206 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 207 229 5 (POTENTIAL).
 FT DOMAIN 230 249 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 250 269 6 (POTENTIAL).
 FT DOMAIN 270 290 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 291 311 7 (POTENTIAL).
 FT DOMAIN 312 356 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 8 8 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT DISULFID 20 20 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT SEQUENCE 356 AA; 40505 MW; 2B67DD4E9DD39B15 CRC64;

Query Match 53.7%; Score 66; DB 1; Length 356;
 Best Local Similarity 71.4%; Pred. No. 0.074;
 Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;


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QY 6 FGFIPLMFIFCY 19
    ||| :||| :|||
Db 216 FGFIPLMFIFCY 229

RESULT 11
CKR7_MOUSE STANDARD; PRT; 378 AA.
AC P47774;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE C-C CHEMOKINE RECEPTOR TYPE 7 PRECURSOR (C-C CKR-7) (CCR-7)
DE (MIP-3 BETA RECEPTOR) (EBV-INDUCED G PROTEIN-COUPLED RECEPTOR 1)
DE (EB11).
GN CKR7 OR CMKBR7 OR EB11 OR EB11H.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B6/CBA; TISSUE=Thymus;
RX MEDLINE=95154835; PubMed=7851893;
RA Schweickart V.L., Raport C.J., Godiska R., Byers M.G., Eddy R.L. Jr.,
RA Shows T.B., Gray P.W.;
RT "Cloning of human and mouse EB11, a lymphoid-specific
RT G-protein-coupled receptor encoded on human chromosome 17q12-q21.2.";
RL Genomics 23:643-650(1994).
CC -!- FUNCTION: RECEPTOR FOR THE MIP-3-BETA CHEMOKINE. PROBABLE MEDIATOR
CC OF EBV EFFECTS ON B LYMPHOCYTES OR OF NORMAL LYMPHOCYTE FUNCTIONS.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; L31580; AAA74232.1;
CC MGD; MGI:103011; Cmkbr7.
CC InterPro; IPR000276;
CC InterPro; IPR001718;
CC Pfam; PF00001; 7tm_1; 1.
CC PRINTS; PR00237; GPCRHHODOPSN.
CC PROSITE; PR00641; CHEMOKINER7.
CC PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
CC PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 24
FT CHAIN 25 378 C-C CHEMOKINE RECEPTOR TYPE 7.
FT DOMAIN 25 59 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 60 86 1 (POTENTIAL).
FT DOMAIN 87 95 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 96 116 2 (POTENTIAL).
FT DOMAIN 117 130 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 131 152 3 (POTENTIAL).
FT DOMAIN 153 170 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 171 191 4 (POTENTIAL).
FT DOMAIN 192 219 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 220 247 5 (POTENTIAL).
FT DOMAIN 248 263 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 264 289 6 (POTENTIAL).
FT DOMAIN 290 313 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 314 331 7 (POTENTIAL).
FT DOMAIN 332 378 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 36 36 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 129 210 BY SIMILARITY.
SQ SEQUENCE 378 AA; 42941 MW; ACBIA422CF54AA54 CRC64;

QY 3 ELLFGFFIPLMFIFCYTEIV 23
    ::||| :||| :||| :|||
Db 227 QMVFGFLVPLMFAMSFYLIIII 247

RESULT 12
BONZ_CERAE
ID BONZ_CERAE STANDARD; PRT; 342 AA.
AC O18983;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE G PROTEIN-COUPLED RECEPTOR BONZO.
GN BONZO.
OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9534;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97373958; PubMed=9230441;
RA Deng H.K., Unutmaz D., Kewalramani V.N., Littman D.R.;
RT "Expression cloning of new receptors used by simian and human
RT immunodeficiency viruses.";
RL Nature 388:296-300(1997).
CC -!- FUNCTION: ORPHAN RECEPTOR. COULD BE A CHEMOKINE RECEPTOR. USED AS
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF007859; AAB64225.1;
CC GCRdb; GCR_2411;
CC InterPro; IPR000276;
CC InterPro; IPR002235;
CC Pfam; PF00001; 7tm_1; 1.
CC PRINTS; PR00237; GPCRHHODOPSN.
CC PRINTS; PR01105; BONZOORPHANR.
CC PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
CC PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 32 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 33 59 1 (POTENTIAL).
FT DOMAIN 60 89 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 69 88 2 (POTENTIAL).
FT DOMAIN 90 103 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 104 125 3 (POTENTIAL).
FT DOMAIN 126 143 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 144 164 4 (POTENTIAL).
FT DOMAIN 165 187 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 188 215 5 (POTENTIAL).
FT DOMAIN 216 231 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 232 259 6 (POTENTIAL).
FT DOMAIN 260 275 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 276 293 7 (POTENTIAL).
FT DOMAIN 294 342 CYTOPLASMIC (POTENTIAL).
FT DISULFID 102 180 BY SIMILARITY.
FT CARBOHYD 16 16 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 342 AA; 39226 MW; 6CBFE389C6E5919E CRC64;
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Query Match      52.8%; Score 65; DB 1; Length 342;
Best Local Similarity 47.6%; Pred. No. 0.096;
Matches 10; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 3 ELLFGFFPLMFIMFYTFIV 23
   : |||: || | : |
Db 195 QMTLGFPLLMAMIVCYSVII 215

RESULT 13
BONZ_HUMAN
ID BONZ_HUMAN STANDARD; PRT; 342 AA.
AC O00574; O00575;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE G PROTEIN-COUPLED RECEPTOR BONZO (G PROTEIN-COUPLED RECEPTOR STRL33).
GN BONZO OR STRL33 OR TYMSTR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97373958; PubMed=9230441;
RA Deng H.K., Unutmaz D., Kewalramani V.N., Littman D.R.;
RT "Expression cloning of new receptors used by simian and human
   immunodeficiency viruses."
RL Nature 388:296-300(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97311099; PubMed=9166430;
RA Liao F., Alkhatib G., Feden K.W.C., Sharma G., Berger E.A.,
RA Farber J.M.;
RT "STRL33, A novel chemokine receptor-like protein, functions as a
   fusion cofactor for both macrophage-tropic and T cell line-tropic
   HIV-1."
RL J. Exp. Med. 185:2015-2023(1997).
RN [3]
RP SEQUENCE FROM N.A.
RX TISSUE=Blood;
RC MEDLINE=97431687; PubMed=9285716;
RA Loetscher M., Amara A., Oberlin E., Brass N., Legler D.F.,
RA Loetscher P., D'Apuzzo M., Meese E.U., Rousset D., Virelizier J.L.,
RA Baggiolini M., Arenzana-Seisdedos F., Moser B.;
RT "TYMSTR, a putative chemokine receptor selectively expressed in
   activated T cells, exhibits HIV-1 coreceptor function."
RL Curr. Biol. 7:652-660(1997).
CC -!- FUNCTION: ORPHAN RECEPTOR. COULD BE A CHEMOKINE RECEPTOR. USED AS
   A CORECEPTOR BY SIVS AND BY STRAINS OF HIV-2 AND M-TROPIC HIV-1.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN LYMPHOID TISSUES AND ACTIVATED T
   CELLS.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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   or send an email to license@isb-sib.ch).
CC EMBL; AF007545; AAB64221.1;
CC EMBL; U73529; AAB61456.1;
CC EMBL; U73531; AAB61457.1;
CC EMBL; Y13248; CAA73698.1;
CC MIM; 605163;
CC GCRDb; GCR_1328;
CC GCRDb; GCR_1330;
CC GCRDb; GCR_2393;

InterPro; IPR000276;
InterPro; IPR002235;
Pfam; PF00001; 7tm.1; 1.
PRINTS; PR00237; GPCRHDOPSN.
PRINTS; PR01105; BONZOORPHANR.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Polymorphism.
FT DOMAIN 1 32
FT TRANSMEM 33 59
FT DOMAIN 60 68
FT TRANSMEM 69 89
FT DOMAIN 90 103
FT TRANSMEM 104 125
FT DOMAIN 126 143
FT TRANSMEM 144 164
FT DOMAIN 165 187
FT TRANSMEM 188 215
FT DOMAIN 216 231
FT TRANSMEM 232 259
FT DOMAIN 260 275
FT TRANSMEM 276 293
FT DOMAIN 294 342
FT DISULFID 102 180
FT CARBOHYD 16 16
FT VARIANT 25 25
SQ SEQUENCE 342 AA; 39280 MW; 9FBC02556D1082E CRC64;

Query Match      52.8%; Score 65; DB 1; Length 342;
Best Local Similarity 47.6%; Pred. No. 0.096;
Matches 10; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 3 ELLFGFFPLMFIMFYTFIV 23
   : |||: || | : |
Db 195 QMTLGFPLLMAMIVCYSVII 215

RESULT 14
BONZ_MACNE
ID BONZ_MACNE STANDARD; PRT; 342 AA.
AC O19024;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE G PROTEIN-COUPLED RECEPTOR BONZO.
GN BONZO.
OS Macaca nemestrina (Pig-tailed macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Macaca.
OX NCBI_TaxID=9545;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97373958; PubMed=9230441;
RA Deng H.K., Unutmaz D., Kewalramani V.N., Littman D.R.;
RT "Expression cloning of new receptors used by simian and human
   immunodeficiency viruses."
RL Nature 388:296-300(1997).
CC -!- FUNCTION: ORPHAN RECEPTOR. COULD BE A CHEMOKINE RECEPTOR. USED AS
   A CORECEPTOR BY SIVS AND BY STRAINS OF HIV-2 AND M-TROPIC HIV-1.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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   or send an email to license@isb-sib.ch).
CC EMBL; AF007545; AAB64221.1;
CC EMBL; U73529; AAB61456.1;
CC EMBL; U73531; AAB61457.1;
CC EMBL; Y13248; CAA73698.1;
CC MIM; 605163;
CC GCRDb; GCR_1328;
CC GCRDb; GCR_1330;
CC GCRDb; GCR_2393;

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DR EMBL: AF007858; AAB64224.1; -;
 DR GCRDB; GCR_2409; -;
 DR InterPro; IPR000276; -;
 DR Pfam; PF00001; 7tm.1; 1.
 DR PRINTS; PR00237; GPCRHHODOPSN.
 DR PRINTS; PR01105; BONZOORPHAN.
 DR PROSITE; PS00237; G-PROTEIN_RECP_FL_1; 1.
 DR PROSITE; PS0262; G-PROTEIN_RECP_FL_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 32
 FT TRANSMEM 33 59
 FT DOMAIN 60 68
 FT TRANSMEM 69 89
 FT DOMAIN 90 103
 FT TRANSMEM 104 125
 FT DOMAIN 126 143
 FT TRANSMEM 144 164
 FT DOMAIN 165 187
 FT TRANSMEM 188 215
 FT DOMAIN 216 231
 FT TRANSMEM 232 259
 FT DOMAIN 260 275
 FT TRANSMEM 276 293
 FT DOMAIN 294 342
 FT DISULFID 102 180
 FT CARBOHYD 16 16
 SQ SEQUENCE 342 AA; 39297 MW; 55F9F68CB62D2DF5 CRC64;

Query Match 52.8%; Score 65; DB 1; Length 342;
 Best Local Similarity 47.6%; Pred. No. 0.096;
 Matches 10; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 3 ELLFGFFPLMFMIFCYTFIV 23
 :: |||:: || ||:
 Db 195 QMTLGFLLAMIVCYSVII 215

RESULT 15
 BONZ_MACMU STANDARD; PRT; 343 AA.
 AC Q9XT45;
 DT 01-OCT-2000 (Rel. 40, Created)
 DT 01-OCT-2000 (Rel. 40, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE G PROTEIN-COUPLED RECEPTOR BONZO (G PROTEIN-COUPLED RECEPTOR STRL33).
 GN BONZO OR STRL33.
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Macaca.
 OX NCBI_TaxID=9544;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Margulies B.J., Hauer D.A., Clements J.E.;
 RT "Identification and characterization of thirteen rhesus macaque
 chemokine receptors and chemokine receptor homologues";
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: ORPHAN RECEPTOR. COULD BE A CHEMOKINE RECEPTOR. USED AS
 CC A CORECEPTOR BY SIVS AND BY STRAINS OF HIV-2 AND M-TROPIC HIV-1.
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AF124380; AAD31419.1; -;

DR InterPro; IPR000276; -;
 DR InterPro; IPR002235; -;
 DR Pfam; PF00001; 7tm.1; 1.
 DR PRINTS; PR00237; GPCRHHODOPSN.
 DR PRINTS; PR01105; BONZOORPHAN.
 DR PROSITE; PS00237; G-PROTEIN_RECP_FL_1; 1.
 DR PROSITE; PS0262; G-PROTEIN_RECP_FL_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 33
 FT TRANSMEM 34 60
 FT DOMAIN 61 69
 FT TRANSMEM 70 90
 FT DOMAIN 91 104
 FT TRANSMEM 105 126
 FT DOMAIN 127 144
 FT TRANSMEM 145 165
 FT DOMAIN 166 188
 FT TRANSMEM 189 216
 FT DOMAIN 217 232
 FT TRANSMEM 233 260
 FT DOMAIN 261 276
 FT TRANSMEM 277 294
 FT DOMAIN 295 343
 FT CARBOHYD 17 17
 FT DISULFID 103 181
 SQ SEQUENCE 343 AA; 39423 MW; 48DB2544949EB83F CRC64;

Query Match 52.8%; Score 65; DB 1; Length 343;
 Best Local Similarity 47.6%; Pred. No. 0.096;
 Matches 10; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 3 ELLFGFFPLMFMIFCYTFIV 23
 :: |||:: || ||:
 Db 196 QMTLGFLLAMIVCYSVII 216

Search completed: May 23, 2001, 15:36:20
 Job time: 651 sec

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	103	83.7	367	11	Q9R1V0	Q9R1V0 mus musculus	
2	71	57.7	368	13	O42444	O42444 oncorhynchus	
3	67	54.5	111	4	Q9P2T6	Q9P2T6 homo sapiens	
4	66	53.7	521	11	Q9QXZ9	Q9QXZ9 mus musculus	
5	65.5	53.3	342	13	Q9XZ39	Q9XZ39 cyprinus carpio	
6	65	52.8	174	6	Q9TU48	Q9TU48 bos taurus	
7	65	52.8	174	6	Q9TQ57	Q9TQ57 bos taurus	
8	65	52.8	339	11	Q9JJ71	Q9JJ71 mus musculus	
9	65	52.8	342	6	Q9TV16	Q9TV16 pan troglodytes	
10	65	52.8	343	6	Q9XT45	Q9XT45 macaca mulatta	
11	65	52.8	343	6	Q9N0Z0	Q9N0Z0 cercocebus	
12	65	52.8	352	11	Q9JK47	Q9JK47 mus musculus	
13	65	52.8	369	4	Q9UQ06	Q9UQ06 homo sapiens	
14	63	51.2	478	4	Q9UHM6	Q9UHM6 homo sapiens	
15	62	50.4	367	11	O88410	O88410 mus musculus	
16	62	50.4	367	11	Q9QWN6	Q9QWN6 mus musculus	
17	62	50.4	415	4	O15185	O15185 homo sapiens	
18	62	50.4	475	11	Q9QWG9	Q9QWG9 cavia porcellus	
19	61	49.6	367	11	Q9JII9	Q9JII9 rattus norvegicus	

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042444
ID O42444 PRELIMINARY; PRT; 368 AA.
AC O42444;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE INTERLEUKIN-8-LIKE RECEPTOR.
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE FROM N.A.
RA Zou J., Daniels G.D., Cunningham C., Secombes C.J.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ003159; CAA05917.1; -
DR INTERPRO: IPR000276; -
DR PFAM: PF00001; 7tm1; 1.
DR PRINTS: PR00237; GPCRHHODOPSN.
DR PROSITE: PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
SQ SEQUENCE 368 AA; 41523 MW; BE28E2D4C47E821A CRC64;

Query Match 57.7%; Score 71; DB 13; Length 368;
Best Local Similarity 47.8%; Pred. NO. 0.029;
Matches 11; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 1 GLELLFGFRLPLMFIFCYTFIV 23
DB 216 GLQICMGFCPLPLLVVFYAGII 238

RESULT 3
Q9P2T6 PRELIMINARY; PRT; 111 AA.
AC Q9P2T6;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE IL-8 RECEPTOR TYPE B (FRAGMENT).
GN CXCR2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kato H., Tsuchiya N., Tokunaga K.;
RT "Detection of single nucleotide polymorphisms in the coding region of
human CXCR2-chemokine receptor CXCR1, CXCR2, and CXCR3."
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB032734; BAA92296.1; -
KW Receptor.
FT NON_TER 1 1
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12947 MW; 1425DC123439A1BB CRC64;

Query Match 54.5%; Score 67; DB 4; Length 111;
Best Local Similarity 62.5%; Pred. NO. 0.037;
Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 6 FGFFPLMFIFCYTF 21
DB 28 FGFIPLLMFICYGF 43

RESULT 4
Q9QXZ9 PRELIMINARY; PRT; 521 AA.
ID Q9QXZ9
AC Q9QXZ9;
DT 01-MAY-2000 (TREMBlrel. 13, Created)

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DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE MELANOPSIN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE-RETINA;
RX MEDLINE=20098934; PubMed=10632589;
RA Provencio I., Rodriguez I.R., Jiang G., Hayes W.P., Moreira E.F.,
RA Rolliag M.D.;
RT "A novel human opsin in the inner retina.";
J. Neurosci. 20:600-605(2000).
DR EMBL: AF147789; AAF24979.1; -
DR INTERPRO: IPR000276; -
DR INTERPRO: IPR001760; -
DR PFAM: PF00001; 7tm1; 1.
DR PRINTS: PR00237; GPCRHHODOPSN.
DR PROSITE: PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
DR PROSITE: PS00238; OPSIN; 1.
SQ SEQUENCE 521 AA; 57231 MW; 50FDICBB05669DA9 CRC64;

Query Match 53.7%; Score 66; DB 11; Length 521;
Best Local Similarity 64.7%; Pred. NO. 0.18;
Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 6 FGFFPLMFIFCYTFI 22
DB 241 FVFPLPLLIIFCYIFI 257

RESULT 5
Q93239 PRELIMINARY; PRT; 342 AA.
ID Q93239;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE CXCR2 CHEMOKINE RECEPTOR-2.
OS Cyprinus carpio (Common carp).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Cyprininae; Cyprinus.
OX NCBI_TaxID=7962;
RN [1]
RP SEQUENCE FROM N.A.
RA Fujiki K., Nakao M., Shin D., Yano T.;
RT "cDNA cloning of a carp homologue-2 of mammalian interleukin-8
receptors."
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB010713; BAA31470.1; -
DR INTERPRO: IPR000276; -
DR PFAM: PF00001; 7tm1; 1.
DR PRINTS: PR00237; GPCRHHODOPSN.
DR PROSITE: PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
SQ SEQUENCE 342 AA; 38481 MW; 8946E5ED5E34B39 CRC64;

Query Match 53.3%; Score 65.5; DB 13; Length 342;
Best Local Similarity 54.2%; Pred. NO. 0.15;
Matches 13; Conservative 3; Mismatches 5; Indels 3; Gaps 1;

QY 1 GLELL---FGFFPLMFIFCYTF 21
DB 191 GLRILHHTLGLFPLVAVMFCYGF 214

RESULT 6
Q9TU48

```

```
ID Q9TU48 PRELIMINARY; PRT; 174 AA.
AC Q9TU48;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE INTERLEUKIN 8 RECEPTOR-LIKE PROTEIN (FRAGMENT).
GN IL8R.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Grosse W.M., Kappes S.M., Laegreid W.W., Keele J.W.,
RA Chitko-McKown C.G., Heaton M.P.;
RT "Single Nucleotide Polymorphism (SNP) Discovery and Linkage Mapping of
RT Bovine Cytokine Genes.";
RL Mamm. Genome 10:1062-1069(1999).
DR EMBL; AF140650; AAF07867.1; -
DR INTERPRO; IPR000174; -
DR INTERPRO; IPR000276; -
DR PFAM; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PRINTS; PR00427; INTRLEUKIN8R.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 174 174
SQ SEQUENCE 174 AA; 20107 MW; D20E223B08FE836 CRC64;

Query Match 52.8%; Score 65; DB 6; Length 174;
Best Local Similarity 62.5%; Pred. No. 0.1;
Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 6 FGFFIPLMFIMFCYTF 21
Db 66 FGFLPLLLVLMFCYGF 81

RESULT 7
Q9TQS7 PRELIMINARY; PRT; 174 AA.
AC Q9TQS7;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE INTERLEUKIN 8 RECEPTOR-LIKE PROTEIN (FRAGMENT).
GN IL8R.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Grosse W.M., Kappes S.M., Laegreid W.W., Keele J.W.,
RA Chitko-McKown C.G., Heaton M.P.;
RT "Single Nucleotide Polymorphism (SNP) Discovery and Linkage Mapping of
RT Bovine Cytokine Genes.";
RL Mamm. Genome 10:1062-1069(1999).
DR EMBL; AF140652; AAF07869.1; -
DR EMBL; AF140648; AAF07865.1; -
DR EMBL; AF140649; AAF07866.1; -
DR EMBL; AF140651; AAF07868.1; -
DR INTERPRO; IPR000174; -
DR INTERPRO; IPR000276; -
DR PFAM; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PRINTS; PR00427; INTRLEUKIN8R.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 174 174
```

```
SQ SEQUENCE 174 AA; 20116 MW; D21C877CEC5BAFC6 CRC64;

Query Match 52.8%; Score 65; DB 6; Length 174;
Best Local Similarity 62.5%; Pred. No. 0.1;
Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 6 FGFFIPLMFIMFCYTF 21
Db 66 FGFLPLLLVLMFCYGF 81

RESULT 8
Q9JJ71 PRELIMINARY; PRT; 339 AA.
AC Q9JJ71;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE CYSLT1.
GN MCYSLT1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=CELL;
RA Ogasawara H., Izumi T., Shimizu T.;
RT "mouse CysLT1.";
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB044087; BAA96809.1; -
SQ SEQUENCE 339 AA; 39160 MW; 27BF72C0F3F0F00F CRC64;

Query Match 52.8%; Score 65; DB 11; Length 339;
Best Local Similarity 50.0%; Pred. No. 0.17;
Matches 11; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

-Oy- 2 LELFGFFIPLMFIMFCYTFIV-23-
Db 194 VSLFFGIIPFVTIIVCYTMII 215

RESULT 9
Q9TV16 PRELIMINARY; PRT; 342 AA.
AC Q9TV16;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE G PROTEIN-COUPLED RECEPTOR STRL33.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=STRL33(BONZO);
RA Brussel A., Pretet J.L., Girard M., Butor C.;
RT "Sequences and Predicted Structures of Chimpanzee STRL33 (Bonzo) and
RT gpr15 (BOB).";
RL AIDS Res. Hum. Retroviruses 15:0-0(1999).
DR EMBL; AF084229; AAD52041.1; -
DR INTERPRO; IPR000248; -
DR INTERPRO; IPR000276; -
DR INTERPRO; IPR000355; -
DR INTERPRO; IPR001277; -
DR INTERPRO; IPR002235; -
DR PFAM; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PRINTS; PR00241; ANGIOTENSINR.
DR PRINTS; PR00645; LCR1ORPHANR.
```

DR PRINTS; PR00657; CCHEMOKINER.
 DR PRINTS; PR01105; BONZOORPHANR.
 DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
 KW Receptor.
 SQ SEQUENCE 342 AA; 39273 MW; 5B58003797806B2A CRC64;

Query Match 52.8%; Score 65; DB 6; Length 342;
 Best Local Similarity 47.6%; Pred. No. 0.18;
 Matches 10; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

OY 3 ELLFGFFIPLMFIFCYTFIV 23
 :: |||::||: || ||: |:
 Db 195 QMTLGFLLPLLMIVCYSVII 215

RESULT 10
 Q9XT45 PRELIMINARY; PRT; 343 AA.
 ID Q9XT45
 AC Q9XT45;
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
 DE CHEMOKINE RECEPTOR BONZO.
 GN STRL33.
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecoidea; Macaca.
 OX NCBI_TaxID=9544;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Margulies B.J., Hauer D.A., Clements J.E.;
 RT "Identification of Thirteen Rhesus Macaque Chemokine Receptors.";
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF124380; AAD31419.1;
 DR INTERPRO; IPR000248;
 DR INTERPRO; IPR000276;
 DR INTERPRO; IPR000355;
 DR INTERPRO; IPR001277;
 DR INTERPRO; IPR002235;
 DR PFAM; PF00001; 7tm_1.
 DR PRINTS; PR00237; GPCRHHODOPSN.
 DR PRINTS; PR00241; ANGIOTENSINR.
 DR PRINTS; PR00645; LCRIORPHANR.
 DR PRINTS; PR00657; CCHEMOKINER.
 DR PRINTS; PR01105; BONZOORPHANR.
 DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
 KW Receptor.
 SQ SEQUENCE 343 AA; 39423 MW; 48DB2544949EB83F CRC64;

Query Match 52.8%; Score 65; DB 6; Length 343;
 Best Local Similarity 47.6%; Pred. No. 0.18;
 Matches 10; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

OY 3 ELLFGFFIPLMFIFCYTFIV 23
 :: |||::||: || ||: |:
 Db 196 QMTLGFLLPLLMIVCYSVII 216

RESULT 11
 Q9N020 PRELIMINARY; PRT; 343 AA.
 ID Q9N020
 AC Q9N020;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE STRL33.
 OS Cercopithecus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecoidea; Cercopithecus.

OX NCBI_TaxID=9531;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=20261727; PubMed=10799581;
 RA Pohlmann S., Lee B., Meister S., Krumbiegel M., Leslie G., Doms R.W.,
 RA Kirchhoff F.;
 RT "Simian immunodeficiency virus utilizes human and sooty mangabey but
 not rhesus macaque STRL33 for efficient entry.";
 RL J. Virol. 74:5075-5082(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Pohlmann S., Lee B., Meister S., Krumbiegel M., Leslie G., Doms R.W.,
 RA Kirchhoff F.;
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF237559; AAF68392.1;
 SQ SEQUENCE 343 AA; 39588 MW; A75B7A0751C13455 CRC64;

Query Match 52.8%; Score 65; DB 6; Length 343;
 Best Local Similarity 47.6%; Pred. No. 0.18;
 Matches 10; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

OY 3 ELLFGFFIPLMFIFCYTFIV 23
 :: |||::||: || ||: |:
 Db 196 QMTLGFLLPLLMIVCYSVII 216

RESULT 12
 Q9JK47 PRELIMINARY; PRT; 352 AA.
 ID Q9JK47
 AC Q9JK47;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE LEUKOTRIENE D4 RECEPTOR.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=BLOOD;
 RA Mollerup J., Jorgensen S., Hougaard C., Hoffmann E.K.;
 RT "Cloning and functional expression of a murine leukotriene D4
 receptor.";
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF263370; AAF73047.1;
 KW Receptor.
 SQ SEQUENCE 352 AA; 40667 MW; F25A465107B4282D CRC64;

Query Match 52.8%; Score 65; DB 11; Length 352;
 Best Local Similarity 50.0%; Pred. No. 0.18;
 Matches 11; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

OY 2 LELLGFFIPLMFIFCYTFIV 23
 : | ||| | : : ||| |:
 Db 207 VSLFFGFIIPFTIIVCYTMI 228

RESULT 13
 Q9U006 PRELIMINARY; PRT; 369 AA.
 ID Q9U006
 AC Q9U006;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE CHEMOKINE RECEPTOR CCR9 (CC CHEMOKINE RECEPTOR 9A).
 GN CCR9.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;

Query Match 51.2%; Score 63; DB 4; Length 478;
Best Local Similarity 58.8%; Pred. No. 0.43;
Matches 10; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Search completed: May 23, 2001, 15:35:16
Job time: 622 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 23, 2001, 15:28:31 ; Search time 184.73 seconds
(without alignments)
4.951 Million cell updates/sec

Title: US-08-887-977-10_COPY_230_245

Perfect score: 78
Sequence: 1 KTLVQAQSKRHKRAIR 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 390729 seqs, 57163235 residues

Total number of hits satisfying chosen parameters: 390729

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_0401.*
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22: /SID56/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	78	100.0	365	19 W48086	Human dendritic ce
2	78	100.0	365	21 Y97077	Primate (human) ch
3	49	62.8	357	21 B19605	Human CC chemokine
4	49	62.8	357	21 Y90615	Human G protein-co
5	48	61.5	358	15 R33745	Partial sequence o
6	48	61.5	358	21 B21689	Human 7TM receptor
7	48	61.5	359	15 R53747	Seven transmembran
8	48	61.5	359	19 W48728	Murine V31 seven t
9	48	61.5	359	21 B21691	Murine 7TM recepto
10	48	61.5	361	20 W97348	An Epstein-barr vi
11	48	61.5	378	15 R34079	Epstein Barr virus

12	48	61.5	378	15 R53744	Putative seven tra
13	48	61.5	378	19 W48724	Human V31 seven tr
14	48	61.5	378	19 W56164	G-protein coupled
15	48	61.5	378	19 W33622	Epstein Barr virus
16	48	61.5	378	21 B21688	Human 7TM receptor
17	48	61.5	378	21 B21699	Human G protein-co
18	48	61.5	378	21 Y90629	Human CCR7. Homo
19	48	61.5	378	22 B50859	Putative seven tra
20	48	61.5	410	15 R53743	Polypeptide sequen
21	48	61.5	410	19 W48723	Genomic clone of 7
22	48	61.5	410	21 B21687	Rodent chemokine r
23	45	57.7	302	19 W70001	A7 times membrane
24	45	57.7	351	20 Y23825	Human mutant G pro
25	45	57.7	357	21 Y90649	Human chemokine re
26	44.5	57.1	332	18 W26766	Human CCR5. Homo
27	44.5	57.1	352	18 W27407	Human chemokine re
28	44.5	57.1	352	18 W27123	Macaque chemokine
29	44.5	57.1	352	18 W27125	Human G-protein ch
30	44.5	57.1	352	18 W07602	Human CC chemokine
31	44.5	57.1	352	19 W23835	Human CC chemokine
32	44.5	57.1	352	20 W88232	HIV-1 co-receptor
33	44.5	57.1	352	21 Y80128	Human G-protein ch
34	44.5	57.1	360	16 R79166	Human monocyte che
35	44.5	57.1	360	18 W35833	Human monocyte che
36	44.5	57.1	371	19 W23834	Human CC chemokine
37	44.5	57.1	374	16 R79165	Human monocyte che
38	44.5	57.1	439	20 Y41280	Fusion protein con
39	43	55.1	355	17 W03376	CC-chemokine recep
40	43	55.1	355	17 W03377	CC-chemokine recep
41	43	55.1	355	17 W03378	CC-chemokine recep
42	43	55.1	355	18 W31850	Human eosinophil e
43	43	55.1	355	18 W27124	Human chemokine re
44	43	55.1	355	18 W10100	Human C-C chemokin
45	43	55.1	355	19 W51744	Human C-C chemokin

ALIGNMENTS

RESULT	1
W48086	
ID	W48086 standard; Protein: 365 AA.
AC	W48086;
XX	
DT	11-JUN-1998 (first entry)
XX	
DE	Human dendritic cell chemokine receptor.
XX	
KW	Human; thymus expressed chemokine; TECK; MIP-3alpha; MIP-3beta;
KW	receptor; dendritic cell; macrophage; inflammation; asthma.
XX	
OS	Homo sapiens.
XX	
PH	Key Location/Qualifiers
FT	Misc-difference 193
FT	/note= "encoded by CAN"
XX	
PN	W09801557-A2.
XX	
PD	15-JAN-1998.
XX	
PF	02-JUL-1997; 97WO-US10819.
XX	
PR	04-JUN-1997; 97US-0048593.
PR	05-JUL-1996; 96US-0675814.
PR	11-OCT-1996; 96US-0028329.
XX	
PA	(SCHE) SCHERING CORP.
XX	
PI	Gish KC, Schall TJ, Vicari A, Wang W, Zlotnik A;
XX	
DR	WPI; 1998-101054/09.

DR N-PSDB; V15418.
 XX Novel chemokines, e.g. thymus expressed chemokine - used for
 PT treating inflammatory conditions including asthma.
 XX
 PS Claim 3; Page 94-95; 202pp; English.
 XX
 CC The present sequence represents human dendritic cell chemokine receptor.
 CC Antibodies which bind to the protein can be used in detecting or
 CC diagnosing various immunological conditions related to expression
 CC of the protein. The nucleic acid can be used for screening and
 CC isolating DNA clones for the chemokines, especially from other
 CC species. The chemokine can be used in the treatment of conditions
 CC associated with abnormal physiology or development, including
 CC inflammatory conditions such as asthma.
 XX
 SQ Sequence 365 AA;

Query Match 100.0%; Score 78; DB 19; Length 365;
 Best Local Similarity 100.0%; Pred. No. 6.3e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KTLVQNSKRHKAIR 16
 |||||
 DB 230 ktlvqnskrhkair 245

RESULT 2
 Y97077
 ID Y97077 standard; Protein; 365 AA.
 XX
 AC Y97077;
 XX
 DT 04-DEC-2000 (first entry)
 XX
 DE Primate (human) chemokine receptor CCR6.
 XX
 KW MIP-3-alpha; chemokine; CCR6 receptor; ligand; cytostatic; agonist;
 KW antagonist; anti-psoriatic; dermatological; immunosuppressive;
 KW anti-inflammatory.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 193
 FT /note= "Encoded by CAN#"
 XX
 PN WO200046248-A1.
 XX
 PD 10-AUG-2000.
 XX
 PF 02-FEB-2000; 2000WO-US00511.
 XX
 PR 03-FEB-1999; 99US-0244281.
 XX
 PA (SCHE) SCHERING CORP.
 XX
 PI Oldham ER, Honey B, Dieu-Nosjean M, Caux C, Zlotnik A;
 XX
 DR WPI; 2000-543477/49.
 DR N-PSDB; A51971.
 XX
 PT Novel methods for modulating the migration of cells within or to the
 PT skin using MIP-3-alpha or CCR6 agonists or antagonists, useful for
 PT treating skin disorders, e.g. cancer
 XX
 PS Disclosure; Page 53-54; 61pp; English.
 XX
 CC The MIP-3-alpha chemokine is expressed in inflamed skin cells. This
 CC chemokine is the ligand for the CCR6 receptor. MIP-3-alpha or CCR6
 CC agonists or antagonists can be used to modulate the migration of a cell
 CC within or to the skin of a mammal. MIP-3-alpha can be used to purify a

CC population of cells expressing a MIP-3-alpha receptor. The methods are
 CC useful for treating a mammalian subject with a skin disease or condition,
 CC e.g. cancer, metastasis, psoriasis, atopic or contact dermatitis,
 CC systemic lupus erythematosus and lichen ruber planus, or for treating
 CC skin transplants or grafts.
 XX
 SQ Sequence 365 AA;

Query Match 100.0%; Score 78; DB 21; Length 365;
 Best Local Similarity 100.0%; Pred. No. 6.3e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KTLVQNSKRHKAIR 16
 |||||
 DB 230 ktlvqnskrhkair 245

RESULT 3
 B19605
 ID B19605 standard; Protein; 357 AA.
 XX
 AC B19605;
 XX
 DT 22-JAN-2001 (first entry)
 XX
 DE Human CC chemokine receptor GPR-9-6.
 XX
 KW GPR-9-6; human; chemokine receptor; TECK; cancer; leukaemia;
 KW lymphoma; carcinoma; inflammation; Crohn's disease; colitis;
 KW therapy; diagnosis.
 XX
 OS Homo sapiens.
 XX
 PN WO200053635-A1.
 XX
 PD 14-SEP-2000.
 XX
 PF 10-MAR-2000; 2000WO-US06240.
 XX
 PR 11-MAR-1999; 99US-0266464.
 XX
 PA (LEUK-) LEUKOSITE INC.
 XX
 PI Andrew DP, Zabel BA, Ponath PD;
 XX
 DR WPI; 2000-572263/53.
 XX
 PT Antibody or its antigen-binding fragment which binds to the mammalian
 PT CC chemokine receptor GPR-9-6, useful for treating inflammatory
 PT diseases, cancer or inhibiting GPR-9-6-mediated homing of leukocytes to
 PT mucosal tissue -
 XX
 PS Disclosure; Fig 14A-B; 114pp; English.
 XX
 CC The present sequence is that of human GPR-9-6, a CC chemokine
 CC receptor that is expressed on the majority of thymocytes and also
 CC on a subset of memory CD4 lymphocytes that traffic to mucosal
 CC sites, suggesting a dual role in T cell development and mucosal
 CC immune response. The invention relates to an antibody that binds
 CC to GPR-9-6 and blocks the binding of a ligand, such as TECK (see
 CC B19607), to the receptor. Also provided is a method of identifying
 CC agents which can bind to GPR-9-6 and inhibit the binding of a
 CC ligand and/or modulate a function of GPR-9-6. The antibodies can
 CC be used to detect or measure expression of GPR-9-6 receptor. They
 CC are useful for treating an inflammatory disease, cancer and
 CC inhibiting GPR-9-6-mediated homing of leukocytes to mucosal tissue.
 CC The cancer treated is acute or chronic leukaemia (e.g., acute T-cell
 CC lymphoblastic leukaemia, acute B-cell lymphoblastic leukaemia,
 CC chronic T-cell lymphoblastic leukaemia, chronic B-cell lymphoblastic
 CC leukaemia), lymphoma (e.g., Hodgkin's disease, T cell lymphoma) or
 CC carcinoma (e.g. breast, melanoma, myeloma, or adenoma). The
 CC inflammatory diseases treated are Crohn's disease, colitis

CC (claimed), inflammatory bowel disease, mastitis, vaginitis,
 CC cholangitis or pericholangitis, chronic bronchitis, asthma, graft
 CC versus host disease, hypersensitivity pneumonitis, collagen
 CC diseases, sarcoidosis, and other idiopathic conditions. Other
 CC diseases that can be treated by the antibodies are autoimmune
 CC diseases (e.g. rheumatoid arthritis, multiple sclerosis), infectious
 CC diseases (e.g. bacterial and viral infections), atherosclerosis,
 CC retinosis, AIDS, pancreatitis, insulin-dependent diabetes mellitus,
 CC and diseases in which angiogenesis or neovascularization play a role.
 XX
 SQ Sequence 357 AA;

Query Match 62.8%; Score 49; DB 21; Length 357;
 Best Local Similarity 53.3%; Pred. No. 0.79;
 Matches 8; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 2 TLVQAQNSKRHKRAIR 16
 ||||| : |||||
 DB 228 tliqakskkhkalk 242

RESULT 4
 Y90615
 ID Y90615 standard; Protein: 357 AA.
 AC Y90615;
 XX
 XX
 DT 21-AUG-2000 (first entry)

DE Human G protein-coupled receptor GPR9-6.

KW G protein-coupled receptor: GPCR: constitutively active;
 KW intracellular loop 3; Transmembrane domain 6; drug screening;
 KW agonist; antagonist.

OS Homo sapiens.

XX WO2000022129-A1.

PD 20-APR-2000.

PF 12-OCT-1999; 99WO-US23938.

PR 13-OCT-1998; 98US-0170496.

XX (AREN-) ARENA PHARM INC.

PI Behan DP, Chalmers DT, Liaw CW;

DR WPI: 2000-329165/28.

DR N-PSDB; A30596.

XX Non-endogenous constitutively activated human G protein-coupled
 PT receptors, useful for identifying agonists for use as pharmaceutical
 PT agents

XX Example 1; Page 119-120; 341pp; English.

XX The invention relates to constitutively active, non-endogenous versions
 CC of endogenous human orphan G protein-coupled receptors (GPCRs, Y90643-
 CC Y90677 and Y90683-Y90687), and to DNA encoding them (A30709-A30743 and
 CC A30775-A30779). The mutant proteins of the invention contain a
 CC mutation in a portion of the protein comprising intracellular loop 3
 CC (IC3) and transmembrane domain 6 (TM6). A non-endogenous amino acid, X,
 CC is substituted for an endogenous residue in IC3 at a position 16 amino
 CC acids N-terminal of an endogenous proline in TM6 to form a sequence
 CC X-(AA)15-Pro. The endogenous amino acid is selected from Lys, His, Arg or
 CC Ala, and is preferably Lys. When the endogenous residue at this position
 CC is Lys, this residue is replaced by His, Arg or preferably Ala. The 15
 CC amino acid stretch between the substituted amino acid and the Pro may be
 CC endogenous, non-endogenous, or a mixture of endogenous and non-endogenous
 CC residues. The constitutively active GPCRs are useful for identifying

CC antagonists, agonists and partial agonists for use as pharmaceutical
 CC agents. The mutant proteins are also useful in research settings for
 CC elucidating the roles of the receptors in normal and diseased conditions.
 CC Antagonists for a particular GPCR are useful for treating diseases and
 CC disorders associated with that receptor. Because the novel mutant GPCRs
 CC are constitutively active, they can be used directly for screening of
 CC compounds without the need for endogenous ligands. The present
 CC sequence represents a human wild-type GPCR referred to in an
 XX exemplification of the invention.
 SQ Sequence 357 AA;

Query Match 62.8%; Score 49; DB 21; Length 357;
 Best Local Similarity 53.3%; Pred. No. 0.79;
 Matches 8; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 2 TLVQAQNSKRHKRAIR 16
 ||||| : |||||
 DB 228 tliqakskkhkalk 242

RESULT 5

R53745
 ID R53745 standard; Protein: 358 AA.
 AC R53745;
 XX
 XX
 DT 02-FEB-1995 (first entry)

DE Partial sequence of seven transmembrane receptor (V31).

KW Primer: seven transmembrane receptor; receptor; amplification; PCR;
 KW polymerase chain reaction.

OS Homo sapiens.

XX WO9412635-A.

PD 09-JUN-1994.

PF 17-NOV-1993; 93WO-US11153.

PR 17-NOV-1992; 92US-0977452.

XX (ICOS-) ICOS CORP.

XX Godiska R, Gray PW, Schweickart VL;

DR WPI: 1994-200264/24.

DR N-PSDB; Q66162.

XX DNA encoding seven transmembrane receptors - used to develop
 PT prods. for use as therapeutic or diagnostic agents for conditions
 PT involving the receptors.

XX Example 3; Page 56-57; 100pp; English.

XX Two primers (Q66148, Q66149) were used to amplify human genomic DNA
 CC purified from leukocytes. Approximately 1000 clones were isolated
 CC after the initial amplification reaction and probed with sequences
 CC specific for seven transmembrane receptors IL8R1, ATR2 and R20.
 CC Clones which did not hybridize were then chosen for sequence
 CC analysis. Three new clones were identified that appeared to encode
 CC seven transmembrane receptor segments. Two more primers (Q66151,
 CC Q66152) were used to isolate a full length version of one of these
 CC clones designated V31 (See Q66153). This is the sequence encoded
 CC by exon 3 of the V31 genomic clone

XX Sequence 358 AA;

Query Match 61.5%; Score 48; DB 15; Length 358;

Best Local Similarity 56.2%; Pred. No. 1.2;
Matches 9; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 KTLVQAQNSKRHKAIR 16
DB 228 rtlqarnfernkalk 243

RESULT 6

ID B21689 standard; Protein; 358 AA.

XX AC B21689;

DT 26-JAN-2001 (first entry)

DE Human 7TM receptor V31-B cDNA clone exon 1 protein.

KW Seven transmembrane receptor; 7TM; heptahelical; serpentine;
KW G-protein-coupled; V28; V31; V112; R20; R2; RM3; gene therapy;
KW cancer.

OS Homo sapiens.

XX US6107475-A.

PN 22-AUG-2000.

XX 26-APR-1999; 99US-0299843.

PR 17-MAY-1994; 94US-0245242.

PR 01-JUN-1998; 98US-0088337.

PR 17-NOV-1992; 92US-0977452.

PR 17-NOV-1993; 93US-0153848.

XX (ICOS-) ICOS CORP.

PI Schweickart VL, Gray PW, Godiska R;
DR WPI; 2000-571335/53.

DR N-PSDB; A91709.

PT Polynucleotide encoding seven transmembrane receptors, antibody
PT specific to the receptor, agonist and antagonist of the receptor useful
PT for treating inflammation in a mammal

PS Example 3; Columns 49-52; 61pp; English.

CC The present sequence is a novel seven transmembrane (7TM) receptors
CC (also known as heptahelical, serpentine or G-protein-coupled receptors).
CC The coding sequence for the present sequence may be used for gene
CC therapy for diseases such as cancer.

XX Sequence 358 AA;

Query Match 61.5%; Score 48; DB 21; Length 358;

Best Local Similarity 56.2%; Pred. No. 1.2;
Matches 9; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 KTLVQAQNSKRHKAIR 16
DB 228 rtlqarnfernkalk 243

RESULT 7

ID R53747 standard; Protein; 359 AA.

XX AC R53747;

XX 03-FEB-1995 (first entry)

DE Seven transmembrane receptor (V31) partial sequence of mouse.

XX Primer: seven transmembrane receptor; receptor; amplification; PCR;
KW polymerase chain reaction.

OS Mus musculus.

XX WO9412635-A.

XX 09-JUN-1994.

XX 17-NOV-1993; 93WO-US11153.

XX 17-NOV-1992; 92US-0977452.

XX (ICOS-) ICOS CORP.

PI Godiska R, Gray PW, Schweickart VL;
DR WPI; 1994-200264/24.

DR N-PSDB; Q66164.

PT DNA encoding seven transmembrane receptors - used to develop
PT prods. for use as therapeutic or diagnostic agents for conditions
PT involving the receptors.

PS Example 5; Page 61-62; 100pp; English.

CC Two primers (Q66148, Q66149) were used to amplify human genomic DNA
CC purified from leukocytes. Approximately 1000 clones were isolated
CC after the initial amplification reaction and probed with sequences
CC specific for seven transmembrane receptors IL8R1, AT2R and R20.
CC Clones which did not hybridise were then chosen for sequence
CC analysis. Three new clones were identified that appeared to encode
CC seven transmembrane receptor segments. Two more primers (Q66151,
CC Q66152) were used to isolate a full length version of one of the
CC human V31 clone (See Q66153). A fragment of the human clone was used
CC to isolate a V31 genomic clone of the mouse from a library.

XX Sequence 359 AA;

Query Match 61.5%; Score 48; DB 15; Length 359;

Best Local Similarity 56.2%; Pred. No. 1.2;
Matches 9; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 KTLVQAQNSKRHKAIR 16

DB 228 rtlqarnfernkalk 243

RESULT 8

ID W48728 standard; Protein; 359 AA.

XX AC W48728;

XX 25-SEP-1998 (first entry)

DE Murine V31 seven transmembrane (7TM) receptor.

KW V28; placenta; seven transmembrane receptor; 7TM; signal transduction;
KW immunology; Inflammation; V31; ss.

OS Mus sp.

XX US5759804-A.

XX 02-JUN-1998.

XX 17-NOV-1993; 93US-0153848.

XX 17-NOV-1992; 92US-0977452.

```

Query Match      61.5%;   Score 48;   DB 21;   Length 359;
Best Local Similarity 56.2%;
Pred. No. 1.2;
Matches 9;   Conservative 6;   Mismatches 1;   Indels 0;   Gaps 0;

QY      1  KTLVQAQNSKRHKAIK 16
        :||:|:|:|:|:|:|:|:|:
Db      228  rllqarnfernkak 243

RESULT      10
W97348
ID      W97348 standard. Protein: 361 AA

```

DI 12-MAY-1999 (first entry)
XX
DE An Epstein-barr virus-induced G-protein coupled receptor.

KW Epstein-Barr virus-induced G-protein coupled receptor; EBI 3;
KW splicing variant; EBI 1; vaccine; infection; HIV-1; HIV-2; pain;
KW cancer; anorexia; bulimia; asthma; Parkinson's disease;
KW acute heart failure; hypotension; hypertension; urinary retention;

KW Gilles de la Tourette's syndrome.

KW Severe mental retardation; dyskinesias; Huntington's disease;
KW Gilles de la Tourette's syndrome.

XX
50
Homo sapiens

XX PN EP894854-A2

XX PD 03-FEB-1999.

XX	04-DEC-1997;	97EP-0309791.
PF		
XX		
PR	29-JUL-1997.	97NS-0902294

XX PA (SMIK) SMTTKLINE BEECHAM CORP.

XX
DT 7h11 v.XX
NR
WPT: 1999-108346/10

DR N-PSDB; X15857.
YY

New Epstein-barr virus-induced G-protein coupled receptor (EBI 3)

PT and treatment of HIV infection

PS Claim 2; Page 7; 20pp; English.

The present sequence represents

CC antibodies are useful for inducing an immune response to immunize a

CC polypeptides by affinity chromatography. EBI 3 polypeptides can be

CC administered directly or as a vaccine to inoculate against disease.

CC Diseases diagnosed, prevented and treated include: bacterial, fungal,

CC viral and protozoan infections, particularly infections caused by HIV1-
 CC or HIV-2; pain; cancers; anorexia; bulimia; asthma; Parkinson's disease;
 CC acute heart failure; hypotension; hypertension; urinary retention;
 CC osteoporosis; angina pectoris; myocardial infarction; ulcers; allergies;
 CC benign prostatic hypertrophy; and psychotic and neurological disorders,
 CC including anxiety, schizophrenia, manic depression, delirium, dementia,
 CC severe mental retardation and dyskinesias, such as Huntington's disease
 CC or Gilles de la Tourette's syndrome.
 XX
 SQ Sequence 361 AA;

Query Match 61.5%; Score 48; DB 20; Length 361;
 Best Local Similarity 56.2%; Pred. No. 1.2;
 Matches 9; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KTLVQAQNSKRHKAIR 16
 Db 231 rtlqarnfernkalk 246

RESULT 11
 R54079
 ID R54079 standard; Protein: 378 AA.
 XX
 AC R54079;

DT 03-FEB-1995 (first entry)

DE Epstein Barr virus induced (EBI-1) polypeptide.

XX Epstein Barr virus; EBV; induction; detection; diagnosis;
 KW lymphocytes; antigen; growth; differentiation; mediator;
 KW infectious mononucleosis.
 XX

OS Homo sapiens.

Key Location/Qualifiers
 FT 1..24
 FT Region

FT /label= Hydrophobic region.
 FT /note= "Predicted to be a signal peptide for
 FT membrane translocation."

FT Modified-site 36
 FT /note= "Potential N-linked glycosylation site."

FT Region 60..86
 FT /label= Hydrophobic region.

FT Region 96..116
 FT /label= Hydrophobic region.

FT Region 131..152
 FT /label= Hydrophobic region.

FT Region 151..159
 FT /note= "This sequences motif
 FT (S-[I/V]-D-R-[Y/F]-X-X-X) is highly
 FT conserved among a large number of G-protein
 FT coupled receptors."

FT Region 171..191
 FT /label= Hydrophobic region.

FT Region 220..247
 FT /label= Hydrophobic region.

FT Region 264..289
 FT /label= Hydrophobic region.

FT Modified-site 292
 FT /note= "Potential N-linked glycosylation site."

FT Region 314..331
 FT /label= Hydrophobic region.

XX WO9412519-A.
 XX PD 09-JUN-1994.

XX 08-OCT-1993; 93WO-US09636.
 XX 25-NOV-1992; 92US-0980518.

XX (BGHM) BRIGHAM & WOMENS HOSPITAL.
 XX Birkenbach M, Kieff E;

XX WPI; 1994-200183/24.
 DR N-PSDB; Q64125.

XX DNA coding for Epstein Barr Virus induced (EBI) polypeptide(s)
 PT and antibodies to EBI1, 2 and 3 - useful for detecting EBV by
 PT hybridisation or by immunoassay

PS Claim 8; Page 54-56; 84pp; English.
 XX

CC EBV infected B lymphocytes recapitulate features of antigen
 CC stimulation in enlarging, increasing RNA synthesis, expressing
 CC activation antigens and adhesion molecules, secreting Ig and
 CC proliferating. Unlike antigen stimulated B lymphocytes, EBV
 CC infected B lymphocytes continue to proliferate (in vitro) as
 CC immortalised lymphoblastoid cell lines. Because of the similar
 CC effects of EBV and antigen, EBV induced genes are likely to include
 CC mediators of antigen induced B lymphocyte growth or differentiation.
 XX
 SQ Sequence 378 AA;

Query Match 61.5%; Score 48; DB 15; Length 378;

Best Local Similarity 56.2%; Pred. No. 1.3;

Matches 9; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KTLVQAQNSKRHKAIR 16

Db 248 rtlqarnfernkalk 263

RESULT 12

R53744

ID R53744 standard; Protein: 378 AA.

AC R53744;

DT 02-FEB-1995 (first entry)

DE Putative seven transmembrane receptor (V31).

XX Primer; seven transmembrane receptor; receptor; amplification; PCR;
 KW polymerase chain reaction.
 XX Homo sapiens.

XX WO9412635-A.
 XX PD 09-JUN-1994.

XX 17-NOV-1993; 93WO-US11153.
 XX 17-NOV-1992; 92US-0977452.

XX (ICOS-) ICOS CORP.
 XX Godiska R, Gray PW, Schweickart VL;

XX WPI; 1994-200264/24.
 DR N-PSDB; Q66160.

XX DNA encoding seven transmembrane receptors - used to develop
 PT prods. for use as therapeutic or diagnostic agents for conditions
 PT involving the receptors.
 XX Claim 1; Page 52-53; 100pp; English.
 XX A human cDNA encoding the seven transmembrane receptor V31 was
 CC isolated by first amplifying a partial cDNA clone from a human

CC tonsil cDNA library using two primers (Q66154, Q66155). The resulting
 CC amplified products were probed using two radioactively labelled
 CC sequences (Q66156, Q66157). A hybridising band was isolated from the
 CC gel and cloned. The resulting clone was named pV31-5'end (Q66158). A
 CC full length cDNA clone was isolated from a peripheral blood
 CC mononuclear cell library using V31 specific primers (Q66159, Q66152).
 CC Clone pBMC75 was isolated and the V31 cDNA insert in the clone was
 CC designated cDNA V31-B (Q66160).
 XX
 SQ Sequence 378 AA;

Query Match 61.5%; Score 48; DB 15; Length 378;

Best Local Similarity 56.2%; Pred. No. 1.3;
 Matches 9; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KTLVQAQNSKRHKAIR 16
 :||:|:|:|:|:|:|:
 Db 248 rtlqarnfernkai 263

RESULT 13

W48724
 ID W48724 standard; Protein; 378 AA.

XX AC W48724;

XX DT 25-SEP-1998 (first entry)

XX DE Human V31 seven transmembrane receptor.

XX KW V28; placenta; seven transmembrane receptor; 7TM; signal transduction;
 XX immunology; inflammation; V31.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Domain 58..86

FT /note= "Transmembrane domain 1"

FT Domain 96..119

FT /note= "Transmembrane domain 2"

FT Domain 131..152

FT /note= "Transmembrane domain 3"

FT Domain 171..196

FT /note= "Transmembrane domain 4"

FT Domain 219..247

FT /note= "Transmembrane domain 5"

FT Domain 264..285

FT /note= "Transmembrane domain 6"

FT Domain 306..331

FT /note= "Transmembrane domain 7"

XX US5759804-A.

XX PD 02-JUN-1998.

XX PE 17-NOV-1993; 93US-0153848.

XX PR 17-NOV-1992; 92US-0977452.

XX (ICOS-) ICOS CORP.

XX PI Godiska R, Gray PW, Schweickart VL;

XX WPI; 1998-332132/29.

XX DR N-PSDB; V18347.

XX DNA encoding V28 seven transmembrane receptor polypeptide - useful

XX for producing recombinant polypeptide and anti-V28 antibodies, and

XX in screening assays for V28 agonists and antagonists

XX Example 3; Columns 39-42; 56pp; English.

XX PS

CC The present sequence represents the V31 seven transmembrane (7TM)
 CC receptor encoded by the V31 cDNA (V18347). The invention claims for
 CC a full length V28 genomic DNA (V18343) and the V28 protein it
 CC encodes (W48722). V28 and V31 proteins are 7TM receptors which
 CC are probably involved in signal transduction. The invention also
 CC claims that cells transformed with V28 DNA can be used to produce the
 CC recombinant polypeptide, to produce anti-V28 antibodies or in screening
 CC assays for V28 agonists or antagonists. The antibodies, agonists and
 CC antagonists could then be used to modulate V28 receptor-ligand binding,
 CC for e.g. in immunological and/or inflammatory events in vivo.
 XX

SQ Sequence 378 AA;

Query Match 61.5%; Score 48; DB 19; Length 378;

Best Local Similarity 56.2%; Pred. No. 1.3;
 Matches 9; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KTLVQAQNSKRHKAIR 16

:||:|:|:|:|:|:|:
 Db 248 rtlqarnfernkai 263

RESULT 14

W56164
 ID W56164 standard; Protein; 378 AA.

XX AC W56164;

XX DT 20-JUL-1998 (first entry)

XX DE G-protein coupled receptor (R7G) designated EB11.

XX KW Lymphocyte R7G; EB11; G-protein coupled receptor;

XX opiate/opioid recognition site; opiate; opioid binding protein;

XX screening; lymphocyte receptor; compound; agonist; antagonist;

XX lymphocyte receptor protein; immune-cell specific lymphocyte receptor;

XX neuronal type opioid receptor.

XX OS Homo sapiens.

XX PN US5753516-A.

XX PD 19-MAY-1998.

XX PF 03-FEB-1995; 95US-0383751.

XX PR 03-FEB-1995; 95US-0383751.

XX (FINB/) FINBERG R W.

XX (HEAG/) HEAGY W E.

XX PI Finberg RW, Heagy WE;

XX WPI; 1998-311410/27.

XX DR N-PSDB; V22684.

XX Screening assay for lymphocyte opioid receptor ligands - using

XX recombinant receptor protein

XX Claim 1; Columns 87-88; 70pp; English.

XX The present sequence represents a novel lymphocyte R7G, termed EB11. R7G

XX proteins are part of the G-protein coupled receptor superfamily. EB11 is

XX a functional opiate/opioid recognition site that probably plays a major

XX role in mediating the effects that opiate/opioids have on lymphocytes.

XX The EB11 protein is an opioid binding protein that is displayed on the

XX surface of lymphocytes. A process for screening a candidate substance for

XX ability to interact with a lymphocyte receptor comprises selecting a

XX candidate substance having a chemical structure or biological activity

XX suggestive of an ability to mimic the biological activity of an

XX opiate, opioid drug or opioid peptide having known binding affinity for

XX EB11. The ability of the candidate substance is tested to interact with

CC the lymphocyte receptor protein. This method can be used to screen for
 CC agonists or antagonists to the lymphocyte receptor protein. The method
 CC can be modified and used to screen for agonists or antagonists to the
 CC immune-cell specific lymphocyte receptor polypeptide or the neuronal type
 CC oploid receptor polypeptide.
 XX
 XX SQ Sequence 378 AA;

Search completed: May 23, 2001, 15:28:32
 Job time: 409 sec

Query Match 61.5%; Score 48; DB 19; Length 378;
 Best Local Similarity 56.2%; Pred. No. 1.3;
 Matches 9; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 KTLVQAQNSKRHKAIR 16
 :||:|:|:|:|:|:
 Db 248 rtilqarnfernkai 263

RESULT 15
 W53622
 ID W53622 standard; Protein; 378 AA.
 XX
 AC W53622;
 XX
 DT 09-JUL-1998 (first entry)
 XX
 DE Epstein Barr virus induced protein 1 (EBI-1).
 XX
 DE Assessing; monitoring; foetal development; placental development;
 KW Epstein Barr virus; EBV; induced gene 1; EBI-1.
 XX
 OS Homo sapiens.
 XX
 PN US5744301-A.
 XX
 PD 28-APR-1998.
 XX
 PF 02-FEB-1995; 95US-0383750.
 XX
 PR 02-FEB-1995; 95US-0383750.
 PR 25-NOV-1992; 92US-0980518.
 PR 30-NOV-1994; 94US-0352678.
 XX
 PA (BGHM) BRIGHAM & WOMENS HOSPITAL.
 XX
 PI Birkenbach M, Kieff E;
 XX
 DR WPI; 1998-271060/24.
 DR N-PSDB; V25490.
 XX

PT Assessing or monitoring foetal or placental development - comprises
 PT detecting the level or size of Epstein Barr virus induced nucleic
 PT acid or protein in maternal serum samples
 XX

PS Example 2; Columns 37-40; 45pp; English.
 XX

CC The present sequence was used in the development of a novel method
 CC for assessing or monitoring foetal or placental development. The
 CC method comprises taking a maternal serum sample, and detecting the
 CC level or size of Epstein Barr virus (EBV) induced gene or protein 3
 CC (EBI-3) to obtain a result, which can be compared to a control to
 CC assess or monitor foetal or placental development.
 XX
 XX SQ Sequence 378 AA;

Query Match 61.5%; Score 48; DB 19; Length 378;
 Best Local Similarity 56.2%; Pred. No. 1.3;
 Matches 9; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 KTLVQAQNSKRHKAIR 16
 :||:|:|:|:|:|:
 Db 248 rtilqarnfernkai 263

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OM protein - protein search, using sw model

Run on: May 23, 2001, 15:30:07 ; Search time 95.91 Seconds
(without alignments)
3.205 Million cell updates/sec

Title: US-08-887-977-10_COPY_230_245

Perfect score: 78

Sequence: 1 KTLVQANSRRHRAIR 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 185757 seqs, 19210857 residues

Total number of hits satisfying chosen parameters: 185757

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Issued Patents_AA:*

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- 2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
- 3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
- 4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
- 5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
- 6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	61.5	358	1	US-08-153-848-19
2	48	61.5	358	3	US-09-299-843A-19
3	48	61.5	358	5	PCT-US93-11153-19
4	48	61.5	359	1	US-08-153-848-24
5	48	61.5	359	3	US-09-299-843A-24
6	48	61.5	359	5	PCT-US93-11153-24
7	48	61.5	361	2	US-08-902-294-2
8	48	61.5	361	3	US-09-178-637-2
9	48	61.5	378	1	US-08-383-750-2
10	48	61.5	378	1	US-08-383-751A-2
11	48	61.5	378	1	US-08-153-848-15
12	48	61.5	378	3	US-08-352-678-2
13	48	61.5	378	3	US-09-299-843A-15
14	48	61.5	378	3	US-09-299-843A-66
15	48	61.5	378	4	US-09-251-545-1
16	48	61.5	378	5	PCT-US93-09636-2
17	48	61.5	378	5	PCT-US93-11153-15
18	48	61.5	410	1	US-08-153-848-7
19	48	61.5	410	3	US-09-299-843A-7
20	48	61.5	410	5	PCT-US93-11153-7
21	44.5	57.1	344	3	US-08-466-343D-9
22	44.5	57.1	347	1	US-08-461-244-3
23	44.5	57.1	352	3	US-08-466-343D-2
24	44.5	57.1	352	4	US-09-087-232A-13
25	44.5	57.1	360	1	US-08-450-393A-4
26	44.5	57.1	360	4	US-08-446-669-4
27	44.5	57.1	360	5	PCT-US95-00476-4

28	44.5	57.1	374	1	US-08-450-393A-2	Sequence 2, Appli
29	44.5	57.1	374	4	US-08-446-669-2	Sequence 2, Appli
30	44.5	57.1	374	5	PCT-US95-00476-2	Sequence 2, Appli
31	42	53.8	3174	2	US-08-477-451-3	Sequence 3, Appli
32	40	51.3	354	1	US-07-759-568-2	Sequence 2, Appli
33	38	48.7	170	4	US-08-875-573-6	Sequence 6, Appli
34	38	48.7	360	4	US-08-875-573-20	Sequence 20, Appli
35	38	48.7	523	4	US-08-948-564-8	Sequence 8, Appli
36	37	47.4	355	1	US-08-012-988A-2	Sequence 2, Appli
37	37	47.4	355	1	US-08-450-393A-5	Sequence 5, Appli
38	37	47.4	355	4	US-08-446-669-5	Sequence 5, Appli
39	37	47.4	355	5	PCT-US95-00476-5	Sequence 5, Appli
40	37	47.4	879	1	US-08-220-151-2	Sequence 2, Appli
41	37	47.4	879	1	US-08-220-151-3	Sequence 3, Appli
42	37	47.4	879	1	US-08-413-118-2	Sequence 2, Appli
43	37	47.4	879	1	US-08-413-118-3	Sequence 3, Appli
44	37	47.4	879	1	US-08-413-118-106	Sequence 106, App
45	37	47.4	879	3	US-08-413-446-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-08-153-848-19
: Sequence 19, Application US/08153848
: Patent No. 5759804
: GENERAL INFORMATION:
: APPLICANT: Godiska, Ronald
: APPLICANT: Gray, Patrick W.
: APPLICANT: Schweikart, Vicki L.
: TITLE OF INVENTION: No. 5759804el Seven Transmembrane Receptors
: NUMBER OF SEQUENCES: 64
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
: ADDRESSEE: Bicknell
: STREET: 6300 Sears Tower, 233 South Wacker Drive
: CITY: Chicago
: STATE: Illinois
: COUNTRY: USA
: ZIP: 60606
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/153.848
: FILING DATE:
: CLASSIFICATION: 514
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/977,452
: FILING DATE: 17-NOV-1992
: ATTORNEY/AGENT INFORMATION:
: NAME: No. 5759804and, Greta E.
: REGISTRATION NUMBER: 35,302
: REFERENCE/DOCKET NUMBER: 31794
: TELEPHONE: (312) 474-6300
: TELEFAX: (312) 474-0448
: TELEX: 25-3856
: INFORMATION FOR SEQ ID NO: 19:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 358 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-153-848-19

Query Match 61.5% Score 48; DB 1; Length 358;
Best Local Similarity 56.2%; Pred. No. 0.62;
Matches 9; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 KTLVQAQNSKRHKAIR 16
:|||||:|:|:|:
Db 228 RTLLQARNFERNKAIR 243

RESULT 2

US-09-299-843A-19
; Sequence 19, Application US/09299843A
; Patent No. 6107475
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schweikart, Vicki L.
; TITLE OF INVENTION: No. 6107475el Seven Transmembrane Receptors
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/299,843A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/088,337
; FILING DATE: 01-JUN-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/153,848
; FILING DATE: 17-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/977,452
; FILING DATE: 17-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Jill E. Uhl
; REGISTRATION NUMBER: 43,213
; REFERENCE/DOCKET NUMBER: 27866/32059B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX:
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 358 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-299-843A-19

Query Match 61.5%; Score 48; DB 3; Length 358;
Best Local Similarity 56.2%; Pred. No. 0.62;
Matches 9; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 KTLVQAQNSKRHKAIR 16
:|||||:|:|:|:
Db 228 RTLLQARNFERNKAIR 243

RESULT 3

PCT-US93-11153-19
; Sequence 19, Application PC/TUS9311153
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald

; APPLICANT: Gray, Patrick W.
; APPLICANT: Schweikart, Vicki L.
; TITLE OF INVENTION: Novel Seven Transmembrane Receptors
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/11153
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/977,452
; FILING DATE: 17-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Noland, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31794
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 358 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US93-11153-19

Query Match 61.5%; Score 48; DB 5; Length 358;
Best Local Similarity 56.2%; Pred. No. 0.62;
Matches 9; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 KTLVQAQNSKRHKAIR 16
:|||||:|:|:|:
Db 228 RTLLQARNFERNKAIR 243

RESULT 4

US-08-153-848-24
; Sequence 24, Application US/08153848
; Patent No. 5759804
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schweikart, Vicki L.
; TITLE OF INVENTION: No. 5759804el Seven Transmembrane Receptors
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/08/153.848
;/ FILING DATE:
;/ CLASSIFICATION: 514
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: US 07/977,452
;/ FILING DATE: 17-NOV-1992
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: No. 5759804and, Greta E.
;/ REGISTRATION NUMBER: 35,302
;/ REFERENCE/DOCKET NUMBER: 31794
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: (312) 474-6300
;/ TELEFAX: (312) 474-0448
;/ TELEX: 25-3856
;/ INFORMATION FOR SEQ ID NO: 24:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 359 amino acids
;/ TYPE: amino acid
;/ TOPOLOGY: linear
;/ MOLECULE TYPE: protein
;/ US-08-153-848-24

Query Match 61.5%; Score 48; DB 1; Length 359;
Best Local Similarity 56.2%; Pred. No. 0.62;
Matches 9; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 KTLVQAQNSKRHKAIR 16
Db 228 RTLLQARNFERNKAIK 243

RESULT 5

US-09-299-843A-24
; Sequence 24, Application US/09299843A
; Patent No. 6107475
; GENERAL INFORMATION:

;/ APPLICANT: Godiska, Ronald
;/ APPLICANT: Gray, Patrick W.
;/ APPLICANT: Schweikart, Vicki L.
;/ TITLE OF INVENTION: No. 6107475el Seven Transmembrane Receptors
;/ NUMBER OF SEQUENCES: 66
;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
;/ ADDRESSEE: Borun
;/ STREET: 6300 Sears Tower, 233 South Wacker Drive
;/ CITY: Chicago
;/ STATE: Illinois
;/ COUNTRY: USA
;/ ZIP: 60606

;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: Floppy disk
;/ COMPUTER: IBM PC compatible
;/ OPERATING SYSTEM: PC-DOS/MS-DOS
;/ SOFTWARE: PatentIn Release #1.0, Version #1.25
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/09/299,843A
;/ FILING DATE:

;/ CLASSIFICATION: 435
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: US 09/088,337
;/ FILING DATE: 01-JUN-1998
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: US 08/153,848
;/ FILING DATE: 17-NOV-1993
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: US 07/977,452
;/ FILING DATE: 17-NOV-1992
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Jill E. Uhl
;/ REGISTRATION NUMBER: 43,213
;/ REFERENCE/DOCKET NUMBER: 27866/32059B

;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: (312) 474-6300
;/ TELEFAX: (312) 474-0448
;/ TELEX:
;/ INFORMATION FOR SEQ ID NO: 24:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 359 amino acids
;/ TYPE: amino acid
;/ TOPOLOGY: linear
;/ MOLECULE TYPE: protein
;/ US-09-299-843A-24

Query Match 61.5%; Score 48; DB 3; Length 359;
Best Local Similarity 56.2%; Pred. No. 0.62;
Matches 9; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 KTLVQAQNSKRHKAIR 16
Db 228 RTLLQARNFERNKAIK 243

RESULT 6

PCT-US93-11153-24
; Sequence 24, Application PC/TUS9311153
; GENERAL INFORMATION:

;/ APPLICANT: Godiska, Ronald
;/ APPLICANT: Gray, Patrick W.
;/ APPLICANT: Schweikart, Vicki L.
;/ TITLE OF INVENTION: Novel Seven Transmembrane Receptors
;/ NUMBER OF SEQUENCES: 64
;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
;/ ADDRESSEE: Bicknell
;/ STREET: 6300 Sears Tower, 233 South Wacker Drive
;/ CITY: Chicago
;/ STATE: Illinois
;/ COUNTRY: USA
;/ ZIP: 60606

COMPUTER-READABLE-FORM:

;/ MEDIUM TYPE: Floppy disk
;/ COMPUTER: IBM PC compatible
;/ OPERATING SYSTEM: PC-DOS/MS-DOS
;/ SOFTWARE: PatentIn Release #1.0, Version #1.25
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: PCT/US93/11153
;/ FILING DATE:

;/ CLASSIFICATION:
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: US 07/977,452
;/ FILING DATE: 17-NOV-1992
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Noland, Greta E.
;/ REGISTRATION NUMBER: 35,302
;/ REFERENCE/DOCKET NUMBER: 31794
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: (312) 474-6300
;/ TELEFAX: (312) 474-0448
;/ TELEX: 25-3856

;/ INFORMATION FOR SEQ ID NO: 24:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 359 amino acids
;/ TYPE: amino acid
;/ TOPOLOGY: linear
;/ MOLECULE TYPE: protein
;/ PCT-US93-11153-24

Query Match 61.5%; Score 48; DB 5; Length 359;
Best Local Similarity 56.2%; Pred. No. 0.62;
Matches 9; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 KTLVQAQNSKRHKAIR 16

Db 228 RTLLQARNFERKAIK 243
:||||:|:|:|:|:

RESULT 7

US-08-902-294-2
; Sequence 2, Application US/08902294
; Patent No. 5874252
; GENERAL INFORMATION:
; APPLICANT: ZHU, YUAN
; TITLE OF INVENTION: A NOVEL SPLICING VARIANT OF
; TITLE OF INVENTION: THE EPSTEIN-BARR VIRUS-INDUCED G-PROTEIN COUPLED
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RATNER & PRESTIA
; STREET: P.O. BOX 980
; CITY: VALLEY FORGE
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/902,294
; FILING DATE: 29-JUL-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GP-70177
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 361 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-902-294-2

Query Match 61.5%; Score 48; DB 2; Length 361;
Best Local Similarity 56.2%; Pred. No. 0.62;
Matches 9; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 KTLVQAQNSKRHKAIK 16
:||||:|:|:|:|:
Db 231 RTLLQARNFERKAIK 246

RESULT 8

US-09-178-637-2
; Sequence 2, Application US/09178637
; Patent No. 6001972
; GENERAL INFORMATION:
; APPLICANT: ZHU, YUAN
; TITLE OF INVENTION: A No. 6001972el Splicing Variant of
; TITLE OF INVENTION: THE EPSTEIN-BARR VIRUS-INDUCED G-PROTEIN COUPLED RECEPTOR
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RATNER & PRESTIA
; STREET: P.O. BOX 980
; CITY: VALLEY FORGE
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/383,750
; FILING DATE: Herewith
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Fox, Samuel, L.
; REGISTRATION NUMBER: 30,353
; REFERENCE/DOCKET NUMBER: 0627.3300001
; TELECOMMUNICATION INFORMATION:

STATE: PA
COUNTRY: USA
ZIP: 19482
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/178,637
FILING DATE: 26-OCT-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/902,294
FILING DATE: 29-JUL-1998
ATTORNEY/AGENT INFORMATION:
NAME: PRESTIA, PAUL F
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GP-70177-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
TELEFAX: 610-407-0701
TELEX: 846169
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 361 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-178-637-2

Query Match 61.5%; Score 48; DB 3; Length 361;
Best Local Similarity 56.2%; Pred. No. 0.62;
Matches 9; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 KTLVQAQNSKRHKAIK 16
:||||:|:|:|:|:
Db 231 RTLLQARNFERKAIK 246

RESULT 9

US-08-383-750-2
; Sequence 2, Application US/08383750
; Patent No. 5744301
; GENERAL INFORMATION:
; APPLICANT: Birkenbach, Mark
; APPLICANT: Kieff, Elliot
; TITLE OF INVENTION: Epstein Barr Virus Induced Genes
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, N.W.,
; STREET: Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/383,750
; FILING DATE: Herewith
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Fox, Samuel, L.
; REGISTRATION NUMBER: 30,353
; REFERENCE/DOCKET NUMBER: 0627.3300001
; TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 378 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-383-750-2

Query Match 61.5%; Score 48; DB 1; Length 378;
Best Local Similarity 56.2%; Pred. No. 0.65;
Matches 9; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KTLVQAQNSKRHKAIR 16
:||:|:|:|:|:|:|:
Db 248 RTLLQARNFERNKAIK 263

RESULT 10
US-08-383-751A-2
Sequence 2, Application US/08383751A
Patent No. 5753516

GENERAL INFORMATION:
APPLICANT: Heagy, Wyrta E.
APPLICANT: Finberg, Robert W.
TITLE OF INVENTION: Identification and Uses of Opioid
TITLE OF INVENTION: Receptors
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: US
ZIP: 77210

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/383,751A
FILING DATE: 03-FEB-1995

ATTORNEY/AGENT INFORMATION:
NAME: Wilson, Mark B.
REGISTRATION NUMBER: 37,259
REFERENCE/DOCKET NUMBER: DFCI:001/WIM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
TELEX: 79-0924

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 378 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-383-751A-2

Query Match 61.5%; Score 48; DB 1; Length 378;
Best Local Similarity 56.2%; Pred. No. 0.65;
Matches 9; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KTLVQAQNSKRHKAIR 16
:||:|:|:|:|:|:|:
Db 248 RTLLQARNFERNKAIK 263

RESULT 11
US-08-153-848-15
Sequence 15, Application US/08153848

Patent No. 5759804
GENERAL INFORMATION:
APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schweikart, Vicki L.
TITLE OF INVENTION: NO. 5759804el Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Bicknell
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/153,848
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992

ATTORNEY/AGENT INFORMATION:
NAME: No. 5759804and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31794
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 378 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-153-848-15

Query Match 61.5%; Score 48; DB 1; Length 378;
Best Local Similarity 56.2%; Pred. No. 0.65;
Matches 9; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KTLVQAQNSKRHKAIR 16
:||:|:|:|:|:|:|:
Db 248 RTLLQARNFERNKAIK 263

RESULT 12

US-08-352-678-2
Sequence 2, Application US/08352678
Patent No. 6043351

GENERAL INFORMATION:
APPLICANT: Birkenbach, Mark
APPLICANT: Kieff, Elliott
TITLE OF INVENTION: EPSTEIN BARR VIRUS INDUCED GENES
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
STREET: 600 Atlantic Avenue
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02210

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

US-09-259-043A-00

CORRESPONDENCE ADDRESS: O'Toole, Gerstel
ADDRESSEE: Marshall, John
ADDRESS: Borun
STREET: 6300 Sears Tower, 233 South W
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, vers
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/299,843A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/088,337
FILING DATE: 01-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/153,848
FILING DATE: 17-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Jill E. Uhl
REGISTRATION NUMBER: 43,213
REFERENCE/DOCKET NUMBER: 27866/32059B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX:
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
LENGTH: 378 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-299-843A-66

QY	1	KT	LV	QA	QNS	KR	H	K	A	I	R	16		
		:	:	:	:	:	:	:	:	:	:			
Db	248	RT	LL	OA	RN	F	E	R	N	K	A	I	K	263

QY	1	KT	LV	QA	QNS	KR	HR	KAIR	16
Db	248	RT	LL	QA	RNF	ER	NA	KAIR	263

Search completed: May 23, 2001, 15:30:08
Job time: 415 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 23, 2001, 15:32:02 ; Search time 110.15 Seconds
(without alignments)
9.982 Million cell updates/sec

Title: US-08-887-977-10_COPY_230_245
Perfect score: 78
Sequence: 1 KTLVQAQNSKRHKRAIR 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 198801 seqs, 68722935 residues
Total number of hits satisfying chosen parameters: 198801

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_67: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	78	100.0	369	2 JC5068	G protein-coupled
2	54	69.2	359	2 I49341	MIP-1 alpha recept
3	48	61.5	378	2 A45680	G protein-coupled
4	48	61.5	378	2 B55735	lymphocyte-specifi
5	48	61.5	378	2 A55735	G protein-coupled
6	44.5	57.1	352	2 A43113	chemokine (C-C) re
7	44.5	57.1	360	2 JC2443	chemokine (C-C) re
8	44.5	57.1	374	2 I38450	chemokine (C-C) re
9	43	55.1	355	2 G02436	chemokine (C-C) re
10	41	52.6	364	2 C83099	hypothetical prote
11	40	51.3	202	2 T52146	ribosomal protein
12	40	51.3	354	2 A23669	interleukin-8 rece
13	40	51.3	355	2 JQ1231	interleukin-8 rece
14	40	51.3	358	2 A53752	interleukin-8 rece
15	40	51.3	639	2 T24972	hypothetical prote
16	40	51.3	698	2 T24970	hypothetical prote
17	40	51.3	1217	2 T13996	pol protein - frui
18	39	50.0	139	2 S06568	finger protein (cl
19	39	50.0	235	2 H81276	N-acyneuraminat
20	39	50.0	318	2 T26364	hypothetical prote
21	39	50.0	4568	2 T08030	dynamin beta heavy
22	38	48.7	150	2 F36809	hypothetical prote
23	38	48.7	360	2 A57160	chemokine (C-C) re
24	38	48.7	360	2 JC4587	chemokine (C-C) re
25	38	48.7	368	2 JC6081	proximal sequence
26	38	48.7	384	2 T19513	hypothetical prote
27	38	48.7	523	2 T05946	cytochrome P450 78
28	38	48.7	668	2 S49639	probable membrane
29	38	48.7	752	2 T16508	hypothetical prote

30 38 48.7 775 2 I49237
31 38 48.7 790 2 A35797
32 37 47.4 290 2 A70208
33 37 47.4 334 2 F83070
34 37 47.4 355 2 A45177
35 37 47.4 380 2 S49116
36 37 47.4 535 2 D75385
37 37 47.4 566 2 C81870
38 37 47.4 566 2 G81151
39 37 47.4 1570 2 T38792
40 37 47.4 1811 2 T39252
41 36 46.2 109 2 D81358
42 36 46.2 183 1 PWEG1
43 36 46.2 333 2 I65989
44 36 46.2 334 2 T02896
45 36 46.2 350 2 A39445

ALIGNMENTS

RESULT 1

JC5068
G protein-coupled receptor CKR-L3 - human
C:Species: Homo sapiens (man)
C:Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 21-Jul-2000
C:Accession: JC5068
R:Zaballos, A.; Varona, R.; Gutierrez, J.; Lind, P.; Marquez, G.
Biochem. Biophys. Res. Commun. 227, 846-853, 1996
A:Title: Molecular cloning and RNA expression of two new human chemokine receptor-lik
A:Reference number: JC5067; MUID:97040707
A:Accession: JC5068
A:Molecule type: DNA
A:Residues: 1-369 <ZAB>
A:Cross-references: EMBL:Z79784; NID:gl668737; PIDN:CAB02144.1; PID:gl668738
C:Comment: This protein belongs to the family of alpha chemokine receptors.
C:Genetics:
A:Gene: GDB:CMKBR6; SPRL22: GPR29; CCR6; CKR-L3; GPR-CY4
A:Cross-references: GDB:5370639; OMIM:601835
A:Map-position: 6q27-6q27

C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; transmembrane protein
F:42-68/Domain: transmembrane #status predicted <TM1>
F:79-99/Domain: transmembrane #status predicted <TM2>
F:115-136/Domain: transmembrane #status predicted <TM3>
F:160-180/Domain: transmembrane #status predicted <TM4>
F:212-233/Domain: transmembrane #status predicted <TM5>
F:250-271/Domain: transmembrane #status predicted <TM6>
F:292-315/Domain: transmembrane #status predicted <TM7>

Query Match 100.0%; Score 78; DB 2; Length 369;
Best Local Similarity 100.0%; Pred. No. 2e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KTLVQAQNSKRHKRAIR 16
| | | | | | | | | | | | | | | | | |
Db 234 KTLVQAQNSKRHKRAIR 249

RESULT 2

I49341
MIP-1 alpha receptor like-2 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 02-Jul-1998
C:Accession: I49341
R:Gao, J.L.; Murphy, P.M.
J. Biol. Chem. 270, 17494-17501, 1995
A:Title: Cloning and differential tissue-specific expression of three mouse beta chem
A:Reference number: I49339; MUID:95340546
A:Accession: I49341
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA

A;Residues: 1-359 <RES>

A;Cross-references: EMBL:U28406; NID:g881551; PID:g881552

C;Superfamily: vertebrate rhodopsin

Query Match 69.2%; Score 54; DB 2; Length 359;
Best Local Similarity 62.5%; Pred. No. 0.043;
Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 KTLVQAOQNSKRHKRAIR 16

||||:|:|:|

Db 228 KTLRCPNKKHKAIR 243

RESULT 3

A45680

G protein-coupled peptide receptor EBI 1 - human

C;Species: Homo sapiens (man)

C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 24-Nov-1999

C;Accession: A45680

R;Birkenbach, M.; Josefsen, K.; Yalamanchilli, R.; Lenoir, G.; Kieff, E.

J. Virol. 67, 2209-2220, 1993

A;Title: Epstein-Barr virus-induced genes: first lymphocyte-specific G protein-coupled p

A;Reference number: A45680; MUID:93188173

A;Accession: A45680

A;Status: preliminary

A;Molecule type: nucleic acid

A;Residues: 1-378 <BIR>

A;Cross-references: GB:L08176; NID:g183484; PID:g183485

A;Experimental source: B-lymphocytes

A;Note: sequence extracted from NCBI backbone (NCBIN:127094, NCBIIP:127095)

C;Superfamily: vertebrate rhodopsin

C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match

Best Local Similarity 61.5%; Score 48; DB 2; Length 378;

Matches 9; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 KTLVQAOQNSKRHKRAIR 16

||||:|:|:|

Db 248 RTLLQARNFERNKAIR 263

RESULT 4

B55735

Lymphocyte-specific G protein-coupled receptor EBII - human

N;Alternate names: Burkitt's lymphoma receptor 2; Epstein-Barr virus induced protein 1

C;Species: Homo sapiens (man)

C;Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 19-May-2000

C;Accession: B55735; S52443

R;Schweickart, V.L.; Raport, C.J.; Godiska, R.; Byers, M.G.; Eddy Jr., R.L.; Shows, T.B.

Genomics 23, 643-650, 1994

A;Title: Cloning of human and mouse EBII, a lymphoid-specific G-protein-coupled receptor

A;Reference number: A55735; MUID:95154835

A;Accession: B55735

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-378 <SCH>

A;Cross-references: GB:L31581; NID:g468319; PIDN:AAA74231.1; PID:g468320

R;Burgstahler, R.; Kempkes, B.; Staebke, K.; Lipp, M.

submitted to the EMBL Data Library, February 1995

A;Description: The expression of the chemokine receptor BLR2/EBII is specifically trans

A;Reference number: S52443

A;Accession: S52443

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 21-378 <BUP>

A;Cross-references: EMBL:X84702

C;Genetics:

A;Gene: GDB:CMKBR7; EBII; BLR2; CCR7

A;Cross-references: GDB:342065; OMIM:600242

A;Map position: 17q12-17q21.2

C;Superfamily: vertebrate rhodopsin

C;Keywords: G protein-coupled receptor

Query Match 61.5%; Score 48; DB 2; Length 378;

Best Local Similarity 56.2%; Pred. No. 0.56;

Matches 9; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 KTLVQAOQNSKRHKRAIR 16

||||:|:|:|

Db 248 RTLLQARNFERNKAIR 263

RESULT 5

A55735

G protein-coupled receptor EBII - mouse

C;Species: Mus musculus (house mouse)

C;Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 24-Nov-1999

C;Accession: A55735

R;Schweickart, V.L.; Raport, C.J.; Godiska, R.; Byers, M.G.; Eddy Jr., R.L.; Shows, T

Genomics 23, 643-650, 1994

A;Title: Cloning of human and mouse EBII, a lymphoid-specific G-protein-coupled recep

A;Reference number: A55735; MUID:95154835

A;Accession: A55735

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-378 <SCH>

A;Cross-references: GB:L31580; NID:g468340; PIDN:AAA74232.1; PID:g468341

C;Superfamily: vertebrate rhodopsin

C;Keywords: G protein-coupled receptor

Query Match

Best Local Similarity 56.2%; Score 48; DB 2; Length 378;

Matches 9; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 KTLVQAOQNSKRHKRAIR 16

||||:|:|:|

Db 248 RTLLQARNFERNKAIR 263

RESULT 6

A43113

chemokine (C-C) receptor 5 - human

N;Alternate names: C-C CKR-5; CCR5

C;Species: Homo sapiens (man)

C;Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 20-Jun-2000

C;Accession: A43113; S71808; A58834; G02653; A58833

R;Samson, M.; Labbe, O.; Mollereau, C.; Vassart, G.; Parmentier, M.

Biochemistry 35, 3362-3367, 1996

A;Title: Molecular cloning and functional expression of a new human CC-chemokine rece

A;Reference number: A43113; MUID:96241590

A;Accession: A43113

A;Molecule type: mRNA

A;Residues: 1-352 <SAM1>

A;Cross-references: GB:X91492; NID:g1262810; PIDN:CAA62796.1; PID:g1262811

R;Samson, M.; Libert, F.; Doranz, B.J.; Rucker, J.; Liesnard, C.; Farber, C.M.; Sarag

M.; Imai, T.; Rana, S.; Yi, Y.; Smyth, R.J.; Collman, R.G.; Doms, R.W.; Vassart, G.;

Nature 382, 722-725, 1996

A;Title: Resistance to HIV-1 infection in caucasian individuals bearing mutant allele

A;Reference number: S71808; MUID:96345670

A;Accession: S71808

A;Status: nucleic acid sequence not shown; not compared with conceptual translation

A;Molecule type: DNA

A;Residues: 182-206;207-230 <SAM2>

A;Accession: A58834

A;Status: nucleic acid sequence not shown; not compared with conceptual translation

A;Molecule type: DNA

A;Residues: 1-184, 'IKDSHLGAGPAACHGHLGNPKNSASVSK' <SAM3>

A;Cross-references: GB:X99393; NID:g1524062; PIDN:CAA67767.1; PID:g1524063

A;Note: this frameshift mutation results in a non-functional receptor but confers a d

nd may have had a selective advantage by conferring resistance to Yersinia plague inf

R;Combadiere, C.; Ahuja, S.K.; Tiffany, H.L.; Murphy, P.M.

J. Leukoc. Biol. 60, 147-152, 1996
A:Title: Cloning and functional expression of CC CKR5, a human monocyte CC chemokine receptor
A:Reference number: A58832; MUID:96295970
A:Accession: A58832
A:Molecule type: mRNA
A:Residues: 1-352 <COM1>
A:Cross-references: GB:U57840; NID:gl502408; PIDN:AA1071.1; PID:gl502409
A:Experimental source: clone 8, endotoxin-stimulated peripheral blood monocytes
R:Combadiere, C.
submitted to the EMBL Data Library, May 1996
A:Reference number: H01541
A:Accession: G02653
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-89, 'L', 91-352 <COM2>
A:Cross-references: EMBL:U57840
R:Raport, C.J.; Gosling, J.; Schweickart, V.L.; Gray, P.W.; Charo, I.F.
J. Biol. Chem. 271, 17161-17166, 1996
A:Title: Molecular cloning and functional characterization of a novel human CC chemokine receptor
A:Reference number: A58833; MUID:96291862
A:Accession: A58833
A:Molecule type: mRNA
A:Residues: 1-352 <RAP>
A:Cross-references: GB:U54994; NID:gl457945; PIDN:AA050598.1; PID:gl457946
C:Comment: This is a receptor for chemokines MIP-1alpha (see PIR:A30574), MIP-1beta (see PIR:A30575) and dual-tropic strains of HIV-1 bind to a complex of chemokine receptor and MIP-1beta.
C:Genetics:
A:Gene: GDB:CMKBR5; CCR5; CXCR-5; CC-CCR-5; CXCR5; ChemR13
A:Cross-references: GDB:1230510; OMIM:601373
A:Map position: 3p21-3p21
C:Function:
A:Description: G protein-coupled receptor for chemokines MIP-1alpha, MIP-1beta and RANTES
A:Note: probably acts to control granulocyte proliferation and differentiation
C:Superfamily: vertebrate rhodopsin
C:Keywords: AIDS; G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane protein
F:32-56/Domain: transmembrane #status predicted <TM1>
F:67-87/Domain: transmembrane #status predicted <TM2>
F:103-124/Domain: transmembrane #status predicted <TM3>
F:142-166/Domain: transmembrane #status predicted <TM4>
F:193-218/Domain: transmembrane #status predicted <TM5>
F:236-257/Domain: transmembrane #status predicted <TM6>
F:285-300/Domain: transmembrane #status predicted <TM7>
F:268/Binding site: disulfide bonds: #status predicted
F:268/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:336,337,342/Binding site: phosphate (Ser) (covalent) #status predicted
F:340,343/Binding site: phosphate (Thr) (covalent) #status predicted

Query Match 57.1%; Score 44.5; DB 2; Length 352;
Best Local Similarity 52.9%; Pred. No. 2.2;
Matches 9; Conservative 5; Mismatches 2; Indels 1; Gaps 1;

QY 1 KTLVQAQN-SKRHKAIR 16
||||: |||:|
DB 219 KTLRCRNEKKRRAVR 235

RESULT 7
JC2443
chemokine (C-C) receptor 2, splice form B - human
N:Alternate names: C-C CKR-2; monocyte chemoattractant protein 1 receptor; monocyte chemoattractant protein 1
C:Species: Homo sapiens (man)
C:Date: 21-Feb-1995 #sequence_revision 05-Apr-1995 #text_change 20-Jun-2000
C:Accession: JC2443; I38463
R:Yamagami, S.; Tokuda, Y.; Ishii, K.; Tanaka, H.; Endo, N.
Biochem. Biophys. Res. Commun. 202, 1156-1162, 1994
A:Title: cDNA cloning and functional expression of a human monocyte chemoattractant protein 1 receptor
A:Reference number: JC2443; MUID:94324942
A:Accession: JC2443
A:Molecule type: mRNA
A:Residues: 1-360 <YAM>
A:Cross-references: DDBJ:D29984; NID:g531246; PIDN:BAA06253.1; PID:g531247
R:Charo, I.F.; Myers, S.J.; Herman, A.; Franci, C.; Connolly, A.J.; Coughlin, S.R.

Proc. Natl. Acad. Sci. U.S.A. 91, 2752-2756, 1994
A:Title: Molecular cloning and functional expression of two monocyte chemoattractant protein 1 receptors
A:Reference number: A53477; MUID:94195821
A:Accession: I38463
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-360 <RES>
A:Cross-references: EMBL:U03905; NID:g472557; PIDN:AAA19120.1; PID:g472558
C:Genetics:
A:Gene: GDB:CMKBR2
A:Cross-references: GDB:337364; OMIM:601267
A:Map position: 3p21-3p21
C:Superfamily: vertebrate rhodopsin
C:Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; transmembrane protein
F:81-100/Domain: transmembrane #status predicted <TM1>
F:115-136/Domain: transmembrane #status predicted <TM2>
F:154-178/Domain: transmembrane #status predicted <TM3>
F:207-226/Domain: transmembrane #status predicted <TM4>
F:244-268/Domain: transmembrane #status predicted <TM5>
F:287-309/Domain: transmembrane #status predicted <TM6>
F:314/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:314/Binding site: disulfide bonds: #status predicted

Query Match 57.1%; Score 44.5; DB 2; Length 360;
Best Local Similarity 52.9%; Pred. No. 2.3;
Matches 9; Conservative 5; Mismatches 2; Indels 1; Gaps 1;

QY 1 KTLVQAQN-SKRHKAIR 16
||||: |||:|
DB 227 KTLRCRNEKKRRAVR 243

RESULT 8
I38450
chemokine (C-C) receptor 2, splice form A - human
N:Alternate names: C-C CKR-2; monocyte chemoattractant protein 1 receptor; monocyte chemoattractant protein 1
C:Species: Homo sapiens (man)
C:Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 13-Aug-1999
R:Charo, I.F.; Myers, S.J.; Herman, A.; Franci, C.; Connolly, A.J.; Coughlin, S.R.
Proc. Natl. Acad. Sci. U.S.A. 91, 2752-2756, 1994
A:Title: Molecular cloning and functional expression of two monocyte chemoattractant protein 1 receptors
A:Reference number: A53477; MUID:94195821
A:Accession: I38450
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-374 <RES>
A:Cross-references: EMBL:U03882; NID:g472555; PIDN:AAA19119.1; PID:g472556
C:Genetics:
A:Gene: GDB:CMKBR2
A:Cross-references: GDB:337364; OMIM:601267
A:Map position: 3p21-3p21
C:Superfamily: vertebrate rhodopsin
C:Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; transmembrane protein
F:44-68/Domain: transmembrane #status predicted <TM1>
F:79-99/Domain: transmembrane #status predicted <TM2>
F:115-136/Domain: transmembrane #status predicted <TM3>
F:154-178/Domain: transmembrane #status predicted <TM4>
F:208-226/Domain: transmembrane #status predicted <TM5>
F:244-265/Domain: transmembrane #status predicted <TM6>
F:292-309/Domain: transmembrane #status predicted <TM7>
F:314/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:32-277,113-190/Disulfide bonds: #status predicted

Query Match 57.1%; Score 44.5; DB 2; Length 374;
Best Local Similarity 52.9%; Pred. No. 2.4;
Matches 9; Conservative 5; Mismatches 2; Indels 1; Gaps 1;

QY 1 KTLVQAQN-SKRHKAIR 16
||||: |||:|

Db 227 KTLRCRNEKKRRRAVR 243

RESULT 9
G02436
chemokine (C-C) receptor 3 - human
N:Alternate names: C-C CKR-3
C:Species: Homo sapiens (man)
C:Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 04-Mar-2000
C:Accession: G02436; A57237
R:Ponath, P.D.
submitted to the EMBL Data Library, February 1996
A:Reference number: H01272
A:Accession: G02436
A:Status: translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-355 <PON>
A:Cross-references: EMBL:U49727; NID:g1477560; PIDN:RAB09726.1; PID:g1477561
R:Combadieere, C.; Ahuja, S.K.; Murphy, P.M.
J. Biol. Chem. 270, 16491-16494, 1995
A:Title: Cloning and functional expression of a human eosinophil CC chemokine receptor.
A:Reference number: A57237; MUID:95348056
A:Accession: A57237
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-106, 'N', 108-275, 'S', 277-280, 'R', 282-355 <COM>
A:Cross-references: GB:U28694; NID:g1199579; PIDN:AAC50469.1; PID:g1199580
A:Note: the translated sequence in GenBank entry HSU28694, release 113.0, PIDN:AAC50469.
C:Genetics:
A:Gene: GDB:CMKBR3
A:Cross-references: GDB:579624; OMIM:601268
A:Map position: 3p21-3p21
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane protein
F:36-60/Domain: transmembrane #status predicted <TM1>
F:71-91/Domain: transmembrane #status predicted <TM2>
F:108-129/Domain: transmembrane #status predicted <TM3>
F:147-171/Domain: transmembrane #status predicted <TM4>
F:205-223/Domain: transmembrane #status predicted <TM5>
F:240-261/Domain: transmembrane #status predicted <TM6>
F:288-305/Domain: transmembrane #status predicted <TM7>
F:24-273,106-183/Disulfide bonds: #status predicted
F:345/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted

Query Match 55.1%; Score 43; DB 2; Length 355;
Best Local Similarity 50.0%; Pred. No. 4.2;
Matches 8; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 KTLVQAQNSKRHKAI 16
||||| : : : : :
DB 224 KTLRCRNEKKRRRAVR 239

RESULT 10
C83099
hypothetical protein PA4373 [imported] - Pseudomonas aeruginosa (strain PAO1)
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathogen.
A:Reference number: A82950; MUID:20437337
A:Accession: C83099
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-364 <STO>
A:Cross-references: GB:AE004853; GB:AE004091; NID:g9950598; PIDN:AAG07761.1; GSPDB:GN001
A:Experimental source: strain PAO1
C:Genetics:

A:Gene: PA4373

Query Match 52.6%; Score 41; DB 2; Length 364;
Best Local Similarity 60.0%; Pred. No. 9.9;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 KTLVQAQNSKRHKAI 15
||| | | | | |
DB 212 ETLAQMNVRHLAI 236

RESULT 11
T52146
ribosomal protein L13e [imported] - yeast (Candida albicans)
C:Species: Candida albicans
C:Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 03-Nov-2000
C:Accession: T52146
R:Taylor, K.; Harris, D.
submitted to the EMBL Data Library, November 1998
A:Reference number: Z25985
A:Accession: T52146
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-202 <TAY>
A:Cross-references: EMBL:AL033497; PIDN:CAA21966.1
A:Experimental source: strain 1161; cosmid Ca49C10
C:Genetics:
A:Gene: Ca49C10.02
A:Map position: 1
C:Superfamily: rat ribosomal protein L13
C:Keywords: protein biosynthesis; ribosome

Query Match 51.3%; Score 40; DB 2; Length 202;
Best Local Similarity 50.0%; Pred. No. 8.4;
Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 KTLVQAQNSKRHKAI 16
||| | : : : : :
DB 170 RTLRLARNEKKYKGI 185

RESULT 12
A23669
interleukin-8 receptor, high affinity - rabbit
N:Alternate names: fMLP receptor
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 05-Nov-1999
C:Accession: A23669
R:Thomas, K.M.; Pyun, H.Y.; Navarrete, J.
J. Biol. Chem. 265, 20061-20064, 1990
A:Title: Molecular cloning of the fMet-Leu-Phe receptor from neutrophils.
A:Reference number: A23669; MUID:91056034
A:Accession: A23669
A:Molecule type: mRNA
A:Residues: 1-354 <THO>
A:Cross-references: GB:M58021; GB:J05705; NID:g165442; PIDN:AAA31377.1; PID:g165443
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; glycoprotein; membrane protein; neutrophil

Query Match 51.3%; Score 40; DB 2; Length 354;
Best Local Similarity 43.8%; Pred. No. 15;
Matches 7; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 KTLVQAQNSKRHKAI 16
||| | | : : : : :
DB 231 RTLFQAHHGQKRRAMR 246

RESULT 13
J01231

interleukin-8 receptor - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 05-Nov-1999
C:Accession: J01231; A46483
R:Beckmann, M.P.; Munger, W.E.; Kozlosky, C.; VandenBos, T.; Price, V.; Lyman, S.; Gerard, B.; Beckmann, M.P.; Res. Commun. 179, 784-789, 1991
A:Title: Molecular characterization of the interleukin-8 receptor.
A:Reference number: J01231; MUID:91378994
A:Accession: J01231
A:Molecule type: DNA
A:Residues: 1-355 <BEC>
A:Cross-references: GB:M74240; NID:q165438; PIDN:AAA31375.1; PID:g165439
R:Lee, J.; Kuang, W.J.; Rice, G.C.; Wood, W.I.
J. Immunol. 148, 1261-1264, 1992
A:Title: Characterization of complementary DNA clones encoding the rabbit IL-8 receptor.
A:Reference number: A46483; MUID:92148149
A:Accession: A46483
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-355 <LEE>
A:Cross-references: GB:M82873; NID:q165440; PIDN:AAA31376.1; PID:g165441
A:Experimental source: neutrophils
A:Note: sequence extracted from NCBI backbone (NCBIN:81526, NCBIP:81530)
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 51.3%; Score 40; DB 2; Length 355;
Best Local Similarity 43.8%; Pred. No. 15;
Matches 7; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 1 KTLVQAQNSKRHKAI 16
||| || :||:|
Db 232 RTLFOAHMGQKHRAMR 247

RESULT 14

A53752
interleukin-8 receptor (clone 5Bla) - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C:Accession: A53752
R:Prado, G.N.; Thomas, K.M.; Suzuki, H.; LaRosa, G.J.; Wilkinson, N.; Folco, E.; Navarro, J. Biol. Chem. 269, 12391-12394, 1994
A:Title: Molecular characterization of a novel rabbit interleukin-8 receptor isotype.
A:Reference number: A53752; MUID:94230294
A:Accession: A53752
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-358 <PRA>
A:Cross-references: GB:L24445; NID:q437661; PIDN:AAA31378.1; PID:g437662
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 51.3%; Score 40; DB 2; Length 358;
Best Local Similarity 43.8%; Pred. No. 15;
Matches 7; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 1 KTLVQAQNSKRHKAI 16
||| || :||:|
Db 234 RTLFOAHMGQKHRAMR 249

RESULT 15

T24972
hypothetical protein T19A6.2b - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T24972
R:Clark, L.
submitted to the EMBL Data Library, January 1998
A:Reference number: Z19963

A:Accession: T24972
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-639 <WIL>
A:Cross-references: EMBL:AL021571; PIDN:CAA16514.1; GSPDB:GN00019; CESP:T19A6.2b
A:Experimental source: clone T19A6
C:Genetics:
A:Gene: CESP:T19A6.2b
A:Map position: 1
A:Introns: 9/2; 41/1; 85/3; 118/3; 186/3; 221/3; 458/3; 505/3; 609/3

Query Match 51.3%; Score 40; DB 2; Length 639;
Best Local Similarity 46.7%; Pred. No. 26;
Matches 7; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 1 KTLVQAQNSKRHKAI 15
||| || :||:|
Db 597 KTIVQAASEKKDKSV 611

Search completed: May 23, 2001, 15:32:02
Job time: 509 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 23, 2001, 15:36:20 ; Search time 62.39 seconds
(without alignments)
8.785 Million cell updates/sec

Title: US-08-887-977-10_COPY_230_245

Perfect score: 78

Sequence: 1 KTLVQAQNSKRRAIR 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	78	100.0	374	1	CCR6_HUMAN
2	75	96.2	367	1	CCR6_MOUSE
3	54	69.2	359	1	CCR3_MOUSE
4	50	64.1	359	1	CCR3_RAT
5	50	64.1	369	1	CCR9_MOUSE
6	49	62.8	357	1	CCR9_HUMAN
7	48	61.5	378	1	CCR7_HUMAN
8	48	61.5	378	1	CCR7_MOUSE
9	44.5	57.1	352	1	CCR5_CERAE
10	44.5	57.1	352	1	CCR5_CERTO
11	44.5	57.1	352	1	CCR5_GORGO
12	44.5	57.1	352	1	CCR5_HUMAN
13	44.5	57.1	352	1	CCR5_HYLLE
14	44.5	57.1	352	1	CCR5_MACMU
15	44.5	57.1	352	1	CCR5_PANTR
16	44.5	57.1	352	1	CCR5_PAPHA
17	44.5	57.1	352	1	CCR5_PONEY
18	44.5	57.1	352	1	CCR5_PYGBI
19	44.5	57.1	352	1	CCR5_PYGNE
20	44.5	57.1	352	1	CCR5_TRAFH
21	44.5	57.1	352	1	CCR5_TRAPE
22	44.5	57.1	374	1	CCR2_HUMAN
23	43	55.1	355	1	CCR3_CERAE
24	43	55.1	355	1	CCR3_HUMAN
25	43	55.1	355	1	CCR3_MACMU
26	43	55.1	358	1	CCR3_CAVPO
27	40	51.3	202	1	RL13_CANAL
28	40	51.3	355	1	IL8A_RABIT
29	40	51.3	358	1	IL8B_RABIT
30	39	50.0	139	1	ZG29_XENLA
31	39	50.0	211	1	VNS3_RSVN
32	39	50.0	211	1	VNS3_RSVT
33	39	50.0	673	1	FOX3_HUMAN

ALIGNMENTS

RESULT	ID	CCR6_HUMAN	STANDARD;	PRT;	374 AA.
34	AC	P51684	O92846; P78553;		
35	DC	01-OCT-1996	(Rel. 34, Created)		
36	DT	15-JUL-1998	(Rel. 36, Last sequence update)		
37	DT	01-OCT-2000	(Rel. 40, Last annotation update)		
38	DE	C-C CHEMOKINE RECEPTOR TYPE 6 (C-C CCR-6) (CCR-6) (LARC			
39	DE	RECEPTOR) (GPR-CY4) (GPCY4) (CHEMOKINE RECEPTOR-LIKE 3) (CCR-L3)			
40	DE	(DRY6).			
41	GN	CCR6 OR CMKBR6 OR STRL22 OR GPR29 OR CCR6L3.			
42	OS	Homo sapiens (Human).			
43	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
44	OC	Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.			
45	OX	NCBI_TaxID=9606;			
	RN	[1]			
	RP	SEQUENCE FROM N.A., AND FUNCTION.			
	RX	MEDLINE=97313465; PubMed=9169459;			
	RA	Baba M., Imal T., Nishimura M., Kakizaki M., Takagi S., Hieshima K.,			
	RA	Nomiyama H., Yoshie O.;			
	RT	"Identification of CCR6, the specific receptor for a novel			
	RT	lymphocyte-directed CC chemokine LARC.";			
	RL	J--BioI--Chem--272:14893-14898(1997).			
	RN	[2]			
	RP	SEQUENCE FROM N.A.			
	RA	Lautens L.L., Modi W., Bonner T.I.;			
	RL	Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.			
	RN	[3]			
	RP	SEQUENCE FROM N.A.			
	RX	MEDLINE=97040707; PubMed=8886020;			
	RA	Zaballos A., Varona R., Gutierrez J., Lind P., Marquez G.;			
	RT	"Molecular cloning and RNA expression of two new human chemokine			
	RT	receptor-like genes.";			
	RL	Biochem. Biophys. Res. Commun. 227:846-853(1996).			
	RN	[4]			
	RP	SEQUENCE FROM N.A.			
	RA	McCoy R., Perlmuter D.H.;			
	RL	Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.			
	RN	[5]			
	RP	SEQUENCE FROM N.A.			
	RX	MEDLINE=97224503; PubMed=9070937;			
	RA	Liao F., Lee H.-H., Farber J.M.;			
	RT	"Cloning of STRL22, a new human gene encoding a G-protein-coupled			
	RT	receptor related to chemokine receptors and located on chromosome			
	RT	6q27.";			
	RL	Genomics 40:175-180(1997).			
	CC	-!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-3-			
	CC	ALPHA/LARC AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE			
	CC	INTRACELLULAR CALCIUM IONS LEVEL.			
	CC	-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.			
	CC	-!- TISSUE SPECIFICITY: SPLEEN, LYMPH NODES, APPENDIX, AND FETAL			
	CC	LIVER. EXPRESSED IN LYMPHOCYTES, T CELLS AND B CELLS BUT NOT IN			
	CC	NATURAL KILLER CELLS, MONOCYTES, OR GRANULOCYTES.			
	CC	-!- INDUCTION: INTERLEUKIN-2.			
	CC	-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.			
	CC	-!- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-6 IS THE INITIATOR.			

Q39565 chlamydomon
O54842 rattus norv
Q01024 herpesvirus
P51679 homo sapien
P51680 mus musculu
Q28003 bos taurus
Q16533 homo sapien
O48927 glycine max
Q04511 saccharomyc
Q60769 mus musculu
P21580 homo sapien
P51682 mus musculu

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 CC EMBL: U45984; AAB62714.1; -
 CC EMBL: 279784; CAB02144.1; ALT_INIT.
 CC EMBL: U60000; AAB06949.1; -
 CC EMBL: U68030; AAC51124.1; -
 CC EMBL: U68032; AAC51125.1; -
 CC HSSP: P34996; 1DDO.
 CC GCRDB: GCR_1037; -
 CC GCRDB: GCR_1075; -
 CC GCRDB: GCR_1906; -
 CC GCRDB: GCR_1919; -
 CC GCRDB: GCR_1941; -
 CC GCRDB: GCR_2110; -
 CC MIM: 601835; -
 CC InterPro: IPR000276; -
 CC Pfam: PF00001; 7tm1.1; -
 CC PRINTS: PR00237; GPCRHHODOPSN.
 CC PROSITE: PS00237; G_PROTEIN_RECF_FL_1; 1.
 CC PROSITE: PS0262; G_PROTEIN_RECF_FL_2; 1.
 CC G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 47 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 48 74 1 (POTENTIAL).
 FT DOMAIN 75 83 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 84 104 2 (POTENTIAL).
 FT DOMAIN 105 119 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 120 141 3 (POTENTIAL).
 FT DOMAIN 142 159 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 160 180 4 (POTENTIAL).
 FT DOMAIN 181 211 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 212 238 5 (POTENTIAL).
 FT DOMAIN 239 254 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 255 279 6 (POTENTIAL).
 FT DOMAIN 280 303 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 304 321 7 (POTENTIAL).
 FT DOMAIN 322 374 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 118 197 BY SIMILARITY.
 FT CARBOHYD 23 23 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 60 60 G -> A (IN REF. 4).
 FT CONFLICT 74 74 Y -> N (IN REF. 4).
 FT CONFLICT 86 86 L -> V (IN REF. 4).
 FT CONFLICT 164 164 S -> T (IN REF. 5).
 FT CONFLICT 182 182 T -> S (IN REF. 4).
 FT CONFLICT 192 192 Q -> L (IN REF. 4).
 FT CONFLICT 206 206 E -> V (IN REF. 4).
 FT CONFLICT 225 225 I -> F (IN REF. 4).
 FT CONFLICT 270 374 SSFTM -> VLVHVIES (IN REF. 4).
 SQ SEQUENCE 374 AA; 42494 MW; D7F963534E990BC4 CRC64;

Query Match 100.0%; Score 78; DB 1; Length 374;
 Best Local Similarity 100.0%; Pred. No. 2.9e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KTLVQAQNSKRHKRAIR 16
 |||||
 DB 239 KTLVQAQNSKRHKRAIR 254

RESULT 2
 ID CKR6_MOUSE STANDARD; PRT; 367 AA.
 AC O54689;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE C-C CHEMOKINE RECEPTOR TYPE 6 (C-C CKR-6) (CCR-6) (KY411).
 GN CCR6 OR CMKBR6.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 ON NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Yanagihara S., Komura E., Yamaguchi Y.;
 RT "Mouse G protein-coupled receptor KY411.";
 RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99077268; PubMed=9862452;
 RA Varona R., Zaballos A., Gutierrez J., Martin P., Roncal F.,
 RA Albar J.P., Ardavin C., Marquez G.;
 RT "Molecular cloning, functional characterization and mRNA expression
 RT analysis of the murine chemokine receptor CCR6 and its specific ligand
 RT MIP-3alpha.";
 RL FEBS Lett. 440:188-194(1998).
 CC -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-3-
 CC ALPHA/LARC AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE
 CC INTRACELLULAR CALCIUM IONS LEVEL.
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 CC EMBL: AB009369; BA237776.1; -
 CC EMBL: AJ222714; CAAL0956.1; -
 CC MGD; MGI:133379; Cmkbr6.
 CC InterPro: IPR000276; -
 CC Pfam: PF00001; 7tm1.1; -
 CC PRINTS: PR00237; GPCRHHODOPSN
 CC PROSITE: PS00237; G_PROTEIN_RECF_FL_1; 1.
 CC PROSITE: PS0262; G_PROTEIN_RECF_FL_2; 1.
 CC G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 39 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 40 66 1 (POTENTIAL).
 FT DOMAIN 67 75 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 76 96 2 (POTENTIAL).
 FT DOMAIN 97 111 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 112 133 3 (POTENTIAL).
 FT DOMAIN 134 151 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 152 172 4 (POTENTIAL).
 FT DOMAIN 173 203 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 204 230 5 (POTENTIAL).
 FT DOMAIN 231 246 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 247 271 6 (POTENTIAL).
 FT DOMAIN 272 295 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 296 313 7 (POTENTIAL).
 FT DOMAIN 314 367 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 110 189 BY SIMILARITY.
 FT CARBOHYD 2 2 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 35 35 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 367 AA; 42102 MW; 6A309AF833B1117E CRC64;

Query Match 96.2%; Score 75; DB 1; Length 367;
 Best Local Similarity 93.8%; Pred. No. 1e-06;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KTLVQAQNSKRHKRAIR 16
 |||||
 DB 231 KTLVQAQNSKRHKRAIR 246

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RESULT 3
CKR3_MOUSE
ID CKR3_MOUSE STANDARD; PRT; 359 AA.
AC P51678;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE PROBABLE C-C CHEMOKINE RECEPTOR TYPE 3 (C-C CKR-3) (CCR-3)
DE (CCR3) (CCR3) (MACROPHAGE INFLAMMATORY PROTEIN-1 ALPHA RECEPTOR-LIKE
2) (MIP-1 ALPHA RL2)
DE CCR3 OR CMKBR3 OR CMKBRIL2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SVJ;
RX MEDLINE=96072806; PubMed=7594543;
RA Post T.W., Bozic C.R., Rothenberg M.E., Luster A.D., Gerard N.,
RA Gerard C.;
RT "Molecular characterization of two murine eosinophil beta chemokine
receptors.";
RL J. Immunol. 155:5299-5305(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SVJ;
RX MEDLINE=95340546; PubMed=7542241;
RA Gao J.-L., Murphy P.M.;
RT "Cloning and differential tissue-specific expression of three mouse
beta chemokine receptor-like genes, including the gene for a
functional macrophage inflammatory protein-1 alpha receptor.";
RL J. Biol. Chem. 270:17494-17501(1995).
CC -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO EOTAXIN,
MCP-3, MCP-4 AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- TISSUE SPECIFICITY: DETECTED IN SKELETAL MUSCLE AND IN TRACE
AMOUNTS IN LEUKOCYTES.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CC EMBL; U29677; AA86118.1; -
CC EMBL; U28406; AA86195.1; -
CC GCRDB; GCR_1673; -
CC GCRDB; GCR_1695; -
CC MGI; MGI:104616; Cmkbril2.
CC InterPro; IPR000276; -
CC InterPro; IPR000355; -
CC Pfam; PF00001; 7tm_1; 1.
CC PRINTS; PR00237; GPCRHHODOPSN.
CC PRINTS; PR00657; CCHEMOKINER.
CC PRINTS; PR01108; CHEMOKINER3.
CC PROSITE; PS00237; G-PROTEIN-RECEP_FL1; 1.
CC PROSITE; PS0262; G-PROTEIN-RECEP_FL2; 1.
KW G-protein coupled receptor; Transmembrane.
FT DOMAIN 1 38 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 39 64 1 (POTENTIAL).
FT DOMAIN 65 68 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 69 95 2 (POTENTIAL).
FT DOMAIN 96 111 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 112 133 3 (POTENTIAL).
FT DOMAIN 134 150 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 151 175 4 (POTENTIAL).

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FT DOMAIN 176 201 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 202 227 5 (POTENTIAL).
FT DOMAIN 228 243 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 244 268 6 (POTENTIAL).
FT DOMAIN 269 285 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 286 309 7 (POTENTIAL).
FT DOMAIN 310 359 CYTOPLASMIC (POTENTIAL).
FT DISULFID 110 187 BY SIMILARITY.
FT CONFLICT 270 270 R -> S (IN REF. 2).
SQ SEQUENCE 359 AA; 41825 MW; ACILED66E283CEAF CRC64;

Query Match 69.2%; Score 54; DB 1; Length 359;
Best Local Similarity 62.5%; Pred. No. 0.0095;
Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 KTLVQAQNSKRHKAIR 16
   |||:: | |::|||
Db 228 KTLRLCPNKKHKAIR 243

RESULT 4
CKR3_RAT
ID CKR3_RAT STANDARD; PRT; 359 AA.
AC O54814; O55169;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE C-C CHEMOKINE RECEPTOR TYPE 3 (C-C CKR-3) (CCR-3) (CCR3)
DE (CCR3).
GN GN Rattus norvegicus (Rat).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A. AND TISSUE SPECIFICITY.
RC STRAIN=Wistar; TISSUE=Spleen;
RX MEDLINE=98318173; PubMed=9855467;
RA Jiang Y., Saifranca M.N., Adhikari S., Xia Y., Feng L., Sonntag M.K.,
RA Defebvre C.M., Pennell N.A., Streit W.J., Harrison J.K.;
RT "Chemokine receptor expression in cultured glia and rat experimental
allergic encephalomyelitis.";
RL J. Neuroimmunol. 86:1-12(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=Spleen;
RA Harrington P.M., Newton D.J., Coleman J.W., Flanagan B.F.;
RA Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO EOTAXIN,
MCP-3, MCP-4 AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
CC -!- TISSUE SPECIFICITY: EXPRESSED IN SPLEEN BUT NOT IN ASTROCYTES OR
MICROGLIA.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CC EMBL; AF003954; AAC03337.1; -
CC EMBL; Y13400; CAA73830.1; -
CC InterPro; IPR000276; -
CC InterPro; IPR000355; -
CC InterPro; IPR002238; -
CC Pfam; PF00001; 7tm_1; 1.
CC PRINTS; PR00237; GPCRHHODOPSN.
CC PRINTS; PR00657; CCHEMOKINER.

```

DR PRINTS; PRO1108; CHEMOKINER3.
 DR PROSITE; PS00237; G-PROTEIN_RECEP_FL_1; 1.
 DR PROSITE; PS0262; G-PROTEIN_RECEP_FL_2; 1.
 KW G-protein coupled receptor; Transmembrane.
 FT DOMAIN 1 43 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 44 64 POTENTIAL.
 FT DOMAIN 65 74 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 75 95 POTENTIAL.
 FT DOMAIN 96 112 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 113 133 POTENTIAL.
 FT DOMAIN 134 154 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 155 175 POTENTIAL.
 FT DOMAIN 176 206 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 207 227 POTENTIAL.
 FT DOMAIN 228 243 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 244 264 POTENTIAL.
 FT DOMAIN 265 288 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 289 309 POTENTIAL.
 FT DOMAIN 310 359 CYTOPLASMIC (POTENTIAL).
 FT CONFLICT 164 164 F -> L (IN REF. 2).
 SQ SEQUENCE 359 AA; 41643 MW; 880F682984F501DA CRC64;

Query Match 64.1%; Score 50; DB 1; Length 359;
 Best Local Similarity 56.2%; Pred. No. 0.054;
 Matches 9; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 KTLVQAQNSKRHRKRAIR 16
 DB 228 KILLRCPNKKKKRAIQ 243
 ||||: | | | | |

RESULT 5
 ID CKR9_MOUSE STANDARD; PRT; 369 AA.
 AC Q9WUT7;

DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE C-C CHEMOKINE RECEPTOR TYPE 9 (C-C CKR-9) (CC-CKR-9) (CCR-9)
 DE (CHEMOKINE C-C RECEPTOR 10).
 GN CKR9 OR CMKBR10.

OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Thymus;

RX MEDLINE=99248139; PubMed=10229797;

RA Zaballios A., Gutierrez J., Varona R., Ardavin C., Marquez G.;

RT "Cutting edge: identification of the orphan chemokine receptor GPR-9-6

as CCR9, the receptor for the chemokine TECK.";

RL J. Immunol. 162:5671-5675(1999).

CC -!- FUNCTION: RECEPTOR FOR CHEMOKINE SCYA25/TECK. SUBSEQUENTLY

TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS

LEVEL.

CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

CC -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN THE THYMUS AND LOW IN

LYMPH NODES AND SPLEEN.

CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

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 CC -----

DR EMBL; AJ132336; CAB43480.1;

DR MGD; MGI:1341902; Cmkbr10.

DR InterPro; IPR000174; -.

DR InterPro; IPR000248; -.
 DR InterPro; IPR000276; -.
 DR InterPro; IPR000355; -.
 DR InterPro; IPR000496; -.
 DR InterPro; IPR001277; -.
 DR InterPro; IPR001718; -.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PRO0237; GPCRHHODPSN.
 DR PRINTS; PRO0241; ANGIOTENSINR.
 DR PRINTS; PRO0425; BRADYKININR.
 DR PRINTS; PRO0437; INTRLEUKINR.
 DR PRINTS; PRO0641; CHEMOKINER7.
 DR PRINTS; PRO0645; LCRIORPHANR.
 DR PRINTS; PRO0657; CCHEMOKINER.
 DR PROSITE; PS00237; G-PROTEIN_RECEP_FL_1; 1.
 DR PROSITE; PS0262; G-PROTEIN_RECEP_FL_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 49 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 50 76 1 (POTENTIAL).
 FT DOMAIN 77 85 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 86 106 2 (POTENTIAL).
 FT DOMAIN 107 120 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 121 142 3 (POTENTIAL).
 FT DOMAIN 143 160 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 161 181 4 (POTENTIAL).
 FT DOMAIN 182 210 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 211 238 5 (POTENTIAL).
 FT DOMAIN 239 254 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 255 280 6 (POTENTIAL).
 FT DOMAIN 281 304 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 305 322 7 (POTENTIAL).
 FT DOMAIN 323 369 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 32 32 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT DISULFID 119 198 BY SIMILARITY.
 SQ SEQUENCE 369 AA; 41913 MW; 6971F76F0A24B4AE CRC64;

Query Match 64.1%; Score 50; DB 1; Length 369;
 Best Local Similarity 60.0%; Pred. No. 0.056;
 Matches 9; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 2 TLVQAQNSKRHRKRAIR 16
 DB 240 TLVQAQNSKRHRKALK 254
 ||||: | | | | |

RESULT 6

ID CKR9_HUMAN

AC P51686; STANDARD; PRT; 357 AA.

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DE 30-MAY-2000 (Rel. 39, Last annotation update)

DE C-C CHEMOKINE RECEPTOR TYPE 9 (C-C CKR-9) (CC-CKR-9) (CCR-9) (GPR-9-

6).

GN CCR9 OR CMKBR9.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RA Lautens L.L., Tiffany H.L., Gao J.-L., Modi W., Murphy P.M.,

RA Bonner T.I.;

RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.

RN [2]

RP CHARACTERIZATION.

RX MEDLINE=99248139; PubMed=10229797;

RA Zaballios A., Gutierrez J., Varona R., Ardavin C., Marquez G.;

RT "Cutting edge: identification of the orphan chemokine receptor GPR-9-6

as CCR9, the receptor for the chemokine TECK.";

RL J. Immunol. 162:5671-5675(1999).

CC -!- FUNCTION: RECEPTOR FOR CHEMOKINE SCYA25/TECK. SUBSEQUENTLY

CC TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS
 CC LEVEL.
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN THE THYMUS AND LOW IN
 CC Lymph Nodes and Spleen.
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 CC -----
 CC EMBL; U45982; AAA93319.1; -
 CC MIM; 604738; -
 CC GCRDB; GCR_1943; -
 CC InterPro; IPR000276; -
 CC Pfam; PF00001; 7tm_1; 1.
 CC PRINTS; PR00237; GPCRHHODOPSN.
 CC PROSITE; PS00237; G-PROTEIN_RECF_FL_1; 1.
 CC PROSITE; PS0262; G-PROTEIN_RECF_FL_2; 1.
 CC G-protein coupled receptor; Transmembrane; Glycoprotein.
 CC DOMAIN 1 37
 CC TRANSMEM 38 64
 CC DOMAIN 65 73
 CC TRANSMEM 74 94
 CC DOMAIN 95 108
 CC TRANSMEM 109 130
 CC DOMAIN 131 148
 CC TRANSMEM 149 169
 CC DOMAIN 170 198
 CC TRANSMEM 199 226
 CC DOMAIN 227 242
 CC TRANSMEM 243 268
 CC DOMAIN 269 292
 CC TRANSMEM 293 310
 CC DOMAIN 311 357
 CC CARBOHYD 20 20 - N-LINKED (GLCNAC...) (POTENTIAL).
 CC DISULFID 107 186 BY SIMILARITY.
 CC SEQUENCE 357 AA; 40713 MW; 96982E0B922F6B31 CRC64;
 SQ
 Query Match 62.8%; Score 49; DB 1; Length 357;
 Best Local Similarity 53.3%; Score No. 0.083;
 Matches 8; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
 Qy 2 TLVQAKSKRHKRAIR 16
 Db 228 TLVQAKSKRHKALK 242
 |||||:|:||||:
 RESULT 7
 ID CKR7_HUMAN STANDARD; PRT; 378 AA.
 AC P32248;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE C-C CHEMOKINE RECEPTOR TYPE 7 PRECURSOR (C-C CKR-7) (CCR-7)
 DE (MIP-3 BETA RECEPTOR) (EBV-INDUCED G PROTEIN-COUPLED RECEPTOR 1)
 DE (EB1) (BLR2).
 GN CCR7 OR CMKBR7 OR EB1 OR EVIL.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93188173; PubMed=8833238;
 RA Birkenbach M.P., Josefsen K., Valamanchili R.R., Lenoir G.M.,
 RA Elliott K.;

RT "Epstein-Barr virus-induced genes: first lymphocyte-specific G
 RT protein-coupled peptide receptors."; J. Virol. 67:2209-2220(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Placenta;
 RX MEDLINE=95154835; PubMed=7851893;
 RA Schweickart V.L., Raport C.J., Godiska R., Byers M.G., Eddy R.L. Jr.,
 RA Shows T.B., Gray P.W.;
 RT "Cloning of human and mouse EB1, a lymphoid-specific
 RT G-protein-coupled receptor encoded on human chromosome 17q12-q21.2.";
 RL Genomics 23:643-650(1994).
 CC -!- FUNCTION: RECEPTOR FOR THE MIP-3-BETA CHEMOKINE. PROBABLE MEDIATOR
 CC OF EBV EFFECTS ON B LYMPHOCYTES OR OF NORMAL LYMPHOCYTE FUNCTIONS.
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN VARIOUS LYMPHOID TISSUES AND
 CC ACTIVATED B AND T LYMPHOCYTES, STRONGLY UPREGULATED IN B CELLS
 CC INFECTED WITH EPSTEIN-BARR VIRUS AND T CELLS INFECTED WITH
 CC HERPESVIRUS 6 OR 7.
 CC -!- INDUCTION: BY EBV.
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 CC -----
 CC EMBL; L08176; AAA58615.1; -
 CC EMBL; L31584; AAA74230.1; -
 CC EMBL; L31582; AAA74230.1; JOINED.
 CC EMBL; L31583; AAA74230.1; JOINED.
 CC EMBL; L31581; AAA74231.1; -
 CC PIR; A45680; A45680.
 CC HSP; P34996; 1DDO.
 CC GCRDB; GCR_0492; -
 CC GCRDB; GCR_0958; -
 CC MIM; 600242; -
 CC InterPro; IPR000276; -
 CC InterPro; IPR001718; -
 CC Pfam; PF00001; 7tm_1; 1.
 CC PRINTS; PR00237; GPCRHHODOPSN.
 CC PRINTS; PR00641; CHEMOKINER7
 CC PROSITE; PS00237; G-PROTEIN_RECF_FL_1; 1.
 CC PROSITE; PS0262; G-PROTEIN_RECF_FL_2; 1.
 CC G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
 CC SIGNAL 1 24
 CC CHAIN 25 378 C-C CHEMOKINE RECEPTOR TYPE 7.
 CC DOMAIN 25 59 EXTRACELLULAR (POTENTIAL).
 CC TRANSMEM 60 86 1 (POTENTIAL).
 CC DOMAIN 87 95 CYTOPLASMIC (POTENTIAL).
 CC TRANSMEM 96 116 2 (POTENTIAL).
 CC DOMAIN 117 130 EXTRACELLULAR (POTENTIAL).
 CC TRANSMEM 131 152 3 (POTENTIAL).
 CC DOMAIN 153 170 CYTOPLASMIC (POTENTIAL).
 CC TRANSMEM 171 191 4 (POTENTIAL).
 CC DOMAIN 192 219 EXTRACELLULAR (POTENTIAL).
 CC TRANSMEM 220 247 5 (POTENTIAL).
 CC DOMAIN 248 263 CYTOPLASMIC (POTENTIAL).
 CC TRANSMEM 264 289 6 (POTENTIAL).
 CC DOMAIN 290 313 EXTRACELLULAR (POTENTIAL).
 CC TRANSMEM 314 331 7 (POTENTIAL).
 CC DOMAIN 332 378 CYTOPLASMIC (POTENTIAL).
 CC CARBOHYD 36 36 N-LINKED (GLCNAC...) (POTENTIAL).
 CC DISULFID 129 210 BY SIMILARITY.
 CC CONFLICT 182 183 IW -> SA (IN REF. 1).
 CC CONFLICT 337 337 L -> I (IN REF. 1).
 CC SEQUENCE 378 AA; 42874 MW; D4CB4213841A1BD4 CRC64;
 SQ
 Query Match 61.5%; Score 48; DB 1; Length 378;

Best Local Similarity 56.2%; Pred. No. 0.14; Mismatches 6; Indels 1; Gaps 0;

Matches 9; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 1 KTLVQAQNSKRHRKPAIR 16
:||:||||:|:||||:
Db 248 RTLLQARNFERNKAIK 263

Query Match 61.5%; Score 48; DB 1; Length 378;
Best Local Similarity 56.2%; Pred. No. 0.14; Indels 0; Gaps 0;
Matches 9; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 1 KTLVQAQNSKRHRKPAIR 16
:||:||||:|:||||:
Db 248 RTLLQARNFERNKAIK 263

RESULT 8
CKR7_MOUSE
ID CKR7_MOUSE STANDARD; PRT; 378 AA.
AC P47774;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE C-C CHEMOKINE RECEPTOR TYPE 7 PRECURSOR (C-C CKR-7) (CCR-7)
DE (MIP-3 BETA RECEPTOR) (EBV-INDUCED G PROTEIN-COUPLED RECEPTOR 1)
DE (EB11).
GN CKR7 OR CMKBR7 OR EB11 OR EB11H.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=B6/CBA; TISSUE=Thymus;
RX MEDLINE=95154835; PubMed=7851893;
RA Schweickart V.L., Raport C.J., Godiska R., Byers M.G., Eddy R.L. Jr.,
RA Shows T.B., Gray P.W.;
RT "Cloning of human and mouse EB11, a lymphoid-specific
RT G-protein-coupled receptor encoded on human chromosome 17q12-q21.2.";
RL Genomics 23:643-650(1994).
CC -!- FUNCTION: RECEPTOR FOR THE MIP-3-BETA CHEMOKINE. PROBABLE MEDIATOR
CC OF EBV EFFECTS ON B LYMPHOCYTES OR OF NORMAL LYMPHOCYTE FUNCTIONS.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC
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CC
CC EMBL; L31580; AAA74232.1; -;
CC MGD; MGI:103011; Cmkbr7.
CC InterPro; IPR000276; -;
CC InterPro; IPR001718; -;
CC Pfam; PF00001; 7tm.1; 1.
CC PRINTS; PR00237; GPCRHHODPSN.
CC PRINTS; PR00641; CHEMOKINER7.
CC PROSITE; PS00237; G_PROTEIN_RECEP_FL_1; 1.
CC PROSITE; PS0262; G_PROTEIN_RECEP_FL_2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 378 C-C CHEMOKINE RECEPTOR TYPE 7.
FT DOMAIN 25 59 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 60 86 1 (POTENTIAL).
FT DOMAIN 87 95 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 96 116 2 (POTENTIAL).
FT DOMAIN 117 130 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 131 152 3 (POTENTIAL).
FT DOMAIN 153 170 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 171 191 4 (POTENTIAL).
FT DOMAIN 192 219 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 220 247 5 (POTENTIAL).
FT DOMAIN 248 263 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 264 289 6 (POTENTIAL).
FT DOMAIN 290 313 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 314 331 7 (POTENTIAL).
FT DOMAIN 332 378 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD N-LINKED (GLCNAC. . .) (POTENTIAL).
FT 36

FT DISULFID 129 210 BY SIMILARITY.
SQ SEQUENCE 378 AA; 42941 MW; ACB1A422CF54AA54 CRC64;

Query Match 61.5%; Score 48; DB 1; Length 378;
Best Local Similarity 56.2%; Pred. No. 0.14; Indels 0; Gaps 0;
Matches 9; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 1 KTLVQAQNSKRHRKPAIR 16
:||:||||:|:||||:
Db 248 RTLLQARNFERNKAIK 263

RESULT 9
CKR5_CERAE
ID CKR5_CERAE STANDARD; PRT; 352 AA.
AC P56493;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE C-C CHEMOKINE RECEPTOR TYPE 5 (C-C CKR-5) (CCR-5) (CCR5).
GN CCR5 OR CMKBR5.
OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9534;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Kidney;
RX MEDLINE=98001387; PubMed=9343222;
RA Kuhlmann S.E., Platt E.J., Kozak S.L., Kabat D.;
RT "Polymorphisms in the CCR5 genes of African green monkeys and mice
RT implicate specific amino acids in infections by simian and human
RT immunodeficiency viruses.";
RL J. Virol. 71:8642-8656(1997).
RN [2]
RP SEQUENCE FROM N.A.
RA Murayama Y., Matsunaga S., Inoue-Murayama M.;
RT "CDNA sequence of African green monkey CCR-5 chemokine receptor
RT gene.";
RT Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
CC MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
CC INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE
CC IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
CC DIFFERENTIATION.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC
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CC
CC EMBL; U83324; AAC51795.1; -;
CC EMBL; U83325; AAC51796.1; -;
CC EMBL; AB015944; BAA31328.1; -;
CC GCRDB; GCR_2465; -;
CC GCRDB; GCR_2466; -;
CC InterPro; IPR000276; -;
CC InterPro; IPR000355; -;
CC InterPro; IPR002240; -;
CC Pfam; PF00001; 7tm.1; 1.
CC PRINTS; PR00237; GPCRHHODPSN.
CC PRINTS; PR00657; CCHEMOKINER.
CC PRINTS; PR01110; CHEMOKINER5.
CC PROSITE; PS00237; G_PROTEIN_RECEP_FL_1; 1.
CC PROSITE; PS0262; G_PROTEIN_RECEP_FL_2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein; Polymorphism.
KW

```

FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 31 58 1 (POTENTIAL).
FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 69 89 2 (POTENTIAL).
FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 103 124 3 (POTENTIAL).
FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 142 166 4 (POTENTIAL).
FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 199 218 5 (POTENTIAL).
FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 236 260 6 (POTENTIAL).
FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 278 301 7 (POTENTIAL).
FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
FT DISULFID 101 178 BY SIMILARITY.
FT VARIANT 14 14 N -> Y.
FT VARIANT 352 352 F -> L.
SQ SEQUENCE 352 AA; 40561 MW; 7F52E690C72EC29A CRC64;

Query Match 57.1%; Score 44.5; DB 1; Length 352;
Best Local Similarity 52.9%; Pred. No. 0.58;
Matches 9; Conservative 5; Mismatches 2; Indels 1; Gaps 1;

QY 1 KTLVQAQN-SKRHKAIR 16
DB 219 KTLRCRNEKRRRAVR 235
||||: :| |||:|

RESULT 10
ID CKR5_CERTO STANDARD; PRT; 352 AA.
AC 062743; 062744; 062745; 062746;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE C-C CHEMOKINE RECEPTOR TYPE 5 (C-C CKR-5) (CCR-5) (CCR5).
GN CKR5 OR CMKBR5.
OS -Cercopithecus torquatus-atys-(Red-crowned-mangabey)-(Sooty-mangabey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Cercopithecinae; Cercopithecidae;
OX NCBI_TaxID=9531;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ISOLATE 079, 085, 087 AND 089;
RX MEDLINE=98321155; PubMed=9656999;
RA Chen Z., Gettle A., Ho D.D., Marx P.A.;
RT "Primary SIVsm isolates use the CCR5 coreceptor from sooty mangabeys
RT naturally infected in west Africa: a comparison of coreceptor usage
RT of primary SIVsm, HIV-2, and SIVmac."
RL Virology 246:113-124(1998).
CC -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
CC MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
CC INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE
CC IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
CC DIFFERENTIATION.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF051902; AAC39830.1; -
CC DR EMBL; AF051903; AAC39831.1; -
CC DR EMBL; AF051904; AAC39832.1; -
CC DR EMBL; AF051905; AAC39833.1; -

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DR InterPro: IPR000276; -
DR InterPro: IPR000355; -
DR InterPro: IPR002240; -
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PRO0237; GPCRHHODPSN.
DR PRINTS: PRO0657; CCHEMOKINER.
DR PRINTS: PRO1110; CHEMOKINER.
DR PROSITE: PS00237; G-PROTEIN_RECF_F1_1; 1.
DR PROSITE: PS00262; G-PROTEIN_RECF_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 31 58 1 (POTENTIAL).
FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 69 89 2 (POTENTIAL).
FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 103 124 3 (POTENTIAL).
FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 142 166 4 (POTENTIAL).
FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 199 218 5 (POTENTIAL).
FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 236 260 6 (POTENTIAL).
FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 278 301 7 (POTENTIAL).
FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
FT DISULFID 101 178 BY SIMILARITY.
FT VARIANT 2 2 D -> E (IN ISOLATE 087).
FT VARIANT 3 3 Y -> D (IN ISOLATE 079).
FT VARIANT 25 25 V -> G (IN ISOLATE 087).
FT VARIANT 100 100 M -> K (IN ISOLATE 079).
FT VARIANT 107 107 L -> V (IN ISOLATE 089).
FT VARIANT 134 134 V -> G (IN ISOLATE 079).
FT VARIANT 146 146 V -> L (IN ISOLATES 085 AND 089).
FT VARIANT 340 340 T -> I (IN ISOLATE 079).
SQ SEQUENCE 352 AA; 40489 MW; 20A196E2D47E49CA CRC64;

Query Match 57.1%; Score 44.5; DB 1; Length 352;
Best Local Similarity 52.9%; Pred. No. 0.58;
Matches 9; Conservative 5; Mismatches 2; Indels 1; Gaps 1;

QY 1 KTLVQAQN-SKRHKAIR 16
DB 219 KTLRCRNEKRRRAVR 235
||||: :| |||:|

RESULT 11
ID CKR5_GORGO STANDARD; PRT; 352 AA.
AC P56439;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE C-C CHEMOKINE RECEPTOR TYPE 5 (C-C CKR-5) (CCR-5) (CCR5).
GN CKR5 OR CMKBR5.
OS Gorilla gorilla gorilla (Lowland gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
OX NCBI_TaxID=9595;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97268687; PubMed=9108095;
RA Edinger A.L., Amodee A., Miller K., Doranz B.J., Endres M.,
RA Sharron M., Samson M., Lu Z.H., Clements J.E., Murphy-Corb M.,
RA Peliper S.C., Parmentier M., Broder C.C., Doms R.W.;
RT "Differential utilization of CCR5 by macrophage and T cell tropic
RT simian immunodeficiency virus strains."
RL Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).
CC -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
CC MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
CC INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE
CC IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
CC DIFFERENTIATION.
CC

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CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AF005659; AAB62953.1; -;
 DR GCRDB; GCR_1372; -;
 DR InterPro; IPR000276; -;
 DR InterPro; IPR000355; -;
 DR InterPro; IPR002240; -;
 DR Pfam; PF00001; 7tm1_1; 1.
 DR PRINTS; PRO0237; GPCRHHODPSN.
 DR PRINTS; PRO0657; CCEMOKINER.
 DR PRINTS; PRO1110; CHEMOKINERS.
 DR PROSITE; PS00237; G-PROTEIN_RECEP_FL_1; 1.
 DR PROSITE; PS00262; G-PROTEIN_RECEP_FL_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 31 58 1 (POTENTIAL).
 FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 69 89 2 (POTENTIAL).
 FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 103 124 3 (POTENTIAL).
 FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 142 166 4 (POTENTIAL).
 FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 199 218 5 (POTENTIAL).
 FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 236 260 6 (POTENTIAL).
 FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 278 301 7 (POTENTIAL).
 FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 101 178 BY SIMILARITY.
 SQ SEQUENCE 352 AA; 40515 MW; D0E6FCB9FE5EAC84 CRC64;

Query Match 57.1%; Score 44.5; DB 1; Length 352;
 Best Local Similarity 52.9%; Pred. No. 0.58;
 Matches 9; Conservative 5; Mismatches 2; Indels 1; Gaps 1;
 QY 1 KILVQAN-SKRHKAIR 16
 DB 219 KTLRCRNEKKRRAVR 235

RESULT 12
 CCR5_HUMAN
 ID CCR5_HUMAN STANDARD; PRT; 352 AA.
 AC P1681; O14692; O14693; O14695; O14696; O14697; O14698; O14699;
 AC O14700; O14701; O14702; O14703; O14704; O14705; O14706; O14707;
 AC O14708;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE C-C CHEMOKINE RECEPTOR TYPE 5 (C-C CCR-5) (CCR-5) (CCR5)
 DE (HIV-1 FUSION CO-RECEPTOR) (CHEMR13).
 GN CCR5 OR CCR5R5
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-96241590; PubMed-8639485;
 RA Samson M., Labbe O., Mollereau C., Vassart G., Parmentier M.;
 RT "Molecular cloning and functional expression of a new human
 CC-chemokine receptor gene.";

Biochemistry 35:3362-3367(1996).
 [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-96291862; PubMed-8663314;
 RA Raport C.J., Gosling J., Schweichart V.L., Gray P.W., Charo I.F.;
 RT "Molecular cloning and functional characterization of a novel human
 CC chemokine receptor (CCR5) for RANTES, MIP-1beta, and MIP-1alpha.";
 J. Biol. Chem. 271:17161-17166(1996).
 [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-96295970; PubMed-8699119;
 RA Combadiere C., Ahuja S.K., Tiffany H.L., Murphy P.M.;
 RT "Cloning and functional expression of CC CKR5, a human monocyte CC
 chemokine receptor selective for MIP-1(alpha), MIP-1(beta), and
 RANTES.";
 J. Leukoc. Biol. 60:147-152(1996).
 [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-98001387; PubMed-9343222;
 RA Kuhnmann S.E., Platt E.J., Kozak S.L., Kabat D.;
 RT "Polymorphisms in the CCR5 genes of African green monkeys and mice
 implicate specific amino acids in infections by simian and human
 immunodeficiency viruses.";
 J. Virol. 71:8642-8656(1997).
 [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-98022612; PubMed-9359654;
 RA Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B.,
 Ho D.D.;
 RT "HIV type 1 subtypes, coreceptor usage, and CCR5 polymorphism.";
 AIDS Res. Hum. Retroviruses 13:1357-1366(1997).
 [7]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-98049523; PubMed-9388201;
 RA Mummidi S., Ahuja S.S., McDaniel B.L., Ahuja S.K.;
 RT "The human CC chemokine receptor 5 (CCR5) gene. Multiple transcripts
 with 5'-end heterogeneity, dual promoter usage, and evidence for
 polymorphisms within the regulatory regions and noncoding exons.";
 J. Biol. Chem. 272:30662-30671(1997).
 [8]
 RP CHARACTERIZATION OF ITS HIV-1 RECEPTOR FUNCTION.
 RX MEDLINE-96260017; PubMed-8649511;
 RA Deng H., Liu R., Elmeier W., Choe S., Unutmaz D., Burkhardt M.,
 di Marzio P., Marmon S., Sutton R.E., Hill C.M., Davis C.B.,
 Peiper S.C., Schall T.J., Littman D.R., Landau N.R.;
 RT "Identification of a major co-receptor for primary isolates of
 HIV-1.";
 Nature 381:661-666(1996).
 [9]
 RP CHARACTERIZATION OF ITS HIV-1 RECEPTOR FUNCTION.
 RX MEDLINE-96260018; PubMed-8649512;
 RA Dragic T., Litwin V., Allaway G.P., Martin S.R., Huang Y.,
 Nagashima K.A., Cayanan C., Maddon P.J., Koup R.A., Moore J.P.,
 Paxton W.A.;
 RT "HIV-1 entry into CD4+ cells is mediated by the chemokine receptor
 CC-CCR-5.";
 Nature 381:667-673(1996).
 CC -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
 CC MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
 CC INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE
 CC IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
 CC DIFFERENTIATION. ACTS AS CO-RECEPTOR WITH CD4 FOR PRIMARY NON-
 CC SYNCYTIIUM-INDUCING STRAINS (NSI) (MACROPHAGE-TROPIC) OF HIV-1

VIRUS. IT PROMOTES ENV-MEDIATED FUSION OF THE VIRUS.
 -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 -1- TISSUE SPECIFICITY: FOUND IN PROMYELOCYTIC CELLS.
 -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

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 DR EMBL; X91492; CAA62796.1; -
 DR EMBL; U54994; AAC50598.1; -
 DR EMBL; U57840; AAB17071.1; -
 DR EMBL; U56626; AAB57793.1; -
 DR EMBL; U83326; AAC51797.1; -
 DR EMBL; AF011500; AAB65700.1; -
 DR EMBL; AF011501; AAB65701.1; -
 DR EMBL; AF011502; AAB65702.1; -
 DR EMBL; AF011503; AAB65703.1; -
 DR EMBL; AF011505; AAB65705.1; -
 DR EMBL; AF011506; AAB65706.1; -
 DR EMBL; AF011507; AAB65707.1; -
 DR EMBL; AF011508; AAB65708.1; -
 DR EMBL; AF011509; AAB65709.1; -
 DR EMBL; AF011510; AAB65710.1; -
 DR EMBL; AF011511; AAB65711.1; -
 DR EMBL; AF011512; AAB65712.1; -
 DR EMBL; AF011513; AAB65713.1; -
 DR EMBL; AF011514; AAB65714.1; -
 DR EMBL; AF011515; AAB65715.1; -
 DR EMBL; AF011517; AAB65717.1; -
 DR EMBL; AF011518; AAB65718.1; -
 DR EMBL; AF011519; AAB65719.1; -
 DR EMBL; AF011520; AAB65720.1; -
 DR EMBL; AF011521; AAB65721.1; -
 DR EMBL; AF011522; AAB65722.1; -
 DR EMBL; AF011523; AAB65723.1; -
 DR EMBL; AF011524; AAB65724.1; -
 DR EMBL; AF011525; AAB65725.1; -
 DR EMBL; AF011526; AAB65726.1; -
 DR EMBL; AF011527; AAB65727.1; -
 DR EMBL; AF011528; AAB65728.1; -
 DR EMBL; AF011529; AAB65729.1; -
 DR EMBL; AF011530; AAB65730.1; -
 DR EMBL; AF011531; AAB65731.1; -
 DR EMBL; AF011532; AAB65732.1; -
 DR EMBL; AF011533; AAB65733.1; -
 DR EMBL; AF011535; AAB65735.1; -
 DR EMBL; AF011537; AAB65737.1; -
 DR EMBL; AF011538; AAB65738.1; -
 DR GCRDb; GCR_1923; -
 DR GCRDb; GCR_1927; -
 DR GCRDb; GCR_2116; -
 DR GCRDb; GCR_2454; -
 DR GCRDb; GCR_2497; -
 DR MIN; 601373; -
 DR InterPro; IPR000276; -
 DR InterPro; IPR000355; -
 DR InterPro; IPR002240; -
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PRINTS; PR00657; CCGHEMOKINER.
 DR PRINTS; PR01110; CHEMOKINERS.
 DR PROSITE; PS00237; G-PROTEIN RECP_F1_1; 1.
 DR PROSITE; PS0262; G-PROTEIN RECP_F1_2; 1.
 DR G-protein coupled receptor; Transmembrane; Glycoprotein; Polymorphism.
 KW DOMAIN 1 30
 FT TRANSMEM 31 58
 FT DOMAIN 59 68
 FT CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 69 89
 FT 2 (POTENTIAL).

FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 103 124 3 (POTENTIAL).
 FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 142 166 4 (POTENTIAL).
 FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 199 218 5 (POTENTIAL).
 FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 236 260 6 (POTENTIAL).
 FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 278 301 7 (POTENTIAL).
 FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 101 178 BY SIMILARITY.
 FT CARBOHYD 268 268 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARIANT 10 10 Y -> D (IN INCCR5-71A).
 FT VARIANT 31 31 R -> H (IN INCCR5-72A).
 FT VARIANT 34 34 P -> L (IN TZCCR5-179).
 FT VARIANT 62 62 K -> R (IN UGCCR5-145B).
 FT VARIANT 68 68 Y -> H (IN ZWCCR5-7).
 FT VARIANT 95 95 D -> N (IN MWCCR5-107).
 FT VARIANT 97 97 G -> E (IN INCCR5-467).
 FT VARIANT 122 122 L -> P (IN ZWCCR5-7).
 FT VARIANT 158 158 F -> S (IN UGCCR5-145A).
 FT VARIANT 176 176 Y -> C (IN KECCR5-116).
 FT VARIANT 177 177 T -> A (IN INCCR5-45C).
 Query Match 57.1%; Score 44.5; DB 1; Length 352;
 Best Local Similarity 52.9%; Pred. No. 0.58;
 Matches 9; Conservative 5; Mismatches 2; Indels 1; Gaps 1;

QY 1 KTLVQAOON-SRRHRAIR 16
 |||:::| |||:|

Db 219 KTLRLCRNKKRRRAVR 235

RESULT 13

CKR5_HYLL STANDARD; PRT; 352 AA.
 AC 097883;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE C-C CHEMOKINE RECEPTOR TYPE 5 (C-C CKR-5) (CCR-5) (CCR5).
 GN CCR5 OR CMKBR5.
 OS Hylobates leucogenys (White-cheeked gibbon).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
 OX NCBI_TaxID=61853;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zhang Y.-W., Zhang Y.-P.;
 RT "Sequence evolution of chemokine receptor CCR5 gene in primates."; Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA, MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR DIFFERENTIATION.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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CC EMBL; AF075451; AAD19863.1; -
DR InterPro; IPR000248; -
DR InterPro; IPR000276; -
DR InterPro; IPR000355; -
DR InterPro; IPR002236; -
DR InterPro; IPR002237; -
DR InterPro; IPR002240; -
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PRINTS; PR00241; ANGIOTENSINR.
DR PRINTS; PR00657; CCHEMOKINER.
DR PRINTS; PR01106; CHEMOKINER1.
DR PRINTS; PR01107; CHEMOKINER2.
DR PRINTS; PR01110; CHEMOKINER3.
DR PROSITE; PS00237; G-PROTEIN_RECEP_FL_2; 1.
DR PROSITE; PS0262; G-PROTEIN_RECEP_FL_1; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 31 58
FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 69 89
FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 124
FT DOMAIN 125 141
FT TRANSMEM 142 166
FT DOMAIN 167 198
FT TRANSMEM 199 218
FT DOMAIN 219 235
FT TRANSMEM 236 260
FT DOMAIN 261 277
FT TRANSMEM 278 301
FT DOMAIN 302 352
FT DISULFID 101 178 BY SIMILARITY.
SQ SEQUENCE 352 AA; 40445 MW; 4F84F344CEB7C91 CRC64;

Query Match 57.1%; Score 44.5; DB 1; Length 352;
Best Local Similarity 52.9%; Pred. No. 0.58;
Matches 9; Conservative 5; Mismatches 1; Indels 1; Gaps 1;

QY 1 KTLVQAOQN-SKRHKAIR 16
|||:::| |||::|
DB 219 KTLRCRNEKRRHRAVR 235

RESULT 14
ID CKR5_MACMU STANDARD; PRT; 352 AA.
AC F79436; O02746;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE C-C CHEMOKINE RECEPTOR TYPE 5 (C-C CKR-5) (CCR-5) (CCR5).
GN CCR5 OR CMKR5.
OS Macaca mulatta (Rhesus macaque),
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey), and
OS Macaca nemestrina (Pig-tailed macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9544, 9541, 9545;
[1]
RN SEQUENCE FROM N.A.
RP SPECIES=M.mulatta;
RC MEDLINE=97184592; PubMed=9032394;
RA Marcon L., Choe H., Martin K.A., Farzan M., Ponath P.D., Wu L.,
RA Newman W., Gerard N., Gerard C., Sodroski J.;
RA "Utilization of C-C chemokine receptor 5 by the envelope

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RT glycoproteins of a pathogenic simian immunodeficiency virus,
RT SIVmac239."
RL J. Virol. 71:2522-2527(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=M.mulatta; STRAIN=INDIAN MACAQUE;
RX MEDLINE=97213934; PubMed=9060623;
RA Chen Z., Zhou P., Ho D.D., Landau N.R., Marx P.A.;
RT "Genetically divergent strains of simian immunodeficiency virus use
RT CCR5 as a coreceptor for entry."
RL J. Virol. 71:2705-2714(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=M.mulatta;
RA Hauer D.A., Margulies B.J., Clements J.E.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC SPECIES=M.mulatta, M.fascicularis, and M.nemestrina;
RX MEDLINE=97268687; PubMed=9108095;
RA Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,
RA Sharron M., Samson M., Lu Z.H., Clements J.E., Murphy-Corb M.,
RA Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;
RT "Differential utilization of CCR5 by macrophage and T cell tropic
RT simian immunodeficiency virus strains."
RL Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).
CC MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
CC INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE
CC IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
CC DIFFERENTIATION.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC
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CC or send an email to license@isb-sib.ch).
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EMBL; U77672; AAC51109.1; -
DR EMBL; U77379; AAC51158.1; -
DR EMBL; U96762; AAC34132.1; -
DR EMBL; AF005660; AAB62554.1; -
DR EMBL; AF005661; AAB82555.1; -
DR EMBL; AF005662; AAB62556.1; -
DR GCRdb; GCR_1296; -
DR GCRdb; GCR_1369; -
DR GCRdb; GCR_1370; -
DR GCRdb; GCR_1371; -
DR GCRdb; GCR_1639; -
DR GCRdb; GCR_1641; -
DR InterPro; IPR000276; -
DR InterPro; IPR000355; -
DR InterPro; IPR002240; -
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PRINTS; PR00657; CCHEMOKINER.
DR PRINTS; PR01110; CHEMOKINER3.
DR PROSITE; PS00237; G-PROTEIN_RECEP_FL_1; 1.
DR PROSITE; PS0262; G-PROTEIN_RECEP_FL_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 31 58
FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 69 89
FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 124
FT DOMAIN 125 141
FT TRANSMEM 142 166
FT DOMAIN 167 198

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FT TRANSMEM 199 218 5 (POTENTIAL).
FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 236 260 6 (POTENTIAL).
FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 278 301 7 (POTENTIAL).
FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
FT DISULFID 101 178 BY SIMILARITY.
FT CARBOHYD 268 268 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 241 241 M -> I (IN REF. 3).
FT CONFLICT 292 292 I -> M (IN REF. 3).
SQ SEQUENCE 352 AA; 58B96C85909FACB2 CRC64;

Query Match 57.1%; Score 44.5; DB 1; Length 352;
Best Local Similarity 52.9%; Pred. No. 0.58;
Matches 9; Conservative 5; Mismatches 2; Indels 1; Gaps 1;

QY 1 KTLVQAOQN-SKRHKAIR 16
DB 219 KTLRCRNEKKRRAVR 235
||||:| |||:|:|

RESULT 15
CKR5_PANTR STANDARD; PRT; 352 AA.
AC P56440; O02778;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DE 30-MAY-2000 (Rel. 39, Last annotation update)
DE C-C CHEMOKINE RECEPTOR TYPE 5 (C-CR-5) (CCR-5) (CCR5).
GN CKR5 OR CMKR5.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=97268687; PubMed=9108095;
RA Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,
RA Sharron M., Samson M., Lu Z.H.; Clements J.E.; Murphy-Corb M.,
RA Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;
RT "Differential utilization of CCR5 by macrophage and T cell tropic
RT simian immunodeficiency virus strains."
RT Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).
RN [2]
SEQUENCE FROM N.A.
RA Zimmerman P.A., Buckler-White A., Alkhatib G.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
SEQUENCE FROM N.A.
RX MEDLINE=98022612; PubMed=9359654;
RA Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B.,
RA Ho D.D.;
RT "HIV type 1 subtypes, coreceptor usage, and CCR5 polymorphism."
RL AIDS Res. Hum. Retroviruses 13:1357-1366(1997).
RN [4]
SEQUENCE FROM N.A.
RX MEDLINE=97426118; PubMed=9282822;
RA Zacharova V., Zachar V., Goustin A.S.;
RT "Sequence of chemokine receptor gene CCR5 in chimpanzees, a natural
RT HIV type 1 host."
RL AIDS Res. Hum. Retroviruses 13:1159-1161(1997).
RN [5]
SEQUENCE FROM N.A.
RX MEDLINE=98090115; PubMed=9430250;
RA Pretet J.-L., Zerbib A., Girard J.-G., Butor C.;
RT "Chimpanzee CXCR4 and CCR5 act as coreceptors for HIV type 1."
RL AIDS Res. Hum. Retroviruses 13:1583-1587(1997).
CC -1- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
CC MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
CC INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE
CC IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
CC DIFFERENTIATION.

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CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF005663; AAB62557.1; -
DR EMBL; U94329; AAB58446.1; -
DR EMBL; AF011542; AAB65742.1; -
DR EMBL; U97666; AAC51670.1; -
DR EMBL; AF011540; AAB65740.1; -
DR EMBL; U89797; AAC03717.1; -
DR GCRDB; GCR_1284; -
DR GCRDB; GCR_1367; -
DR GCRDB; GCR_2432; -
DR InterPro; IPR000276; -
DR InterPro; IPR000355; -
DR InterPro; IPR002240; -
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PRINTS; PR00657; CCHEMOKINER.
DR PRINTS; PR01110; CHEMOKINER5.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 31 58 1 (POTENTIAL).
FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 69 89 2 (POTENTIAL).
FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 124 3 (POTENTIAL).
FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 142 166 4 (POTENTIAL).
FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 199 218 5 (POTENTIAL).
FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 236 260 6 (POTENTIAL).
FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 278 301 7 (POTENTIAL).
FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
FT DISULFID 101 178 BY SIMILARITY.
FT CARBOHYD 268 268 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 123 123 T -> S (IN REF. 1).
SQ SEQUENCE 352 AA; 40539 MW; 4A33E698B80FE34C CRC64;

Query Match 57.1%; Score 44.5; DB 1; Length 352;
Best Local Similarity 52.9%; Pred. No. 0.58;
Matches 9; Conservative 5; Mismatches 2; Indels 1; Gaps 1;

QY 1 KTLVQAOQN-SKRHKAIR 16
DB 219 KTLRCRNEKKRRAVR 235
||||:| |||:|:|

Search completed: May 23, 2001, 15:36:20
Job time: 651 sec

```


GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 23, 2001, 15:35:16 ; Search time 189.03 Seconds
(without alignments)
9.921 Million cell updates/sec

Title: US-08-887-977-10_COPY_230_245

Perfect score: 78

Sequence: 1 KTLVQAQNSKRHKRAIR 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: sp.archaea.*

2: sp.bacteria.*

3: sp.fungi.*

4: sp.human.*

5: sp.invertebrate.*

6: sp.mammal.*

7: sp.mhc.*

8: sp.organelle.*

9: sp.phase.*

10: sp.plant.*

11: sp.rodent.*

12: sp.unclassified.*

13: sp.vertebrate.*

14: sp.virus.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	75	96.2	367	11	Q9R1V0	Q9R1V0 mus musculu
2	49	62.8	369	4	Q9UQ06	Q9UQ06 homo sapien
3	48.5	62.2	339	6	Q9TQU7	Q9TQU7 cercopithec
4	47.5	60.9	339	6	Q9TUS4	Q9TUS4 lemur varie
5	47.5	60.9	339	6	Q9TUS3	Q9TUS3 lemur catia
6	47.5	60.9	339	6	Q9TUS2	Q9TUS2 lemur catia
7	47.5	60.9	339	6	Q9TUS1	Q9TUS1 lemur varie
8	47.5	60.9	339	6	Q9TQU3	Q9TQU3 lemur catia
9	44.5	57.1	140	4	Q9S950	Q9S950 homo sapien
10	44.5	57.1	316	6	Q9TUV7	Q9TUV7 saguinus sp
11	44.5	57.1	333	4	O14694	O14694 homo sapien
12	44.5	57.1	334	6	Q9TU07	Q9TU07 erythrocebu
13	44.5	57.1	339	4	Q9UN28	Q9UN28 homo sapien
14	44.5	57.1	339	4	Q9UN27	Q9UN27 homo sapien
15	44.5	57.1	339	4	Q9UN26	Q9UN26 homo sapien
16	44.5	57.1	339	4	Q9UN25	Q9UN25 homo sapien
17	44.5	57.1	339	4	Q9UN24	Q9UN24 homo sapien
18	44.5	57.1	339	4	Q9UN23	Q9UN23 homo sapien
19	44.5	57.1	339	4	Q9UBT9	Q9UBT9 homo sapien

20	44.5	57.1	339	4	Q9UBJ7	Q9UBJ7 homo sapien
21	44.5	57.1	339	6	Q9TUX1	Q9TUX1 hyllobates c
22	44.5	57.1	339	6	Q9TUX0	Q9TUX0 hyllobates c
23	44.5	57.1	339	6	Q9TUN9	Q9TUN9 hyllobates c
24	44.5	57.1	339	6	Q9TUN8	Q9TUN8 gorilla gor
25	44.5	57.1	339	6	Q9TUN7	Q9TUN7 pan troglod
26	44.5	57.1	339	6	Q9TUN6	Q9TUN6 pan troglod
27	44.5	57.1	339	6	Q9TUN5	Q9TUN5 pan troglod
28	44.5	57.1	339	6	Q9TUN4	Q9TUN4 pan troglod
29	44.5	57.1	339	6	Q9TUN3	Q9TUN3 pongo pygma
30	44.5	57.1	339	6	Q9TUN2	Q9TUN2 saguinus sp
31	44.5	57.1	339	6	Q9TUN1	Q9TUN1 saguinus sp
32	44.5	57.1	339	6	Q9TUN0	Q9TUN0 saguinus sp
33	44.5	57.1	339	6	Q9TUV9	Q9TUV9 saguinus sp
34	44.5	57.1	339	6	Q9TUV8	Q9TUV8 saguinus sp
35	44.5	57.1	339	6	Q9TUV6	Q9TUV6 saguinus sp
36	44.5	57.1	339	6	Q9TUV5	Q9TUV5 saguinus sp
37	44.5	57.1	339	6	Q9TUV2	Q9TUV2 alouatta ca
38	44.5	57.1	339	6	Q9TUV1	Q9TUV1 aotus trivi
39	44.5	57.1	339	6	Q9TUV0	Q9TUV0 aotus trivi
40	44.5	57.1	339	6	Q9TUU9	Q9TUU9 cercopithec
41	44.5	57.1	339	6	Q9TUU8	Q9TUU8 cercopithec
42	44.5	57.1	339	6	Q9TUU7	Q9TUU7 macaca fusc
43	44.5	57.1	339	6	Q9TUU6	Q9TUU6 macaca fusc
44	44.5	57.1	339	6	Q9TUU5	Q9TUU5 macaca fusc
45	44.5	57.1	339	6	Q9TUU4	Q9TUU4 macaca mula

ALIGNMENTS

RESULT 1
Q9R1V0
ID Q9R1V0 PRELIMINARY; PRT; 367 AA.
AC Q9R1V0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE CC CHEMOKINE LARC SPECIFIC RECEPTOR.
GN MCCR6.

OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Tanaka Y.;
RT "Molecular Cloning of Murine Homologue of CCR6, the Specific Receptor for CC Chemokine LARC."
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB016031; BAA82443.1;
DR INTERPRO; IPR000190;
DR INTERPRO; IPR000276;
DR INTERPRO; IPR000355;
DR PFAM; PF000001; 7tm.1.1;
DR PRINTS; PR00237; GPCRHDOPSN.
DR PRINTS; PR00635; ANGIOTENSINR.
DR PRINTS; PR00657; CCHEMOKINR.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
KW Receptor.
SQ SEQUENCE 367 AA; 42082 MW; 207FD98B2F7A6DD3 CRC64;

Query Match 96.2%; Score 75; DB 11; Length 367;
Best Local Similarity 93.8%; Pred. No. 6.8e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KTLVQAQNSKRHKRAIR 16

|||||
Db 231 KTLVQAQNSKRHKRAIR 246

RESULT 2


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FT NON_TER 1 1
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 38664 MW; B53CFB4F66B09E1A CRC64;

Query Match 60.9%; Score 47.5; DB 6; Length 339;
Best Local Similarity 58.8%; Pred. No. 0.73;
Matches 10; Conservative 4; Mismatches 2; Indels 1; Gaps 1;

QY 1 KTLVQAQN-SKRHKAIR 16
    |||:::| |||||:|
Db 212 KTLRCRNEKKRHKAVR 228

RESULT 5
Q9TUS3 PRELIMINARY; PRT; 339 AA.
AC Q9TUS3;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TReMBLrel. 15, Last annotation update)
DE C-C CHEMOKINE RECEPTOR 5 (FRAGMENT).
GN CCR5.
OS Lemur catta (Ring-tailed lemur).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Strepsirrhini; Lemnidae; Lemur.
OX NCBI_TaxID=9447;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wollinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162012; AAD47767.1; -
DR INTERPRO; IPR000248; -
DR INTERPRO; IPR000276; -
DR INTERPRO; IPR000355; -
DR INTERPRO; IPR001277; -
DR INTERPRO; IPR002236; -
DR INTERPRO; IPR002237; -
DR INTERPRO; IPR002238; -
DR INTERPRO; IPR002240; -
DR PFAM; PF00001; 7tm1.1;
DR PRINTS; PR00237; GPCRHHODPSN.
DR PRINTS; PR00241; ANGIOTENSINR.
DR PRINTS; PR00645; LCRIORPHANR.
DR PRINTS; PR00657; CCHEMOKINER.
DR PRINTS; PR01106; CHEMOKINER1.
DR PRINTS; PR01107; CHEMOKINER2.
DR PRINTS; PR01108; CHEMOKINER3.
DR PRINTS; PR01110; CHEMOKINER5.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 38646 MW; BA7E73C6F05E2CA4 CRC64;

Query Match 60.9%; Score 47.5; DB 6; Length 339;
Best Local Similarity 58.8%; Pred. No. 0.73;
Matches 10; Conservative 4; Mismatches 2; Indels 1; Gaps 1;

QY 1 KTLVQAQN-SKRHKAIR 16
    |||:::| |||||:|
Db 212 KTLRCRNEKKRHKAVR 228

RESULT 7
Q9TUS1 PRELIMINARY; PRT; 339 AA.
AC Q9TUS1;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
DE C-C CHEMOKINE RECEPTOR 5 (FRAGMENT).
GN CCR5.
OS Lemur variegatus (Ruffed lemur) (Varecia variegata).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Strepsirrhini; Lemnidae; Varecia.
OX NCBI_TaxID=9455;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wollinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162013; AAD47768.1; -
DR INTERPRO; IPR000248; -
DR INTERPRO; IPR000276; -
DR INTERPRO; IPR000355; -

Query Match 60.9%; Score 47.5; DB 6; Length 339;
Best Local Similarity 58.8%; Pred. No. 0.73;
Matches 10; Conservative 4; Mismatches 2; Indels 1; Gaps 1;

QY 1 KTLVQAQN-SKRHKAIR 16
    |||:::| |||||:|
Db 212 KTLRCRNEKKRHKAVR 228

RESULT 6
Q9TUS2 PRELIMINARY; PRT; 339 AA.
AC Q9TUS2;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
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DR INTERPRO: IPR001277; -
DR INTERPRO: IPR002236; -
DR INTERPRO: IPR002237; -
DR INTERPRO: IPR002238; -
DR INTERPRO: IPR002240; -
DR PFAM: PF00001; 7tm_1; 1
DR PRINTS: PR00237; GPCRHHODOPS.
DR PRINTS: PR00241; ANGIOTENSINR.
DR PRINTS: PR00645; LCRJOPHARN.
DR PRINTS: PR00657; CCHEMOKINER.
DR PRINTS: PR01106; CHEMOKINER1.
DR PRINTS: PR01107; CHEMOKINER2.
DR PRINTS: PR01108; CHEMOKINER3.
DR PRINTS: PR01110; CHEMOKINER5.
DR PROSITE: PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 38682 MW; 6A770AFCAF7E02F6 CRC64;

Query Match 60.9%; Score 47.5; DB 6; Length 339;
Best Local Similarity 58.8%; Pred. No. 0.73; Mismatches 4; Indels 1; Gaps 1;
Matches 10; Conservative 4;

OY 1 KTLVQAQN-SKRHKAIR 16
DB 212 KTLRCRNEKRRHKAVR 228
||||: :| |||||:|

RESULT 8
O9TQU3 PRELIMINARY; PRT; 339 AA.
AC O9TQU3
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE C-C CHEMOKINE RECEPTOR 5 (FRAGMENT).
GN CCR5.
OS Lemur catta (Ring-tailed lemur).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Strepsirhini; Lemuridae; Lemur.
OX NCBI_TaxID=9447;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=MONOCYTIC LINE;
RX MEDLINE=97211835; PubMed=9058802;
RA Polentarutti N., Allavena P., Bianchi G., Giardina G., Basile A.,
RA Sozzani S., Mantovani A., Introna M.;
RT "IL-2-regulated expression of the monocyte chemotactic protein-1
RT receptor (CCR2) in human NK cells: characterization of a predominant
RT 3.4-kilobase transcript containing CCR2B and CCR2A sequences.";
RL J. Immunol. 158:2689-2694(1997).
DR EMBL: X95583; CAA64835.1; -
DR INTERPRO: IPR000276; -
DR INTERPRO: IPR002238; -
DR PFAM: PF00001; 7tm_1; 1
DR PRINTS: PR00237; GPCRHHODOPS.
DR PRINTS: PR01108; CHEMOKINER3.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
SQ SEQUENCE 140 AA; 16273 MW; 63BE2A527757D8C2 CRC64;

Query Match 57.1%; Score 44.5; DB 4; Length 140;
Best Local Similarity 52.9%; Pred. No. 1.1; Mismatches 5; Indels 1; Gaps 1;
Matches 9; Conservative 5;

OY 1 KTLVQAQN-SKRHKAIR 16
DB 7 KTLRCRNEKRRHKAVR 23
||||: :| ||||:|

RESULT 10
O9TUV7 PRELIMINARY; PRT; 316 AA.
ID O9TUV7
AC O9TUV7
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE C-C CHEMOKINE RECEPTOR 5 (FRAGMENT).
GN CCR5.
OS Saginus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Saginus.
OX NCBI_TaxID=100754;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF162011; AAD47766.1; -
DR EMBL: AF162008; AAD47763.1; -
DR INTERPRO: IPR000248; -
DR INTERPRO: IPR000276; -
DR INTERPRO: IPR000355; -
DR INTERPRO: IPR001277; -
DR INTERPRO: IPR002236; -
DR INTERPRO: IPR002237; -
DR INTERPRO: IPR002238; -
DR INTERPRO: IPR002240; -
DR PFAM: PF00001; 7tm_1; 1
DR PRINTS: PR00237; GPCRHHODOPS.
DR PRINTS: PR00241; ANGIOTENSINR.
DR PRINTS: PR00645; LCRJOPHARN.
DR PRINTS: PR00657; CCHEMOKINER.
DR PRINTS: PR01106; CHEMOKINER1.
DR PRINTS: PR01107; CHEMOKINER2.
DR PRINTS: PR01108; CHEMOKINER3.
DR PRINTS: PR01110; CHEMOKINER5.
DR PROSITE: PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
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RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF161930; AAD47687.1; -
DR INTERPRO; IPR000248; -
DR INTERPRO; IPR000276; -
DR INTERPRO; IPR000355; -
DR INTERPRO; IPR000923; -
DR INTERPRO; IPR002236; -
DR INTERPRO; IPR002237; -
DR INTERPRO; IPR002240; -
DR PFAM; PF00001; 7tm_1.1;
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PRINTS; PR00241; ANGIOTENSINR.
DR PRINTS; PR00657; CCHEMOKINER.
DR PRINTS; PR01106; CHEMOKINER1.
DR PRINTS; PR01107; CHEMOKINER2.
DR PRINTS; PR01110; CHEMOKINER5.
DR PROSITE; PS00196; COPPER_BLUE; UNKNOWN_1.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
KW Receptor.
FT NON_TER 1
FT NON_TER 316
FT NON_TER 316
SQ SEQUENCE 316 AA; 4DAD95C3848F04EA CRC64;

Query Match 57.1%; Score 44.5; DB 6; Length 316;
Best Local Similarity 52.9%; Pred. No. 2.4;
Matches 9; Conservative 5; Mismatches 2; Indels 1; Gaps 1;

QY 1 KTLVQAQN-SKRHKAIR 16
||||: |||:|
DB 189 KTLRCRNEKKRRAVR 205

RESULT 11

OL14694 ID O14694 PRELIMINARY; PRT; 333 AA.
AC O14694
DT 01-JAN-1998 (TRENBLrel. 05, Created)
DT 01-JAN-1998 (TRENBLrel. 05, Last sequence update)
DT 01-OCT-2000 (TRENBLrel. 15, Last annotation update)
DE CCR5 RECEPTOR (FRAGMENT).
GN CCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B.,
RA Ho D.D.;
RL AIDS Res. Hum. Retroviruses 0:0-0(1997).
DR EMBL; AF011504; AAB65704.1; -
DR INTERPRO; IPR000190; -
DR INTERPRO; IPR000276; -
DR INTERPRO; IPR000355; -
DR INTERPRO; IPR000355; -
DR INTERPRO; IPR001277; -
DR INTERPRO; IPR002236; -
DR INTERPRO; IPR002237; -
DR INTERPRO; IPR002238; -
DR INTERPRO; IPR002240; -
DR PFAM; PF00001; 7tm_1.1;
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PRINTS; PR00635; ANGIOTENSINR.
DR PRINTS; PR00645; LCR1ORPHANR.
DR PRINTS; PR00657; CCHEMOKINER.
DR PRINTS; PR01106; CHEMOKINER1.
DR PRINTS; PR01107; CHEMOKINER2.
DR PRINTS; PR01108; CHEMOKINER3.
DR PRINTS; PR01110; CHEMOKINER5.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
FT NON_TER 333
FT NON_TER 333
SQ SEQUENCE 333 AA; 38174 MW; AEFBA07A67893AEB CRC64;

Query Match 57.1%; Score 44.5; DB 4; Length 333;
Best Local Similarity 52.9%; Pred. No. 2.6;
Matches 9; Conservative 5; Mismatches 2; Indels 1; Gaps 1;

QY 1 KTLVQAQN-SKRHKAIR 16
||||: |||:|
DB 200 KTLRCRNEKKRRAVR 216

RESULT 12

Q9TUQ7 ID Q9TUQ7 PRELIMINARY; PRT; 334 AA.
AC Q9TUQ7
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TRENBLrel. 14, Last annotation update)
DE C-C CHEMOKINE RECEPTOR 5 (FRAGMENT).
GN CCR5.
OS Erythrocebus patas (Red quonon) (Hussar).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Erythrocebus.
OX NCBI_TaxID=9538;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162049; AAD47804.1; -
DR INTERPRO; IPR000248; -
DR INTERPRO; IPR000276; -
DR INTERPRO; IPR000355; -
DR INTERPRO; IPR001277; -
DR INTERPRO; IPR002236; -
DR INTERPRO; IPR002237; -
DR INTERPRO; IPR002240; -
DR PFAM; PF00001; 7tm_1.1;
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PRINTS; PR00241; ANGIOTENSINR.
DR PRINTS; PR00645; LCR1ORPHANR.
DR PRINTS; PR00657; CCHEMOKINER.
DR PRINTS; PR01106; CHEMOKINER1.
DR PRINTS; PR01107; CHEMOKINER2.
DR PRINTS; PR01110; CHEMOKINER5.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
KW Receptor.
FT NON_TER 1
FT NON_TER 334
FT NON_TER 334
SQ SEQUENCE 334 AA; 38460 MW; B19D0CEC667B69F0 CRC64;

Query Match 57.1%; Score 44.5; DB 6; Length 334;
Best Local Similarity 52.9%; Pred. No. 2.6;
Matches 9; Conservative 5; Mismatches 2; Indels 1; Gaps 1;

QY 1 KTLVQAQN-SKRHKAIR 16
||||: |||:|
DB 207 KTLRCRNEKKRRAVR 223

RESULT 13

Q9UN28 ID Q9UN28 PRELIMINARY; PRT; 339 AA.
AC Q9UN28
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TRENBLrel. 15, Last annotation update)
DE C-C CHEMOKINE RECEPTOR 5 (FRAGMENT).
GN CCR5.
OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 [1]
 RP SEQUENCE FROM N.A.
 RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
 RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
 RT "Sequences of the CCR5 genes from diverse simian and prosimian
 RT species."
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF161913; RAD47670.1; -
 DR INTERPRO: IPR000190; -
 DR INTERPRO: IPR000248; -
 DR INTERPRO: IPR000276; -
 DR INTERPRO: IPR000355; -
 DR INTERPRO: IPR001277; -
 DR INTERPRO: IPR002236; -
 DR INTERPRO: IPR002237; -
 DR INTERPRO: IPR002240; -
 DR PFAM: PF00001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCRHHODPSN.
 DR PRINTS: PR00241; ANGIOTENSINR.
 DR PRINTS: PR00635; ANGIOTENSINR.
 DR PRINTS: PR00645; LCR1ORPHANR.
 DR PRINTS: PR00657; CCHEMOKINER.
 DR PRINTS: PR01106; CHEMOKINER1.
 DR PRINTS: PR01107; CHEMOKINER2.
 DR PRINTS: PR01110; CHEMOKINER5.
 DR PROSITE: PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
 KW Receptor.
 FT NON_TER 1 1
 FT NON_TER 339 339
 SQ SEQUENCE 339 AA; 39183 MW; 56C819F92D6DB1A6 CRC64;

Query Match 57.1%; Score 44.5; DB 4; Length 339;
 Best Local Similarity 52.9%; Pred. No. 2.6;
 Matches 9; Conservative 5; Mismatches 2; Indels 1; Gaps 1;

QY 1 KTLVQAO-N-SKRHKAIR 16
 |||:::| |||:|
 DB 212 KTLRCRNEKRRRAVR 228

RESULT 14
 Q9UN27
 ID Q9UN27 PRELIMINARY; PRT; 339 AA.
 AC Q9UN27;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE C-C CHEMOKINE RECEPTOR 5 (FRAGMENT).
 GN CCR5.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
 RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
 RT "Sequences of the CCR5 genes from diverse simian and prosimian
 RT species."
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF161914; AAD47671.1; -
 DR INTERPRO: IPR000190; -
 DR INTERPRO: IPR000248; -
 DR INTERPRO: IPR000276; -
 DR INTERPRO: IPR000355; -
 DR INTERPRO: IPR001277; -
 DR INTERPRO: IPR002236; -
 DR INTERPRO: IPR002237; -
 DR INTERPRO: IPR002240; -

DR PFAM: PF00001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCRHHODPSN.
 DR PRINTS: PR00241; ANGIOTENSINR.
 DR PRINTS: PR00635; ANGIOTENSINR.
 DR PRINTS: PR00645; LCR1ORPHANR.
 DR PRINTS: PR00657; CCHEMOKINER.
 DR PRINTS: PR01106; CHEMOKINER1.
 DR PRINTS: PR01107; CHEMOKINER2.
 DR PRINTS: PR01110; CHEMOKINER5.
 DR PROSITE: PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
 KW Receptor.
 FT NON_TER 1 1
 FT NON_TER 339 339
 SQ SEQUENCE 339 AA; 39086 MW; 88AD8B44E2CB4EC2 CRC64;

Query Match 57.1%; Score 44.5; DB 4; Length 339;
 Best Local Similarity 52.9%; Pred. No. 2.6;
 Matches 9; Conservative 5; Mismatches 2; Indels 1; Gaps 1;

QY 1 KTLVQAO-N-SKRHKAIR 16
 |||:::| |||:|
 DB 212 KTLRCRNEKRRRAVR 228

RESULT 15
 Q9UN26
 ID Q9UN26 PRELIMINARY; PRT; 339 AA.
 AC Q9UN26;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE C-C CHEMOKINE RECEPTOR 5 (FRAGMENT).
 GN CCR5.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
 RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
 RT "Sequences of the CCR5 genes from diverse simian and prosimian
 RT species."
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF161916; AAD47673.1; -
 DR INTERPRO: IPR000190; -
 DR INTERPRO: IPR000248; -
 DR INTERPRO: IPR000276; -
 DR INTERPRO: IPR000355; -
 DR INTERPRO: IPR001277; -
 DR INTERPRO: IPR002236; -
 DR INTERPRO: IPR002237; -
 DR INTERPRO: IPR002240; -
 DR PFAM: PF00001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCRHHODPSN.
 DR PRINTS: PR00241; ANGIOTENSINR.
 DR PRINTS: PR00635; ANGIOTENSINR.
 DR PRINTS: PR00645; LCR1ORPHANR.
 DR PRINTS: PR00657; CCHEMOKINER.
 DR PRINTS: PR01106; CHEMOKINER1.
 DR PRINTS: PR01107; CHEMOKINER2.
 DR PRINTS: PR01110; CHEMOKINER5.
 DR PROSITE: PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
 KW Receptor.
 FT NON_TER 1 1
 FT NON_TER 339 339
 SQ SEQUENCE 339 AA; 39162 MW; A56369FE0529F4AB CRC64;

Query Match 57.1%; Score 44.5; DB 4; Length 339;
 Best Local Similarity 52.9%; Pred. No. 2.6;
 Matches 9; Conservative 5; Mismatches 2; Indels 1; Gaps 1;

QY 1 KTLVQON-SRRHKAIR 16
| | | : : | | | : : |
Db 212 KTLRCRNEKKRRRAVR 228

Search completed: May 23, 2001, 15:35:16
Job time: 622 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 23, 2001, 15:28:32 ; Search time 184.73 Seconds
(without alignments)
7.736 Million cell updates/sec

Title: US-08-887-977-10_COPY_246_270

Perfect score: 119

Sequence: 1 VIIAVVFLACQIPHNMVLLVTA 25

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 390729 seqs, 57163235 residues

Total number of hits satisfying chosen parameters: 390729

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

A_Geneseq_0401.*
1: /SID56/qcgdata/geneseq/geneseq/AA1980.DAT.*
2: /SID56/qcgdata/geneseq/geneseq/AA1981.DAT.*
3: /SID56/qcgdata/geneseq/geneseq/AA1982.DAT.*
4: /SID56/qcgdata/geneseq/geneseq/AA1983.DAT.*
5: /SID56/qcgdata/geneseq/geneseq/AA1984.DAT.*
6: /SID56/qcgdata/geneseq/geneseq/AA1985.DAT.*
7: /SID56/qcgdata/geneseq/geneseq/AA1986.DAT.*
8: /SID56/qcgdata/geneseq/geneseq/AA1987.DAT.*
9: /SID56/qcgdata/geneseq/geneseq/AA1988.DAT.*
10: /SID56/qcgdata/geneseq/geneseq/AA1989.DAT.*
11: /SID56/qcgdata/geneseq/geneseq/AA1990.DAT.*
12: /SID56/qcgdata/geneseq/geneseq/AA1991.DAT.*
13: /SID56/qcgdata/geneseq/geneseq/AA1992.DAT.*
14: /SID56/qcgdata/geneseq/geneseq/AA1993.DAT.*
15: /SID56/qcgdata/geneseq/geneseq/AA1994.DAT.*
16: /SID56/qcgdata/geneseq/geneseq/AA1995.DAT.*
17: /SID56/qcgdata/geneseq/geneseq/AA1996.DAT.*
18: /SID56/qcgdata/geneseq/geneseq/AA1997.DAT.*
19: /SID56/qcgdata/geneseq/geneseq/AA1998.DAT.*
20: /SID56/qcgdata/geneseq/geneseq/AA1999.DAT.*
21: /SID56/qcgdata/geneseq/geneseq/AA2000.DAT.*
22: /SID56/qcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	119	100.0	365	19	W48086 Human dendritic ce
2	119	100.0	365	21	Y97077 Primate (human) ch
3	74	62.2	350	13	R27791 Interleukin-8 rece
4	74	62.2	350	16	R68811 Interleukin-8 rece
5	74	62.2	350	16	R80756 Interleukin 8 rece
6	74	62.2	350	16	R80951 Recombinant high a
7	74	62.2	350	17	B09889 Human IL-8 recepto
8	74	62.2	354	15	R53932 Interleukin 8 (IL
9	74	62.2	355	13	R28272 Sequence in a high
10	74	62.2	355	14	R33420 Human IL-8 recepto
11	74	62.2	355	16	R80950 Recombinant high a

12	74	62.2	355	17	B09990 Human IL-8 recepto
13	74	62.2	358	16	R80952 Recombinant high a
14	74	62.2	360	13	R28273 Sequence in a low
15	74	62.2	360	16	R80758 Interleukin 8 rece
16	74	62.2	360	16	R80953 Recombinant high a
17	74	62.2	1060	16	R70123 IL8-R type 1-GBP 1
18	74	62.2	1064	16	R70124 IL8-R type 2-GBP 1
19	73	61.3	358	13	R28274 Sequence in a lowh
20	72	60.5	312	15	R48717 G-protein coupled
21	72	60.5	312	17	W02689 G-protein coupled
22	70	58.8	371	19	W69599 Human G-protein co
23	70	58.8	371	19	W69970 Human 7-transmembr
24	70	58.8	371	21	Y11302 Human orphan G pro
25	70	58.8	371	21	B02836 Human G protein co
26	70	58.8	380	20	Y06215 Human G protein co
27	67	56.3	382	20	Y06214 Mouse G protein co
28	63	52.9	358	15	R53745 Partial sequence o
29	63	52.9	358	21	B21689 Human 7TM receptor
30	63	52.9	359	15	R53747 Seven transmembran
31	63	52.9	359	19	W48728 Murine V31 seven t
32	63	52.9	359	21	B21691 Murine 7TM recepto
33	63	52.9	361	20	W97348 An Epstein-Barr vi
34	63	52.9	378	15	R54079 Epstein Barr virus
35	63	52.9	378	15	R53744 Putative seven tra
36	63	52.9	378	19	W48724 Human V31 seven tr
37	63	52.9	378	19	W56164 G-protein coupled
38	63	52.9	378	19	W53622 Epstein Barr virus
39	63	52.9	378	21	B21688 Human 7TM receptor
40	63	52.9	378	21	B21699 7TM receptor prote
41	63	52.9	378	21	Y90629 Human G protein-co
42	63	52.9	378	21	Y90663 Human mutant G pro
43	63	52.9	378	22	B50859 Human CCR7, Homo
44	63	52.9	410	15	R53743 Putative seven tra
45	63	52.9	410	19	W48723 Polypeptide sequen

ALIGNMENTS

RESULT 1

ID	W48086	standard; Protein; 365 AA.
XX	XX	
AC	W48086;	
XX	XX	
DT	11-JUN-1998	(first entry)
XX	XX	
DE	Human dendritic cell chemokine receptor.	
XX	XX	
KW	Human; thymus expressed chemokine; TECK; MIP-3alpha; MIP-3beta;	
KW	receptor; dendritic cell; macrophage; inflammation; asthma.	
XX	XX	
OS	Homo sapiens.	
XX	XX	
FH	Key	Location/Qualifiers
FT	Misc-difference 193	
FT		/note= "encoded by CAN"
XX	XX	
PN	W09801557-A2.	
XX	XX	
PD	15-JAN-1998.	
XX	XX	
PF	02-JUL-1997;	97WO-US10819.
XX	XX	
PR	04-JUN-1997;	97US-0048593.
PR	05-JUL-1996;	96US-0675814.
PR	11-OCT-1996;	96US-0028329.
XX	XX	
PA	(SCHE) SCHERING CORP.	
XX	XX	
PI	Gish KC, Schall TJ, Vicari A, Wang W, Zlotnik A;	
XX	XX	
DR	WPI; 1998-101054/09.	

2

PT polypeptide and corresp. antibodies and DNA - useful as
 PT diagnostic and screening agents, and for treating inflammation or
 PS PF4AR-mediated disorders

XX Claim 7; Fig 2; 78pp; English.

XX A cDNA library constructed from human neutrophil mRNA in the mammalian
 CC expression vector pRK5B was transfected into COS-7 cells as pools of
 CC 2500 clones. One positive pool from the first 58 transfections was
 CC partitioned into smaller pools until a pure clone (pRK5B.118r1.1)
 CC was obtained. The ORF encodes a protein of 350 amino acids which
 CC shares several features with the G-protein coupled receptors of the
 CC rhodopsin superfamily, including 7 hydrophobic (transmembrane)
 CC domains. The IL-8 receptor is a preferred PF4AR superfamily member
 CC of the invention. See also Q29506 and Q37107.

XX Sequence 350 AA;

Query Match 62.2%; Score 74; DB 13; Length 350;
 Best Local Similarity 66.7%; Pred. No. 0.00047;
 Matches 14; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 VIIAVLVFLACQIPHNWLL 21
 || ||||| || | : ||: |||
 Db 243 vifavvlflcwlcpynlavl 263

RESULT 4

R68811 ID R68811 standard; Protein; 350 AA.

XX AC R68811;

DT 18-JUL-1995 (first entry)

XX DE Interleukin-8 receptor.

XX KW Interleukin-8 receptor; IL-8 receptor; PF4AR;

XX KW--platelet factor-superfamily receptor; neutrophil; chemotactic;
 KW inflammation; inflammatory disease; arthritis; emphysema; cystic;
 KW fibrosis; colitis; bronchitis; meningitis; therapeutic.

XX OS Homo sapiens.

XX PN W09428931-A.

XX PD 22-DEC-1994.

XX PF 07-JUN-1994; 94WO-US06380.

XX PR 11-JUN-1993; 93US-0076093.

XX PA (GETH) GENENTECH INC.

XX PI Chuntharapai A, Hebert C, Kim KJ, Lee J;

XX WPI; 1995-036114/05.

DR N-PSDB; Q80520.

XX Treatment of inflammatory disorders - by administering an
 PT antibody capable of binding a platelet factor 4 superfamily
 PT receptor polypeptide

XX PS Disclosure; Page 51-54; 83pp; English.

XX A cDNA library constructed from human neutrophil mRNA in pRK5B was
 CC transfected into COS-7 cells, and the cells were screened with 125I-
 CC IL-8. The DNA sequence of isolated cDNA clone pRK5B.118r1.1,
 CC encoding human IL-8 receptor, is given in Q80520 and the predicted
 CC amino acid sequence in R68811. The receptor is used to raise
 CC antibodies that neutralize the activity of PF4AR, e.g. IL-8 receptor.

XX

SQ Sequence 350 AA;

Query Match 62.2%; Score 74; DB 16; Length 350;
 Best Local Similarity 66.7%; Pred. No. 0.00047;
 Matches 14; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 VIIAVLVFLACQIPHNWLL 21
 || ||||| || | : ||: |||
 Db 243 vifavvlflcwlcpynlavl 263

RESULT 5

R80756 ID R80756 standard; Protein; 350 AA.

XX AC R80756;

XX DT 26-MAR-1996 (first entry)

XX DE Interleukin 8 receptor A partial sequence.

XX KW Interleukin; IL-8; inflammation; psoriasis; dermatitis;

XX KW rheumatoid arthritis; inflammatory bowel disease;

XX KW chronic lung inflammation; treatment; antibody;

XX KW affinity purification; detection.

XX OS Homo sapiens.

XX PN US5440021-A.

XX PD 08-AUG-1995.

XX PF 29-MAR-1991; 91US-0677211.

XX PR 25-FEB-1994; 94US-0202056.

XX PR 29-MAR-1991; 91US-0677211.

XX PA (CHUN/) CHUNTHARAPAI A.

XX PA (HEBE/) HEBERT C.

XX PA (KIMK/) KIM K J.

XX PA (LEEJ/) LEE J.

XX PI Chuntharapai A, Hebert C, Kim KJ, Lee J;

XX WPI; 1995-283151/37.

DR N-PSDB; Q99006.

XX New antibodies against interleukin 8 type B receptor - used to treat
 PT or prevent inflammation, also for detecting receptor expression and
 PT purification.

XX Example 2; Columns 41-44; 62pp; English.

XX Antibodies directed against the interleukin-8 receptor B can be used
 CC to treat or prevent inflammation e.g. psoriasis, dermatitis,
 CC rheumatoid arthritis and particularly inflammatory bowel disease and
 CC chronic lung inflammation. When immobilised, these antibodies may
 CC be used to detect interleukin-8 receptor B expression in cells and
 CC tissues and for affinity purification of interleukin-8 receptor B
 CC from cells. A sequence encoding amino acids 23-314 of this fragment
 CC of the high affinity interleukin-8 receptor, was used to probe lambda
 CC gt10 cDNA libraries for the human interleukin-8 type B receptor.

XX Sequence 350 AA;

Query Match 62.2%; Score 74; DB 16; Length 350;
 Best Local Similarity 66.7%; Pred. No. 0.00047;
 Matches 14; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 VIIAVLVFLACQIPHNWLL 21
 || ||||| || | : ||: |||

AC R53932;
 XX 23-FEB-1995 (first entry)
 XX Interleukin 8 (IL-8) receptor.
 XX Interleukin; receptor; antiinflammatory; psoriasis; reperfusion;
 KW rheumatoid arthritis; allograft; graft rejection.
 XX Homo sapiens.
 XX JP06100595-A.
 XX 12-APR-1994.
 XX 27-MAY-1991; 91JP-0149245.
 XX 27-MAY-1991; 91JP-0149245.
 XX (UYBO-) UNIV BOSTON.
 XX WPI: 1994-156656/19.
 XX N-PSDB; Q63919.
 XX Recombinant interleukin-8 receptor polypeptide - having
 PT antiinflammatory properties
 XX Claim 1; Figure 1; 13pp; Japanese.
 XX Anti-inflammatory agents containing the interleukin-8 receptor
 CC polypeptide can be used for the treatment of psoriasis, rheumatoid
 CC arthritis and other acute and chronic inflammatory diseases,
 CC including reperfusion and allograft rejection.
 XX Sequence 354 AA;
 SQ

Query Match 62.2%; Score 74; DB 15; Length 354;
 Best Local Similarity 66.7%; Pred. No. 0.00048;
 Matches 14; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
 QY 1 VIIAVLVFLACQIPHNVL 21
 DB 247 vifavvlflcwlpynlvll 267

RESULT 9
 R28272
 ID R28272 standard; Protein; 355 AA.
 AC R28272;
 XX 04-APR-1993 (first entry)
 XX Sequence in a high affinity recombinant rabbit interleukin-8
 DE (IL-8) receptor polypeptide in F3R.
 XX IL-8 receptor polypeptide; G-protein-coupled receptor.
 XX Oryctolagus cuniculus.
 XX WO9218641-A.
 XX 29-OCT-1992.
 XX 10-APR-1992; 92WO-US02977.
 XX 10-APR-1991; 91US-0685101.
 PR 09-JUL-1991; 91US-072606.
 PR 09-DEC-1991; 91US-0803842.
 XX (REPK) REPLIGEN CORP.
 PA (UYBO-) UNIV BOSTON.

XX Navarro J, Thomas KM, Witt DP;
 XX WPI: 1992-382123/46.
 DR N-PSDB; Q30011.
 XX Recombinant mammalian interleukin-8 receptor - used for screening
 PT interleukin-8 binding antagonists, used to treat inflammation
 XX Claim 2; Fig 1; 71pp; English.
 XX Rabbit high affinity IL-8 receptor gene was isolated from rabbit
 CC peritoneal neutrophils and used as a source of poly(A)+ RNA, to
 CC produce a rabbit neutrophil cDNA library. 250,000 recombinant
 CC plaques were screened for those which hybridized to an antisense
 CC oligonucleotide (Q30015). This probe was designed based on the
 CC sequence derived from the second transmembrane domain of G-protein-
 CC coupled receptors. After tertiary screening, six plaques were
 CC isolated. The insert of one of these plaques, termed F3R was of 2.5
 CC kb in size. This insert was sequenced. The protein deduced from
 CC the F3R clone demonstrates that it belongs to the family of
 CC G-protein-coupled receptors. The deduced protein sequence
 CC indicates seven putative transmembrane segments.
 XX Sequence 355 AA;
 SQ

Query Match 62.2%; Score 74; DB 13; Length 355;
 Best Local Similarity 66.7%; Pred. No. 0.00048;
 Matches 14; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
 QY 1 VIIAVLVFLACQIPHNVL 21
 DB 248 vifavvlflcwlpynlvll 268

RESULT 10
 R33420
 ID R33420 standard; Protein; 355 AA.
 XX R33420;
 XX 26-JUL-1993 (first entry)
 XX Human IL-8 receptor from clone p2.
 DE Interleukin-8 receptor; probes; gene therapy; gro receptor;
 KW intracellular-calcium mobilising; ligand-binding; MIP-2 receptor.
 XX Homo sapiens.
 XX WO9306229-A.
 XX 01-APR-1993.
 XX 14-SEP-1992; 92WO-US07641.
 XX 13-SEP-1991; 91US-0759568.
 XX (USSH) US DEPT HEALTH & HUMAN SERVICE.
 XX Murphy PM;
 XX WPI: 1993-117549/14.
 DR N-PSDB; Q38747.
 XX New interleukin-8 receptor aminoacid sequence - and corresp. cDNA
 PT expressed in Xenopus laevis oocytes or transfected host cells,
 PT for screening ligands of IL-8 receptor and gene therapy
 XX Claim 1; Fig 3; 39pp; English.
 XX cDNA libraries from 2 and 3.5 kb fractions of poly(A)+ RNA from HL60
 CC

CC neutrophils sepd. of a sucrose gradient were made in UnizAP. The
 CC libraries were screened with F3R oligonucleotide probe (from rabbit
 CC IL-8 receptor) and under low stringency with a p2 cDNA probe
 CC synthesised from random primers, to isolated the clone p2, encoding
 CC human IL-8 receptor protein. The presence or absence of the DNA
 CC encoding IL-8R or related MIP-2 receptor may be detected using
 CC portions of the p2 clone as probes. p2 may also be used to screen
 CC for ligands of IL-8R and may also be used in gene therapy to treat a
 CC patient deficient in IL-8R. The IL-8R is a gro receptor and has
 CC intracellular calcium-mobilising and ligand-binding properties.
 XX
 XX Sequence 355 AA;

Query Match 62.2%; Score 74; DB 14; Length 355;
 Best Local Similarity 66.7%; Pred. No. 0.00048;
 Matches 14; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 VIIAVLVFLACQIPHNVL 21
 II IIII:II I :I:IIII
 Db 247 vifavvlflcwlpynlvll 267

RESULT 11

R80950
 ID R80950 standard; Protein; 355 AA.

XX AC R80950;

XX DT 24-APR-1996 (first entry)

XX DE Recombinant high affinity interleukin-8 receptor subtype A.

XX KW IL-8A; IL-8B; receptor; monoclonal antibody; inflammatory disorder;
 KW anaphylaxis; systemic lupus erythematosus; rheumatoid arthritis;
 KW systemic necrotising vasculitis; psoriasis; asthma; allergy; ARDS;
 KW adult respiratory distress syndrome; neutrophil detection.

XX OS Oryctolagus cuniculus.

XX PN W09525126-A1.

XX PD 21-SEP-1995.

XX PF 09-MAR-1995; 95WO-US03032.

XX PR 02-MAY-1994; 94US-0237937.

XX PR 15-MAY-1994; 94US-0210250.

XX PA (REPK) REPLIGEN CORP.

XX PA (UYBO-) UNIV BOSTON.

XX PI Greenfield EA, Larosa GJ, Navarro J, Thomas KM;

XX PI Witt DP;

XX DR WPI; 1995-336945/43.

XX DR N-PSDB; Q99949.

XX PT Monoclonal antibody against recombinant IL-8 receptor polypeptide -
 PT useful for treating inflammatory disorders, for detecting
 PT neutrophil(s) and for isolating IL-8 receptor from liq.mixt.

XX PS Claim 2; Fig 1A-B; 74pp; English.

XX CC Monoclonal antibodies were raised against recombinant interleukin-8
 CC (IL-8) receptor subtypes A and B from both human and rabbit sources
 CC (R80950-53 encoded by Q99949-52). The A subtype receptor (IL-8rA) is
 CC a high affinity receptor and the B subtype receptor (IL-8rB) is a
 CC low affinity receptor. The monoclonal antibody (mAb) pref. binds to
 CC the IL-8 binding domain thus blocking its activation. The mAbs are
 CC useful for treating inflammatory disorders (see key words) and for
 CC detecting the presence of neutrophils in a biological sample. The
 CC mAbs are also useful in the isolation of IL-8 receptors from a mixture.

XX SQ Sequence 355 AA;

Query Match 62.2%; Score 74; DB 16; Length 355;
 Best Local Similarity 66.7%; Pred. No. 0.00048;
 Matches 14; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 VIIAVLVFLACQIPHNVL 21
 II IIII:II I :I:IIII
 Db 248 vifavvlflcwlpynlvll 268

RESULT 12

B09990
 ID B09990 standard; Protein; 355 AA.

XX AC B09990;

XX DT 20-OCT-2000 (first entry)

XX DE Human IL-8 receptor protein hIL8RB.

XX KW IL-8 receptor protein; hIL8RA; hIL8RB; human; interleukin-8; drug;
 KW treatment; inflammatory disease; anti-tumor.

XX OS Homo sapiens.

XX PN JP08103276-A.

XX PD 23-APR-1996.

XX PF 06-OCT-1994; 94JP-0242534.

XX PR 06-OCT-1994; 94JP-0242534.

XX PA (TAKE) TAKEDA CHEM IND LTD.

XX DR WPI; 1996-253878/26.

XX DR N-PSDB; A40128.

XX PT Recombinant human interleukin 8 receptor protein, - its prepn. and
 PT application.

XX PS Example 2; Fig 4; 22pp; Japanese.

XX CC This invention describes a novel expression vector which carries a DNA
 CC encoding human interleukin 8 receptor protein and is expressed by
 CC pAKK01.11/hrIL8RA or pAKK01.11/hIL8RB. Also claimed are (I) CHO cell
 CC containing the above expression vector, (II) the preparation of a
 CC recombinant human interleukin 8 receptor protein in which the above CHO
 CC cell is cultured under a condition enabling the expression of a DNA
 CC coding human interleukin 8 receptor protein, (III) a CHO cell
 CC containing a recombinant human interleukin 8 receptor protein which can
 CC be prepared, by culturing the above CHO cell under a condition enabling
 CC the expression of a DNA coding human interleukin 8 receptor protein or
 CC its cell membrane fraction, (IV) a recombinant human interleukin 8
 CC receptor protein isolated from a CHO cell containing the above
 CC recombinant human interleukin 8 receptor protein, its partial peptide or
 CC their salt, (V) the screening of human interleukin 8 receptor agonist or
 CC antagonist in which the above CHO cell or its cell membrane fraction is
 CC used or the above recombinant human interleukin 8 receptor protein, its
 CC partial peptide or their salt is used (VI) a kit for screening the human
 CC interleukin 8 receptor agonist or antagonist containing the above CHO
 CC cell or its cell membrane fraction or the above recombinant human
 CC interleukin 8 receptor protein, its partial peptide or their salt, (VII)
 CC a human interleukin 8 receptor agonist or antagonist prepared by using
 CC the above screening method or the above screening kit or its salt, (VII)
 CC an activation promoter or a migration promoter of neutrophils containing
 CC the above agonist or its salt, and an activation inhibitor or a migration
 CC inhibitor containing the above antagonist or its salt. The agonist or the
 CC antagonist can be used in drug compositions for the prevention and
 CC treatment of inflammatory diseases and anti-tumor agents. The screening

CC method can select an agonist or an antagonist advantageously. This
 CC sequence represents the human IL-8 receptor protein hIL8RB which is
 CC described in the method of the invention.

XX Sequence 355 AA;

Query Match 62.2%; Score 74; DB 17; Length 355;
 Best Local Similarity 66.7%; Pred. No. 0.00048;
 Matches 14; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 VIIAVLVFLACQIPHNVL 21
 II IIII:II I :I:I:II
 Db 247 vifavvlflcwpynl 267

RESULT 13

R80952
 ID R80952 standard; Protein; 358 AA.

XX AC R80952;

XX DT 24-APR-1996 (first entry)

XX DE Recombinant high affinity interleukin-8 receptor subtype B.

XX KW IL-8A; IL-8B; receptor; monoclonal antibody; inflammatory disorder;
 KW anaphylaxis; systemic lupus erythematosus; rheumatoid arthritis;
 KW systemic necrotizing vasculitis; psoriasis; asthma; allergy; ARDS;
 KW adult respiratory distress syndrome; neutrophil detection.

XX OS Oryctolagus cuniculus.

XX PN WO9525126-A1.

XX PD 21-SEP-1995.

XX PF 09-MAR-1995; 95WO-US03032.

XX PR 02-MAY-1994; 94US-0237937.

XX PR 15-MAR-1994; 94US-0210250.

XX PA (REPK) REPLIGEN CORP.

XX PA (UYBO-) UNIV BOSTON.

XX PI Greenfield EA, Larosa GJ, Navarro J, Thomas KM;

XX PI Witt DT;

XX DR WPI; 1995-336945/43.

XX DR N-PSDB; Q99951.

XX PT Monoclonal antibody against recombinant IL-8 receptor polypeptide -
 PT useful for treating inflammatory disorders, for detecting
 PT neutrophil(s) and for isolating IL-8 receptor from liq.mixt.

XX PS Claim 6; Fig 3A-B; 74pp; English.

XX CC Monoclonal antibodies were raised against recombinant interleukin-8
 CC (IL-8) receptor subtypes A and B from both human and rabbit sources
 CC (R80950-53 encoded by 099949-52). The A subtype receptor (IL-8rA) is
 CC a high affinity receptor and the B subtype receptor (IL-8rB) is a
 CC low affinity receptor. The monoclonal antibody (mAb) pref. binds to
 CC the IL-8 binding domain thus blocking its activation. The mAbs are
 CC useful for treating inflammatory disorders (see key words) and for
 CC detecting the presence of neutrophils in a biological sample. The
 CC mAbs are also useful in the isolation of IL-8 receptors from a mixture.

XX SQ Sequence 358 AA;

Query Match 62.2%; Score 74; DB 16; Length 358;
 Best Local Similarity 66.7%; Pred. No. 0.00048;
 Matches 14; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 VIIAVLVFLACQIPHNVL 21
 II IIII:II I :I:I:II
 Db 250 vifavvlflcwpynl 270

RESULT 14

R28273
 ID R28273 standard; Protein; 360 AA.

XX AC R28273;

XX DT 04-APR-1993 (first entry)

XX DE Sequence in a low affinity recombinant human interleukin-8
 DE (IL-8) receptor polypeptide in 4AB.

XX KW IL-8 receptor polypeptide; G-protein-coupled receptor.

XX OS Homo sapiens.

XX PN WO9218641-A.

XX PD 29-OCT-1992.

XX PF 10-APR-1992; 92WO-US02977.

XX PR 10-APR-1991; 91US-0685101.

XX PR 09-JUL-1991; 91US-0726606.

XX PR 09-DEC-1991; 91US-0803842.

XX PA (REPK) REPLIGEN CORP.

XX PA (UYBO-) UNIV BOSTON.

XX PI Navarro J, Thomas KM, Witt DP;

XX DR WPI; 1992-382123/46.

XX DR N-PSDB; Q30012.

XX PT Recombinant mammalian interleukin-8 receptor - used for screening
 PT interleukin-8 binding antagonists, used to treat inflammation

XX PS Disclosure; Fig 2; 71pp; English.

XX CC Rabbit high affinity IL-8 receptor gene was isolated from rabbit
 CC peritoneal neutrophils and used as a source of poly(A)⁺ RNA, to
 CC produce a rabbit neutrophil cDNA library. 250,000 recombinant
 CC plaques were screened for those which hybridized to an antisense
 CC oligonucleotide (Q30015). This probe was designed based on the
 CC sequence derived from the second transmembrane domain of G-protein-
 CC coupled receptors. After tertiary screening, six plaques were
 CC isolated. The insert of one of these plaques, termed F3R was of 2.5
 CC kb in size. This insert was sequenced. The protein deduced from
 CC the F3R clone demonstrates that it belongs to the family of
 CC G-protein-coupled receptors. The deduced protein sequence
 CC indicates seven putative transmembrane segments. A human
 CC peripheral blood leukocyte lambda gt11 cDNA library (5' stretch) was
 CC screened with a 652 bp EcoRI/BamHI fragment (including nucleotides
 CC -27 to 625) of the rabbit F3R clone. After tertiary screening
 CC several human clones which hybridized to the rabbit IL-8 probe
 CC were isolated. The insert of one such clone, termed 4AB was
 CC sequenced (Q30012).

XX SQ Sequence 360 AA;

Query Match 62.2%; Score 74; DB 13; Length 360;
 Best Local Similarity 66.7%; Pred. No. 0.00048;
 Matches 14; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 VIIAVLVFLACQIPHNVL 21
 II IIII:II I :I:I:II
 Db 252 vifavvlflcwpynl 272

RESULT 15

R80758
ID R80758 standard; Protein; 360 AA.

XX AC R80758;

XX DT 26-MAR-1996 (first entry)

XX DE Interleukin 8 receptor B.

XX KW Interleukin; IL-8; inflammation; psoriasis; dermatitis;

XX KW rheumatoid arthritis; inflammatory bowel disease;

XX KW chronic lung inflammation; treatment; antibody;

XX KW affinity purification; detection.

OS Homo sapiens.

XX PN US5440021-A.

XX PD 08-AUG-1995.

XX PF 29-MAR-1991; 91US-0677211.

XX PR 25-FEB-1994; 94US-0202056.

XX PR 29-MAR-1991; 91US-0677211.

XX PA (CHUN/) CHUNTHARAPAI A.

XX PA (HEBE/) HEBERT C.

XX PA (KIMK/) KIM K J.

XX PA (LEEJ/) LEE J.

XX PI Chuntharapai A, Hebert C, Kim KJ, Lee J;

XX DR WPI; 1995-283151/37.

XX DR N-PSDB; Q99008.

XX PT New antibodies against interleukin 8 type B receptor - used to treat or prevent inflammation, also for detecting receptor expression and purification.

XX PS Disclosure; Columns 53-56; 62pp; English.

XX CC Antibodies directed against the interleukin-8 receptor B can be used to treat or prevent inflammation e.g. psoriasis, dermatitis, rheumatoid arthritis and particularly inflammatory bowel disease and chronic lung inflammation. When immobilised, these antibodies may be used to detect interleukin-8 receptor B expression in cells and tissues and for affinity purification of interleukin-8 receptor B from cells.

XX SQ Sequence 360 AA;

Query Match 62.2%; Score 74; DB 15; Length 360;

Best Local Similarity 66.7%; Pred. No. 0.00048;

Matches 14; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Oy 1 VIIAVVLVFLACQIPHNVL 21

|||:|:|:|:|:|:|

Db 252 vifavvlflcwlpylnvl 272

Search completed: May 23, 2001, 15:28:32
Job time: 409 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 23, 2001, 15:30:08 ; Search time 95.91 Seconds
(without alignments)
5.008 Million cell updates/sec

Title: US-08-887-977-10_COPY_246_270
Perfect score: 119
Sequence: 1 VIIIAVLVFLACQIPHNVLIVTAA 25

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 185757 seqs, 19210857 residues

Total number of hits satisfying chosen parameters: 185757

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA.*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
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5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	74	62.2	350	1	US-08-202-056-1
2	74	62.2	350	1	US-08-076-093A-2
3	74	62.2	350	1	US-08-450-393A-7
4	74	62.2	350	1	US-08-410-453A-1
5	74	62.2	350	1	US-08-701-265-2
6	74	62.2	350	1	US-08-410-454A-1
7	74	62.2	350	2	US-08-284-586-2
8	74	62.2	350	2	US-08-410-456A-1
9	74	62.2	350	2	US-08-805-478-2
10	74	62.2	350	2	US-08-802-627A-2
11	74	62.2	350	2	US-08-801-238-2
12	74	62.2	350	2	US-08-801-228-2
13	74	62.2	350	3	US-09-104-296-2
14	74	62.2	350	4	US-08-446-669-7
15	74	62.2	350	5	PCT-US95-00476-7
16	74	62.2	354	1	US-07-759-568-2
17	74	62.2	355	1	US-07-759-568-1
18	74	62.2	355	1	US-08-450-393A-8
19	74	62.2	355	2	US-08-390-000A-5
20	74	62.2	355	4	US-08-446-669-8
21	74	62.2	355	5	PCT-US95-00476-8
22	74	62.2	360	1	US-08-202-056-7
23	72	60.5	312	1	US-08-118-270-38
24	72	60.5	312	5	PCT-US93-08528-38
25	70	58.8	380	4	US-08-969-815-4
26	67	56.3	382	4	US-08-969-815-2
27	63	52.9	358	1	US-08-153-848-19

28	63	52.9	358	3	US-09-299-843A-19	Sequence 19, Appl
29	63	52.9	358	5	PCT-US93-11153-19	Sequence 19, Appl
30	63	52.9	359	1	US-08-153-848-24	Sequence 24, Appl
31	63	52.9	359	3	US-09-299-843A-24	Sequence 24, Appl
32	63	52.9	359	5	PCT-US93-11153-24	Sequence 24, Appl
33	63	52.9	361	2	US-08-902-294-2	Sequence 2, Appl
34	63	52.9	361	3	US-09-178-637-2	Sequence 2, Appl
35	63	52.9	378	1	US-08-383-750-2	Sequence 2, Appl
36	63	52.9	378	1	US-08-383-751A-2	Sequence 2, Appl
37	63	52.9	378	1	US-08-153-848-15	Sequence 15, Appl
38	63	52.9	378	3	US-08-352-678-2	Sequence 2, Appl
39	63	52.9	378	3	US-09-299-843A-15	Sequence 15, Appl
40	63	52.9	378	3	US-09-299-843A-66	Sequence 66, Appl
41	63	52.9	378	4	US-09-251-545-1	Sequence 1, Appl
42	63	52.9	378	5	PCT-US93-09636-2	Sequence 2, Appl
43	63	52.9	378	5	PCT-US93-11153-15	Sequence 15, Appl
44	63	52.9	410	1	US-08-153-848-7	Sequence 7, Appl
45	63	52.9	410	3	US-09-299-843A-7	Sequence 7, Appl

ALIGNMENTS

```

RESULT 1
US-08-202-056-1
: Sequence 1, Application US/08202056
: Patent No. 5440021
: GENERAL INFORMATION:
: APPLICANT: Chuntharapai, Anan
: APPLICANT: Hebert, Caroline
: APPLICANT: Kim, Kyung Jin
: APPLICANT: Lee, James
: TITLE OF INVENTION: Antibodies to Human IL-8 Type B Receptor
: NUMBER OF SEQUENCES: 8
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Genentech, Inc.
: STREET: 460 Point San Bruno Blvd
: CITY: South San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94080
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: patin (Genentech)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/202,056
: FILING DATE: 25-FEB-1994
: CLASSIFICATION: 436
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/677211
: FILING DATE: 29-MAR-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: Love, Richard B.
: REGISTRATION NUMBER: 34,659
: REFERENCE/DOCKET NUMBER: 706P3
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 415/225-5530
: TELEFAX: 415/952-9881
: TELEX: 910/371-7168
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 350 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: US-08-202-056-1

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Query Match 62.2%; Score 74; DB 1; Length 350;
Best Local Similarity 66.7%; Pred. No. 0.00089;
Matches 14; Conservative 4; Mismatches 3; Indels 0; Caps 0;

QY 1 VIIAVVLVFLACQIPHNVLL 21
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 Db 243 VIFAVVLFLCWLCPYNLVL 263

RESULT 2

US-08-076-093A-2
 ; Sequence 2, Application US/08076093A
 ; Patent No. 5543503
 ; GENERAL INFORMATION:
 ; APPLICANT: Chuntharapai, Anan
 ; APPLICANT: Lee, James
 ; APPLICANT: Hebert, Caroline
 ; APPLICANT: Jin Kim, K.
 ; TITLE OF INVENTION: Antibodies to Human PF4A Receptors
 ; NUMBER OF SEQUENCES: 6
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genentech, Inc.
 ; STREET: 460 Point San Bruno Blvd
 ; CITY: South San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94080
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: WinPatIn (Genentech)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/076,093A
 ; FILING DATE: 11-Jun-1993
 ; CLASSIFICATION: 530
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/810782
 ; FILING DATE: 19-DEC-1991
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/677211
 ; FILING DATE: 29-MAR-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Love, Richard B.
 ; REGISTRATION NUMBER: 34,659
 ; REFERENCE/DOCKET NUMBER: 706P2
 ; TELEPHONE: 415/225-5530
 ; TELEFAX: 415/952-9881
 ; TELEX: 910/371-7168
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 350 amino acids
 ; TYPE: Amino Acid
 ; TOPOLOGY: Linear
 ; US-08-076-093A-2

Query Match 62.2%; Score 74; DB 1; Length 350;
 Best Local Similarity 66.7%; Pred. No. 0.00089;
 Matches 14; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 VIIAVVLVFLACQIPHNVLL 21
 || |||||:| | :|:|:|
 Db 243 VIFAVVLFLCWLCPYNLVL 263

RESULT 3

US-08-450-393A-7
 ; Sequence 7, Application US/08450393A
 ; Patent No. 5707815
 ; GENERAL INFORMATION:
 ; APPLICANT: Charo, Israel
 ; APPLICANT: Coughlin, Shaun
 ; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
 ; TITLE OF INVENTION: PROTEIN RECEPTORS
 ; NUMBER OF SEQUENCES: 14

; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
 ; STREET: 5 Palo Alto Square
 ; CITY: Palo Alto
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94306-2155
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/450,393A
 ; FILING DATE: May 25, 1995
 ; CLASSIFICATION: 424
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Cseri, Luann
 ; REGISTRATION NUMBER: 31,822
 ; REFERENCE/DOCKET NUMBER: UCAL-237/0205
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-843-5165
 ; TELEFAX: 415-8857-0663
 ; TELEX: 380816Cooileypa
 ; INFORMATION FOR SEQ ID NO: 7:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 350 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; US-08-450-393A-7

Query Match 62.2%; Score 74; DB 1; Length 350;
 Best Local Similarity 66.7%; Pred. No. 0.00089;
 Matches 14; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 VIIAVVLVFLACQIPHNVLL 21
 || |||||:| | :|:|:|
 Db 243 VIFAVVLFLCWLCPYNLVL 263

RESULT 4

US-08-410-453A-1
 ; Sequence 1, Application US/08410453A
 ; Patent No. 5767063
 ; GENERAL INFORMATION:
 ; APPLICANT: Lee, James,
 ; APPLICANT: Holmes, William E.,
 ; APPLICANT: Woods, William I.,
 ; TITLE OF INVENTION: Human PF4A Receptors and Their Use
 ; NUMBER OF SEQUENCES: 2
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genentech, Inc.
 ; STREET: 1 DNA Way
 ; CITY: South San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94080
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: WinPatIn (Genentech)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/410,453A
 ; FILING DATE: 24-Mar-1995
 ; CLASSIFICATION: 514
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/234494
 ; FILING DATE: 28-APR-1994

RESULT 8
US-08-410-456A-1
; Sequence 1, Application US/08410456A
; Patent No. 5856457
; GENERAL INFORMATION:
; APPLICANT: Lee, James,
; APPLICANT: Holmes, William E.,
; APPLICANT: Woods, William I.
; TITLE OF INVENTION: Human PF4A Receptors and Their Use
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESS: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California

COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPacIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/805,478
FILING DATE: 25-Feb-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/284586
FILING DATE: 10-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/076093

```

Query Match          62.2%; Score 74; DB 2; Length 350;
Best Local Similarity 66.7%; Pred. No. 0.00089;
Matches 14; Conservative 4; Mismatches 3; Indels

QY . 1 VITAVLVFLACQIPHNVL 21
    || ||||| | | : | : |||
Db 243 VIFAVLVFLLCWLPYNVL 263

```

```

12
RESULT 12
US-08-801-228-2
; Sequence 2, Application US/08801228
; Patent No. 5922541
; GENERAL INFORMATION:
; APPLICANT: Lee, James
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: METHODS FOR DETECTION AND AMPLIFICATION OF
; TITLE OF INVENTION: PF4A RECEPTOR NUCLEIC ACID
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/801.228
; FILING DATE: 19-Feb-1997
; CLASSIFICATION: 435.
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/284586
; FILING DATE: 10-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/076093
; FILING DATE: 11-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/810782
; FILING DATE: 19-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P0706P2PID3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5530
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 2:
; LENGTH: 350 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-801-228-2
Query Match 62.2%; Score 74; DB 2; Length 350;
Best Local Similarity 66.7%; Pred. No. 0.00089;
Matches 14; Conservative 3; Indels 0;
Gaps 0;
QY 1 VITAVLVFLACQIPHNVL 21
|| |||:|| | :|:||||
Db 243 VIFAVLFLCWLPLNVL 263
RESULT 13
US-09-104-296-2
; Sequence 2, Application US/09104296
; Patent No. 6087475
; GENERAL INFORMATION:
; APPLICANT: Lee, James
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: PF4A Receptors
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
13
RESULT 13
US-09-104-296-2
; Sequence 2, Application US/09104296
; Patent No. 6087475
; GENERAL INFORMATION:
; APPLICANT: Lee, James
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: PF4A Receptors
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
14
RESULT 14
US-08-446-669-7
; Sequence 7, Application US/08446669
; Patent No. 6132987
; GENERAL INFORMATION:
; APPLICANT: Charo, Israel
; APPLICANT: Coughlin, Shaun
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
; TITLE OF INVENTION: PROTEIN RECEPTORS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
; STREET: 5 Palo Alto Square
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
14
RESULT 14
US-08-446-669-7
; Sequence 7, Application US/08446669
; Patent No. 6132987
; GENERAL INFORMATION:
; APPLICANT: Charo, Israel
; APPLICANT: Coughlin, Shaun
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
; TITLE OF INVENTION: PROTEIN RECEPTORS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
; STREET: 5 Palo Alto Square
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

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APPLICATION NUMBER: US/08/446,669
FILING DATE: May 25, 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Neeley, Richard
REGISTRATION NUMBER: 30,092
REFERENCE/DOCKET NUMBER: USAL-237/01US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-843-5000
TELEFAX: 415-857-0663
TELEX: 380816CcoleyPA
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 350 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-446-669-7

Query Match 62.2%; Score 74; DB 4; Length 350;
Best Local Similarity 66.7%; Pred. No. 0.00089;
Matches 14; Conservative 4; Mismatches 3; Indels

Qy 1 VIIAVLVFLACQIPHNMLL 21
|| ||||:| | :|:| | |
Db 243 VIFAVVLIFLLCWLPLYNLVL 263

RESULT 15

```

PCT-US95-00476-7
; Sequence 7, Application PC/TUS9500476
; GENERAL INFORMATION:
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
; TITLE OF INVENTION: PROTEIN RECEPTORS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Robbins, Berliner & Carson
; STREET: 201 N. Figueroa Street, 5th Floor
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90012-2628
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/00476
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Berliner, Robert
; REGISTRATION NUMBER: 20,121
; REFERENCE/DOCKET NUMBER: 5555-291
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 310-977-1001
; TELEFAX: 310-977-1003
; TELEX:
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 350 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
PCT-US95-00476-7

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 23, 2001, 15:32:02 ; Search time 110.15 seconds
(without alignments)
15.598 Million cell updates/sec

Title: US-08-887-977-10_COPY_246_270

Perfect score: 119

Sequence: 1 VIIAVLVFLACQIPHNMLLVTTAA 25

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 198801 seqs, 68722935 residues

Total number of hits satisfying chosen parameters: 198801

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_67:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	119	100.0	369	JC5068	G protein-coupled
2	74	62.2	350	A39445	interleukin-8 rece
3	74	62.2	354	A23669	interleukin-8 rece
4	74	62.2	355	QJ1231	interleukin-8 rece
5	74	62.2	358	A53752	interleukin-8 rece
6	74	62.2	360	A53611	interleukin-8 rece
7	71	59.7	359	A48921	interleukin-8 rece
8	70	58.8	356	S42096	interleukin-8 rece
9	63	52.9	378	A45680	G protein-coupled
10	63	52.9	378	B55735	lymphocyte-specific
11	63	52.9	378	A55735	G protein-coupled
12	61	51.3	361	JC5653	G protein-coupled
13	61	51.3	365	S68208	G protein-coupled
14	59	49.6	358	G02670	IL8-related recept
15	59	49.6	375	JC5069	G protein-coupled
16	56	47.1	362	A30341	G protein-coupled
17	56	47.1	375	JC5509	G protein-coupled
18	55	46.2	323	Q0BED3	HHRE3 protein - hu
19	55	46.2	354	T09353	G protein-coupled
20	55	46.2	354	B57333	G protein-coupled
21	54.5	45.8	473	JC5835	anaphylatoxin C3a
22	54	45.4	349	JC5490	opsin, pineal glan
23	54	45.4	350	JN0621	G protein-coupled
24	53	44.5	342	S13638	platelet-activatin
25	53	44.5	363	I57940	somatostatin recep
26	52	43.7	351	A55962	opsin, pineal glan
27	52	43.7	362	A39714	G protein-coupled
28	50	42.0	341	S63666	platelet activatin
29	50	42.0	342	A40191	platelet-activatin

30	50	42.0	362	2	JN0694	angiotensin II rec
31	50	42.0	367	2	JE0349	interferon-inducib
32	50	42.0	394	2	JC7209	galanin receptor -
33	50	42.0	465	1	JQ1517	neurokinin 3 recep
34	50	42.0	519	2	S17783	tachykinin recepto
35	49	41.2	341	2	S43252	platelet-activatin
36	49	41.2	359	2	I49341	MIP-1 alpha recept
37	49	41.2	360	2	A57160	chemokine (C-C) re
38	49	41.2	385	2	S55524	neurokinin 3 recep
39	49	41.2	440	2	A44081	kappa-type opioid
40	49	41.2	449	2	A41738	neuropeptide Y rec
41	49	41.2	452	2	A34916	neurokinin 3 recep
42	48	40.3	363	2	I57955	somatostatin recep
43	48	40.3	364	2	JN0763	somatostatin recep
44	48	40.3	380	2	JC2434	kappa opioid recep
45	48	40.3	380	2	A48227	kappa opioid recep

ALIGNMENTS

RESULT 1

JC5068

G protein-coupled receptor CKR-L3 - human

C:Species: Homo sapiens (man)

C:Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 21-Jul-2000

C:Accession: JC5068

R:Zaballos, A.; Varona, R.; Gutierrez, J.; Lind, P.; Marquez, G.

Biochem. Biophys. Res. Commun. 227, 846-853, 1996

A:Title: Molecular cloning and RNA expression of two new human chemokine receptor-lik

A:Reference number: JC5067; MUID:97040707

A:Accession: JC5068

A:Molecule type: DNA

A:Residues: 1-369 <ZAB>

A:Cross-references: EMBL:Z79784; NID:gl668737; PIDN:CA802144.1; PID:gl668738

C:Comment: This protein belongs to the family of alpha chemokine receptors.

C:Genetics:

A:Gene: GDB:CMKBR6; STRL22; GPR29; CCR6; CKR-L3; GPR-CY4

A:Cross-references: GDB:5370639; OMIM:601835

A:Map position: 6q27-q27

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor; transmembrane protein

F:42-68/Domain: transmembrane #status predicted <TM1>

F:79-99/Domain: transmembrane #status predicted <TM2>

F:115-136/Domain: transmembrane #status predicted <TM3>

F:160-180/Domain: transmembrane #status predicted <TM4>

F:212-233/Domain: transmembrane #status predicted <TM5>

F:250-271/Domain: transmembrane #status predicted <TM6>

F:292-315/Domain: transmembrane #status predicted <TM7>

Query Match 100.0%; Score 119; DB 2; Length 369;

Best Local Similarity 100.0%; Pred. No. 6.5e-10;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VIIAVLVFLACQIPHNMLLVTTAA 25

DB 250 VIIAVLVFLACQIPHNMLLVTTAA 274

RESULT 2

A39445

interleukin-8 receptor type A - human

N:Alternate names: interleukin-8 receptor, high-affinity

C:Species: Homo sapiens (man)

C:Date: 22-Jan-1993 #sequence_revision 12-Apr-1996 #text_change 05-Nov-1999

C:Accession: I37449; I38710; I38711; A39445

R:Mollereau, C.; Muscatelli, F.; Mattei, M.G.; Vassart, G.; Parmentier, M.

Genomics 16, 248-251, 1993

A:Title: The high-affinity interleukin 8 receptor gene (IL8RA) maps to the 2q33-q36 r

A:Reference number: I37449; MUID:93252387

A:Accession: I37449

A:Molecule type: DNA

A:Residues: 1-350 <RES>
 A:Cross-references: EMBL:X65858; NID:9312046; PIDN:CAA46688.1; PID:g312047
 R:Ahuja, S.K.; Shetty, A.; Tiffany, H.L.; Murphy, P.M.
 J. Biol. Chem. 269, 26381-26389, 1994
 A:Title: Comparison of the genomic organization and promoter function for human interleukin-8 receptor.
 A:Reference number: 137898; MUID:95014476
 A:Accession: J38710
 A:Molecule type: DNA
 A:Residues: 1-350 <RE2>
 A:Cross-references: EMBL:U11870; NID:9511804; PIDN:AAA64378.1; PID:g511805
 A:Accession: J38711
 A:Molecule type: mRNA
 A:Residues: 1-16 <RE3>
 A:Cross-references: EMBL:U11871; NID:9511806; PIDN:AAA64379.1; PID:g733002
 R:Holmes, W.E.; Lee, J.; Kuang, W.J.; Rice, G.C.; Wood, W.I.
 Science 253, 1278-1280, 1991
 A:Title: Structure and functional expression of a human interleukin-8 receptor.
 A:Reference number: A39445; MUID:91368199
 A:Accession: A39445
 A:Molecule type: mRNA
 A:Residues: 1-275, 'T', 277-350 <HO1>
 A:Cross-references: GB:M68932; NID:g186369; PIDN:AAA59159.1; PID:g186370
 C:Genetics:
 A:Gene: GDB:IL8RA
 A:Cross-references: GDB:135039; OMIM:146929
 A:Map position: 2q35-2q35
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: G protein-coupled receptor; glycoprotein; membrane protein

Query Match 62.2%; Score 74; DB 2; Length 350;
 Best Local Similarity 66.7%; Pred. No. 0.002;
 Matches 14; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 VITAVVLVFLACQIPHNVL 21
 || ||||| || | : : : |||
 DB 243 VIFAVVLIFLLCWLPLNVL 263

RESULT 3

A23669
 Interleukin-8 receptor, high affinity - rabbit
 N:Alternate names: fMLP receptor
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C:Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 05-Nov-1999
 C:Accession: A23669
 R:Thomas, K.M.; Pyun, H.Y.; Navarro, J.
 J. Biol. Chem. 265, 20061-20064, 1990
 A:Title: Molecular cloning of the fMet-Leu-Phe receptor from neutrophils.
 A:Reference number: A23669; MUID:91056034
 A:Accession: A23669
 A:Molecule type: mRNA
 A:Residues: 1-354 <THO>
 A:Cross-references: GB:M58021; GB:J05705; NID:g165442; PIDN:AAA31377.1; PID:g165443
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: G protein-coupled receptor; glycoprotein; membrane protein; neutrophil

Query Match 62.2%; Score 74; DB 2; Length 354;
 Best Local Similarity 66.7%; Pred. No. 0.002;
 Matches 14; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 VITAVVLVFLACQIPHNVL 21
 || ||||| || | : : : |||
 DB 247 VIFAVVLIFLLCWLPLNVL 267

RESULT 4

J01231
 Interleukin-8 receptor - rabbit
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 05-Nov-1999
 C:Accession: J01231; A46483

R:Beckmann, M.P.; Munger, W.E.; Kozlosky, C.; VandenBos, T.; Price, V.; Lyman, S.; Ge
 Biochem. Biophys. Res. Commun. 179, 784-789, 1991
 A:Title: Molecular characterization of the interleukin-8 receptor.
 A:Reference number: J01231; MUID:91378994
 A:Accession: J01231
 A:Molecule type: DNA
 A:Residues: 1-355 <BEC>
 A:Cross-references: GB:M74240; NID:g165438; PIDN:AAA31375.1; PID:g165439
 R:Lee, J.; Kuang, W.J.; Rice, G.C.; Wood, W.I.
 J. Immunol. 148, 1261-1264, 1992
 A:Title: Characterization of complementary DNA clones encoding the rabbit IL-8 receptor
 A:Reference number: A46483; MUID:92148149
 A:Accession: A46483
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-355 <LEE>
 A:Cross-references: GB:M82873; NID:g165440; PIDN:AAA31376.1; PID:g165441
 A:Experimental source: neutrophils
 A:Note: sequence extracted from NCBI backbone (NCBI:81526, NCBIP:81530)
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 62.2%; Score 74; DB 2; Length 355;
 Best Local Similarity 66.7%; Pred. No. 0.002;
 Matches 14; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 VITAVVLVFLACQIPHNVL 21
 || ||||| || | : : : |||
 DB 248 VIFAVVLIFLLCWLPLNVL 268

RESULT 5

A53752
 Interleukin-8 receptor (clone 5Bla) - rabbit
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
 C:Accession: A53752
 R:Prado, G.N.; Thomas, K.M.; Suzuki, H.; LaRosa, G.J.; Wilkinson, N.; Folco, E.; Nava
 J. Biol. Chem. 269, 12391-12394, 1994
 A:Title: Molecular characterization of a novel rabbit interleukin-8 receptor isotype.
 A:Reference number: A53752; MUID:94230294
 A:Accession: A53752
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-358 <PRA>
 A:Cross-references: GB:L24445; NID:g437661; PIDN:AAA31378.1; PID:g437662
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 62.2%; Score 74; DB 2; Length 358;
 Best Local Similarity 66.7%; Pred. No. 0.002;
 Matches 14; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 VITAVVLVFLACQIPHNVL 21
 || ||||| || | : : : |||
 DB 250 VIFAVVLIFLLCWLPLNVL 270

RESULT 6

A53611
 Interleukin-8 receptor type B - human
 C:Species: Homo sapiens (man)
 C:Date: 07-Oct-1994 #sequence_revision 12-Apr-1996 #text_change 05-Nov-1999
 C:Accession: J37898; J38712; A53611; A39446
 R:Ahuja, S.K.; Shetty, A.; Tiffany, H.L.; Murphy, P.M.
 J. Biol. Chem. 269, 26381-26389, 1994
 A:Title: Comparison of the genomic organization and promoter function for human interleukin-8 receptor
 A:Reference number: J37898; MUID:95014476
 A:Accession: J37898
 A:Status: preliminary
 A:Molecule type: DNA

A:Accession: I49348
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-359 <RES>
A:Cross-references: EMBL:U31207; NID:g950174; PIDN:AAC52239.1; PID:g950175
R:Bozic, C.R.; Garard, N.P.; von Uexkull-Guldenband, C.; Kolakowski, L.F.
J. Biol. Chem. 269, 29355-29358, 1994
A:Title: The murine interleukin 8 type B receptor homologue and its ligand
A:Reference number: I55421; MUID:95050766
A:Accession: I55421
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-359 <RE2>
A:Cross-references: GB:I13239; NID:g293665; PIDN:AAA62109.1; PID:g293666
R:Wilkie, T.M.; Chen, Y.; Gilbert, D.J.; Moore, K.J.; Yu, L.; Simon, M.I.;
Genomics 18, 175-184, 1993
A:Title: Identification, chromosomal location, and genome organization of
A:Reference number: A48909; MUID:94116980
A:Accession: H48909
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 145-258 <WIL>
A:Cross-references: GB:I20337; NID:g438800; PIDN:AAA16853.1; PID:g438801
R:Harada, A.; Kuno, K.; Nomura, H.; Mukaida, N.; Murakami, S.; Matsushima,
Gene 142, 297-300, 1994
A:Title: Cloning of a cDNA encoding a mouse homolog of the interleukin-8 r
A:Reference number: I53774; MUID:94252584
A:Accession: I53774
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-359 <RE3>
A:Cross-references: GB:J17630; NID:g493671; PIDN:BAAO4536.1; PID:g493672

C; Superfamily: vertebrate rhodopsin
C; Keywords: G protein-coupled receptor; glycoprotein; transmembrane protein
F; 49-74/Domain: transmembrane #status predicted <TM1>
F; 84-106/Domain: transmembrane #status predicted <TM2>
F; 120-141/Domain: transmembrane #status predicted <TM3>
F; 163-182/Domain: transmembrane #status predicted <TM4>
F; 213-234/Domain: transmembrane #status predicted <TM5>
F; 251-271/Domain: transmembrane #status predicted <TM6>
F; 308-328/Domain: transmembrane #status predicted <TM7>

Query Match 59.7%; Score 71; DB 2; Length 359;
Best Local Similarity 70.0%; Pred. No. 0.0054;
Matches 14; Conservative 3; Mismatches 3; Indels 0; Gaps

QY 1 VIIAVLVFLACQIPHNVL 20
|| ||||| | :|:|:|
DB 251 VIFAVLVFLCLWPNLVL 270

RESULT 8
S42096
interleukin-8 receptor - rat
C; Species: Rattus norvegicus (Norway rat)
C; Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 26-Aug-1999
C; Accession: S42096
R; Gobl, A.E.; Wang, S.; Zhou, Y.; Oeberg, K.
submitted to the EMBL Data Library, February 1994
A; Description: Molecular cloning of the rat IL8 receptor.
A; Reference number: S42096
A; Accession: S42096
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-356 <GOB>
A; Cross-references: EMBL:X77797
C; Superfamily: vertebrate rhodopsin
C; Keywords: G protein-coupled receptor; transmembrane protein

Query Match 58.8%; Score 70; DB 2; Length 356;
Best Local Similarity 70.0%; Pred. No. 0.0075;
Matches 14; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 VTIATVVLFLACQIPHNWVL 20
|||||:|:| |:|:| |:
DB 251 VIFAVVVLFLCLWLPYNI 270

RESULT 9

G protein-coupled peptide receptor EBI 1 - human
C:Species: Homo sapiens (man)
C:Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 24-Nov-1999
C:Accession: A45680
R:Birkenbach, M.; Josefsen, K.; Yalamanchili, R.; Lenoir, G.; Kieff, E.
J. Virol. 67, 2209-2220, 1993
A:Title: Epstein-Barr virus-induced genes: first lymphocyte-specific G protein-coupled R
A:Reference number: A45680; MUID:93188173
A:Accession: A45680
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-378 <BIR>
A:Cross-references: GB:L08176; NID:g183484; PID:g183485
A:Experimental source: B-lymphocytes
A:Note: sequence extracted from NCBI backbone (NCBI:127094, NCBI:P:127095)
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 52.9%; Score 63; DB 2; Length 378;
Best Local Similarity 61.9%; Pred. No. 0.081;
Matches 13; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 VTIATVVLFLACQIPHNWVL 21
|||||:|:| |:|:| |:
DB 264 VTIATVVLFLCLWLPYNI 284

RESULT 10

B55735
Lymphocyte-specific G protein-coupled receptor EBI1 - human
N:Alternate names: Burkitt's lymphoma receptor 2; Epstein-Barr virus induced protein 1
C:Species: Homo sapiens (man)
C:Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 19-May-2000
C:Accession: B55735; S52443
R:Schweickart, V.L.; Raport, C.J.; Godiska, R.; Byers, M.G.; Eddy Jr., R.L.; Shows, T.B.
Genomics 23, 643-650, 1994
A:Title: Cloning of human and mouse EBI1, a lymphoid-specific G-protein-coupled receptor
A:Reference number: A55735; MUID:95154835
A:Accession: B55735
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-378 <SCH>
A:Cross-references: GB:L31581; NID:g468319; PIDN:AAA74231.1; PID:g468320
R:Burgstahler, R.; Kempkes, B.; Staube, K.; Lipp, M.
submitted to the EMBL Data Library, February 1995
A:Description: The expression of the chemokine receptor BLR2/EBI1 is specifically trans
A:Reference number: S52443
A:Accession: S52443
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 21-378 <BUR>
A:Cross-references: EMBL:X84702
C:Genetics:
A:Gene: GDB:CMKBR7; EBI1; BLR2; CCR7
A:Cross-references: GDB:342065; OMIM:600242
A:Map position: 17q12-17q21.2
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor

Query Match 52.9%; Score 63; DB 2; Length 378;
Best Local Similarity 61.9%; Pred. No. 0.081;
Matches 13; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 VIIAVVVLFLACQIPHNWVL 21
|||||:|:| |:|:| |:
DB 264 VIIAVVVLFLCLWLPYNI 284

RESULT 11

A55735
G protein-coupled receptor EBI1 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 24-Nov-1999
C:Accession: A55735
R:Schweickart, V.L.; Raport, C.J.; Godiska, R.; Byers, M.G.; Eddy Jr., R.L.; Shows, T.
Genomics 23, 643-650, 1994
A:Title: Cloning of human and mouse EBI1, a lymphoid-specific G-protein-coupled recep
A:Reference number: A55735; MUID:95154835
A:Accession: A55735
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-378 <SCH>
A:Cross-references: GB:L31580; NID:g468340; PIDN:AAA74232.1; PID:g468341
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor

Query Match 52.9%; Score 63; DB 2; Length 378;
Best Local Similarity 61.9%; Pred. No. 0.081;
Matches 13; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 VIIAVVVLFLACQIPHNWVL 21
|||||:|:| |:|:| |:
DB 264 VIIAVVVLFLCLWLPYNI 284

RESULT 12

JC5653
G protein-coupled receptor - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 17-Nov-1997 #sequence_revision 17-Nov-1997 #text_change 21-Jul-2000
C:Accession: JC5653
R:Freder-Martinez, A.; Felipe, A.; Mata, J.F.; Casado, F.J.; Pastor-Anglada, M.
Biochem. Biophys. Res. Commun. 238, 107-112, 1997
A:Title: Molecular cloning of a bovine renal G-protein coupled receptor gene (bRGR):
A:Reference number: JC5653; MUID:97445134
A:Accession: JC5653
A:Molecule type: mRNA
A:Residues: 1-361 <FER>
A:Cross-references: GB:U88366; NID:g2827875; PIDN:AAC05611.1; PID:g2827876
A:Experimental source: renal epithelial cell
C:Superfamily: G protein-coupled receptor 4
C:Keywords: glycoprotein; phosphoprotein
F:24-46/Domain: transmembrane #status predicted <TM1>
F:58-79/Domain: transmembrane #status predicted <TM2>
F:96-117/Domain: transmembrane #status predicted <TM3>
F:137-159/Domain: transmembrane #status predicted <TM4>
F:189-207/Domain: transmembrane #status predicted <TM5>
F:229-253/Domain: transmembrane #status predicted <TM6>
F:265-289/Domain: transmembrane #status predicted <TM7>
F:3-8,62/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:134,218,293,313/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #sta
F:204,221,328/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status

Query Match 51.3%; Score 61; DB 2; Length 361;
Best Local Similarity 40.9%; Pred. No. 0.15;
Matches 9; Conservative 11; Mismatches 2; Indels 0; Gaps 0;

QY 1 VIIAVVVLFLACQIPHNWVL 22
||||:|:| |:|:| |:
DB 229 LVLTSTWIFLCLWLPYNI 250

RESULT 13

S68208

G protein-coupled receptor 12A - human

C:Species: Homo sapiens (man)

C>Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 29-Sep-1999

C:Accession: S68208

R:An, S.; Tsai, C.; Goetzl, E.J.

FEBS Lett. 375, 121-124, 1995

A:Title: Cloning, sequencing and tissue distribution of two related G protein-coupled re

A:Reference number: S68207; MUID:96087098

A:Accession: S68208

A:Status: preliminary; nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-365 <ANS>

A:Cross-references: EMBL:U35398; NID:gl1015418; PIDN:AAA79060.1; PID:gl1015419

C:Superfamily: G protein-coupled receptor 4

C:Keywords: G protein-coupled receptor

Query Match 51.3%; Score 61; DB 2; Length 365;
Best Local Similarity 40.9%; Pred. No. 0.15;
Matches 11; Conservative 11; Mismatches 2; Indels 0; Gaps 0;

Qy 1 VIIAVLVFLACQIPHNMLLV 22

::: |::||| |::|||

Db 229 LVLSNVVFLACFLPYHVLV 250

RESULT 14

G02670

IL8-related receptor - human

C:Species: Homo sapiens (man)

C>Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 24-Nov-1999

C:Accession: G02670

R:McCoy, R.L.; Perlmuter, D.H.

submitted to the EMBL Data Library, May 1996

A:Reference number: H01575

A:Accession: G02670

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-358 <MCC>

A:Cross-references: EMBL:U58928; NID:gl1381668; PIDN:AAB02736.1; PID:gl1381669

C:Genetics:

A:Gene: DRV12

C:Superfamily: vertebrate rhodopsin

Query Match 49.6%; Score 59; DB 2; Length 358;
Best Local Similarity 50.0%; Pred. No. 0.29;
Matches 11; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

Qy 1 VIIAVLVFLACQIPHNMLLV 22

:|:||||| |::|||

Db 243 MILAVLVFFVCWLPENVFISV 264

RESULT 15

JC5069

G protein-coupled receptor CMKRL2 - human

N:Alternate names: constitutively expressed peptide-like receptor; flow-induced endothel

C:Species: Homo sapiens (man)

C>Date: 31-Jan-1997 #sequence_revision 28-Aug-1998 #text_change 21-Jul-2000

C:Accession: JC5069; JC5786; JC5294

R:Oman, C.; Blay, P.; Nilsson, C.; Lolait, S.J.

Biochem. Biophys. Res. Commun. 228, 285-292, 1996

A:Title: Cloning of human cDNA encoding a novel heptahelix receptor expressed in Burkitt

A:Reference number: JC5069; MUID:97079175

A:Accession: JC5069

A:Molecule type: mRNA

A:Residues: 1-375 <OWN>

A:Cross-references: GB:Y08162; NID:gl1707499; PIDN:CAA69354.1; PID:gl1707500

A:Experimental source: B-cell lymphoblast
R:Takada, Y.; Kato, C.; Kondo, S.; Korenaga, R.; Ando, J.
Biochem. Biophys. Res. Commun. 240, 737-741, 1997
A:Title: Cloning of cDNAs encoding G protein-coupled receptor expressed in human endo
A:Reference number: JC5786; MUID:98063308
A:Accession: JC5786
A:Molecule type: mRNA
A:Residues: 1-375 <TAK>
A:Cross-references: GB:AF015257; NID:g2353152; PIDN:AAC51904.1; PID:g2353153
A:Experimental source: umbilical vein endothelial cell
R:Feng, Y.; Gregor, P.
Biochem. Biophys. Res. Commun. 231, 651-654, 1997
A:Title: Cloning of a novel member of the G protein-coupled receptor family related t
A:Reference number: JC5294; MUID:97224403
A:Accession: JC5294
A:Molecule type: DNA
A:Residues: 1-311, 'T', 313-375 <FEN>
A:Cross-references: GB:U77827; NID:g1906591; PIDN:AAC51173.1; PID:g1906592
C:Comment: This protein plays a role in B-cell functions and is involved in endotheli
C:Genetics:
A:Gene: GDB:CMKRL2; CEPR
A:Cross-references: GDB:3929190
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; glycoprotein; transmembrane protein
F:64-83/Domain: transmembrane #status predicted <TM1>
F:96-114/Domain: transmembrane #status predicted <TM2>
F:126-148/Domain: transmembrane #status predicted <TM3>
F:180-198/Domain: transmembrane #status predicted <TM4>
F:221-238/Domain: transmembrane #status predicted <TM5>
F:260-283/Domain: transmembrane #status predicted <TM6>
F:308-327/Domain: transmembrane #status predicted <TM7>
F:25,32,44/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 49.6%; Score 59; DB 2; Length 375;
Best Local Similarity 50.0%; Pred. No. 0.3;
Matches 11; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

Qy 1 VIIAVLVFLACQIPHNMLLV 22

:|:||||| |::|||

Db 260 MILAVLVFFVCWLPENVFISV 281

Search completed: May 23, 2001, 15:32:02
Job time: 509 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 23, 2001, 15:36:20 ; Search time 62.39 Seconds
(without alignments)

13.726 Million cell updates/sec

Title: US-08-887-977-10_COPY_246_270

Perfect score: 119

Sequence: 1 VITAVLVFLACQIPHNVLVTAA 25

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Match	Length	DB	ID	Description
1	119	100.0	374	1	CKR6_HUMAN	P51684	homo sapien
2	114	95.8	367	1	CKR6_MOUSE	O54689	mus musculus
3	74	62.2	349	1	IL8A_RAT	P70612	rattus norv
4	74	62.2	350	1	IL8A_GORGO	P55919	gorilla gor
5	74	62.2	350	1	IL8A_HUMAN	P25024	homo sapien
6	74	62.2	350	1	IL8A_PANTR	P55920	pan troglod
7	74	62.2	353	1	IL8B_GORGO	Q28422	gorilla gor
8	74	62.2	353	1	IL8B_PANTR	Q28807	pan troglod
9	74	62.2	355	1	IL8A_RABIT	P21109	oryctolagus
10	74	62.2	358	1	IL8B_RABIT	P35344	oryctolagus
11	74	62.2	360	1	IL8B_HUMAN	P25025	homo sapien
12	73	61.3	360	1	IL8B_BOVIN	Q28003	bos taurus
13	71	59.7	359	1	IL8B_MOUSE	P35343	mus musculus
14	70	58.8	359	1	IL8B_RAT	P35407	rattus norv
15	69	58.0	353	1	IL8B_MACMU	Q28519	macaca mula
16	67	56.3	356	1	IL8B_CANFA	O97571	canis famil
17	63	52.9	378	1	CKR7_HUMAN	P32248	homo sapien
18	63	52.9	378	1	CKR7_MOUSE	P47774	mus musculus
19	61	51.3	365	1	GP68_HUMAN	Q17543	homo sapien
20	59	49.6	375	1	CM12_HUMAN	O99527	homo sapien
21	57	47.9	362	1	CKRA_MOUSE	O99121	mus musculus
22	56	47.1	362	1	RDC1_CANFA	P11613	canis famil
23	56	47.1	363	1	AG2S_XENLA	P35373	xenopus lae
24	56	47.1	375	1	CM12_RAT	O08878	rattus norv
25	55	46.2	354	1	US28_HCMVA	P09704	human cytom
26	55	46.2	362	1	CKRA_HUMAN	P46092	homo sapien
27	55	46.2	362	1	RDC1_MOUSE	P56485	mus musculus
28	55	46.2	362	1	RDC1_RAT	O89039	rattus norv
29	55	46.2	369	1	CKR9_MOUSE	Q9WU77	mus musculus
30	54	45.8	473	1	C3AR_RAT	O55197	rattus norv
31	54	45.4	349	1	OPSP_COLLI	P51476	columba liv
32	54	45.4	350	1	GUSB_BOVIN	P35350	bos taurus
33	54	45.4	357	1	CKR9_HUMAN	P51686	homo sapien

RESULT 1

ID	CKR6_HUMAN	STANDARD;	PRT;	374 AA.
AC	P51684: Q92846; P78553;			
DT	01-OCT-1996 (Rel. 34, Created)			
DT	15-JUL-1998 (Rel. 36, Last sequence update)			
DT	01-OCT-2000 (Rel. 40, Last annotation update)			
DE	C-C CHEMOKINE RECEPTOR TYPE 6 (C-C CKR-6) (CCR-6) (LARC			
DE	RECEPTOR) (GPR-CY4) (GPCY4) (CHEMOKINE RECEPTOR-LIKE 3) (CKR-L3)			
DE	(DRY6).			
GN	CCR6 OR CMKBR6 OR STRL22 OR GPR29 OR CKRL3.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RX	SEQUENCE FROM N.A., AND FUNCTION.			
RX	MEDLINE=97313465; PubMed=9169459;			
RA	Baba M., Imai T., Nishimura M., Kakizaki M., Takagi S., Hieshima K.,			
RA	Nomiya H., Yoshie O.;			
RT	"Identification of CCR6, the specific receptor for a novel			
RT	lymphocyte-directed CC chemokine LARC.";			
RL	J. Biol. Chem. 272:14893-14898(1997).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RP	Lautens L.L., Modi W., Bonner T.L.;			
RL	Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=97040707; PubMed=8886020;			
RA	Zaballos A., Varona R., Gutierrez J., Lind P., Marquez G.;			
RT	"Molecular cloning and RNA expression of two new human chemokine			
RT	receptor-like genes.";			
RL	Biochem. Biophys. Res. Commun. 227:846-853(1996).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RP	McCoy R., Perlmutter D.H.;			
RL	Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=97224503; PubMed=9070937;			
RA	Liao F., Lee H.-H., Farber J.M.;			
RT	"Cloning of STRL22, a new human gene encoding a G-protein-coupled			
RT	receptor related to chemokine receptors and located on chromosome			
RT	6q27.";			
RL	Genomics 40:175-180(1997).			
CC	-!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-3-			
CC	ALPHA/LARC AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE			
CC	INTRACELLULAR CALCIUM IONS LEVEL.			
CC	-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.			
CC	-!- TISSUE SPECIFICITY: SPLEEN, LYMPH NODES, APPENDIX, AND FETAL			
CC	LIVER. EXPRESSED IN LYMPHOCYTES, T CELLS AND B CELLS BUT NOT IN			
CC	NATURAL KILLER CELLS, MONOCYTES, OR GRANULOCYTES.			
CC	-!- INDUCTION: INTERLEUKIN-2.			
CC	-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.			
CC	-!- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-6 IS THE INITIATOR.			

P21556 cavia porce
O08858 mus musculus
P30938 rattus norv
O09047 mus musculus
P51475 gallus gall
P25106 homo sapien
O54814 rattus norv
P49682 homo sapien
Q62035 mus musculus
P25105 homo sapien
P51682 mus musculus
O08556 rattus norv

34 53 44.5 342 1 PAFR_CAVPO
35 53 44.5 362 1 SSR5_MOUSE
36 53 44.5 363 1 SSR5_RAT
37 52.5 44.1 477 1 C3AR_MOUSE
38 52 43.7 351 1 OPSP_CHICK
39 52 43.7 362 1 RDC1_HUMAN
40 51 42.9 359 1 CCR3_RAT
41 51 42.9 368 1 CCR3_HUMAN
42 50 42.0 341 1 PAFR_MOUSE
43 50 42.0 342 1 PAFR_HUMAN
44 50 42.0 354 1 CKR5_MOUSE
45 50 42.0 354 1 CKR5_RAT

ALIGNMENTS

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EMBL; U45984; AAB62714.1; -
EMBL; Z79784; CAB02144.1; ALT_INIT.
EMBL; U60000; AAB06949.1; -
EMBL; U68030; AAC51124.1; -
EMBL; U68032; AAC51125.1; -
DR HSP; P34966; IDDD.
DR GCRDB; GCR_1037; -
DR GCRDB; GCR_1075; -
DR GCRDB; GCR_1906; -
DR GCRDB; GCR_1919; -
DR GCRDB; GCR_1941; -
DR GCRDB; GCR_2110; -
DR MIM; 601835; -
DR InterPro: IPR000276; -
DR Pfam: PF00001; 7tm1.1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 47 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 48 74 1 (POTENTIAL).
FT DOMAIN 75 83 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 84 104 2 (POTENTIAL).
FT DOMAIN 105 119 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 120 141 3 (POTENTIAL).
FT DOMAIN 142 159 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 160 180 4 (POTENTIAL).
FT DOMAIN 181 211 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 212 238 5 (POTENTIAL).
FT DOMAIN 239 254 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 255 279 6 (POTENTIAL).
FT DOMAIN 280 303 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 304 321 7 (POTENTIAL).
FT DOMAIN 322 374 BY SIMILARITY.
FT DISULFID 118 197 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 7 7 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 23 23 G -> A (IN REF. 4).
FT CONFLICT 60 60 Y -> N (IN REF. 4).
FT CONFLICT 74 74 L -> V (IN REF. 4).
FT CONFLICT 86 86 S -> T (IN REF. 5).
FT CONFLICT 164 164 T -> S (IN REF. 4).
FT CONFLICT 182 182 Q -> L (IN REF. 4).
FT CONFLICT 192 192 E -> V (IN REF. 4).
FT CONFLICT 206 206 I -> F (IN REF. 4).
FT CONFLICT 225 225 SPTM -> VLVHVIIES (IN REF. 4).
FT CONFLICT 370 374
FT SEQUENCE 374 AA; 42494 MR; D7F963534E990BC4 CRC64;
Query Match 100.0%; Score 119; DB 1; Length 374;
Best Local Similarity 100.0%; Pred. No. 9,1e-10;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VIIAVLVFLACQIPHNVLVTA 25
DB 255 VIIAVLVFLACQIPHNVLVTA 279
RESULT 2
ID CKR6_MOUSE STANDARD; PRT; 367 AA.
AC O54689;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE C-C CHEMOKINE RECEPTOR TYPE 6 (C-C CKR-6) (CCR-6) (KY411).
GN CCR6 OR CMKBR6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Yanagihara S., Komura E., Yamaguchi Y.;
RT "Mouse G protein-coupled receptor Ky411.";
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99077268; PubMed=9862452;
RA Varona R., Zaballós A., Gutierrez J., Martín P., Roncal F.,
RA Albar J.P., Ardavin C., Marquez G.;
RT "Molecular cloning, functional characterization and mRNA expression
RT analysis of the murine chemokine receptor CCR6 and its specific ligand
RT MIP-3alpha.";
RL FEBS Lett. 440:188-194 (1998).
CC -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-3-
CC ALPHA/LARC AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE
CC INTRACELLULAR CALCIUM IONS LEVEL.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----
DR EMBL; AB009369; BAA23776.1; -
DR EMBL; AJ227114; CAA10956.1; -
DR MGD; MGI:133379; Cmkbr6.
DR InterPro: IPR000276; -
DR Pfam; PF00001; 7tm1.1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 39 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 40 66 1 (POTENTIAL).
FT DOMAIN 67 75 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 76 96 2 (POTENTIAL).
FT DOMAIN 97 111 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 112 133 3 (POTENTIAL).
FT DOMAIN 134 151 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 152 172 4 (POTENTIAL).
FT DOMAIN 173 203 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 204 230 5 (POTENTIAL).
FT DOMAIN 231 246 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 247 271 6 (POTENTIAL).
FT DOMAIN 272 295 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 296 313 7 (POTENTIAL).
FT DOMAIN 314 367 CYTOPLASMIC (POTENTIAL).
FT DISULFID 110 189 BY SIMILARITY.
FT CARBOHYD 2 2 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 35 35 N-LINKED (GLCNAC...) (POTENTIAL).
FT SEQUENCE 367 AA; 42102 MW; 6A309AF833B1117E CRC64;
Query Match 95.8%; Score 114; DB 1; Length 367;
Best Local Similarity 95.8%; Pred. No. 4,5e-09;
Matches 23; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 VIIAVLVFLACQIPHNVLVTA 24
DB 247 VIIAVLVFLACQIPHNVLVTA 270

```
RESULT 3
IL8A_RAT
ID IL8A_RAT STANDARD; PRT; 349 AA.
AC P70612,
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE HIGH AFFINITY INTERLEUKIN-8 RECEPTOR A (IL-8R A) (CXCR-1).
GN IL8A OR CXCR1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
ON NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC SPRAIN-WISTAR; TISSUE=Lung;
RX MEDLINE=97115810; PubMed=8955112;
RA Dunstan C.-A.N., Salafra M.N., Adhikari S., Xia Y., Feng L.,
RA Harrison J.K.;
RT "Identification of two rat genes orthologous to the human
interleukin-8 receptors";
RL J. Biol. Chem. 271:32770-32776(1996).
CC -1- FUNCTION: RECEPTOR TO INTERLEUKIN-8, WHICH IS A POWERFUL
CC NEUTROPHILS CHEMOTACTIC FACTOR. BINDING OF IL-8 TO THE RECEPTOR
CC CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA A
CC G-PROTEIN THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND
CC MESSENGER SYSTEM (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC
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CC
CC EMBL; U71089; AAC52962.1; -
CC HSPSP; P34996; IIDD.
CC GCRDB; GCR_1404; -
CC InterPro; IPR000276; -
CC Pfam; PF00001; 7tm.1; 1.
CC PRINTS; PR00237; GPCRHHODOPSN.
CC PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
CC PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein;
CC Chemotaxis.
CC
CC DOMAIN 1 44 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 45 71 1 (POTENTIAL).
CC DOMAIN 72 80 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 81 101 2 (POTENTIAL).
CC DOMAIN 102 116 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 117 138 3 (POTENTIAL).
CC DOMAIN 139 159 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 160 179 4 (POTENTIAL).
CC DOMAIN 180 204 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 205 225 5 (POTENTIAL).
CC DOMAIN 226 247 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 248 269 6 (POTENTIAL).
CC DOMAIN 270 290 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 291 313 7 (POTENTIAL).
CC DOMAIN 314 349 CYTOPLASMIC (POTENTIAL).
CC CARBOHYD 22 22 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC DISULFID 115 192 BY SIMILARITY.
CC SEQUENCE 349 AA; 39944 MW; 9B1CDCE61568EABA CRC64;
Query Match 62.2%; Score 74; DB 1; Length 349;
Best Local Similarity 71.4%; Pred. No. 0.0017;
Matches 15; Conservative 3; Mismatches 3; Indels 0; Gaps. 0;
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QY 1 VIIAVLVFLACQIPHNMLL 21
II IIIIIII I :I:I:II
Db 248 VIFAVLVFLCCLPYNLVLL 268

RESULT 4
IL8A_GORGO
ID IL8A_GORGO STANDARD; PRT; 350 AA.
AC P55919; P55921;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE HIGH AFFINITY INTERLEUKIN-8 RECEPTOR A (IL-8R A) (IL-8 RECEPTOR TYPE
DE 1) (CXCR-1) (CDW128).
GN IL8A OR CXCR1.
OS Gorilla gorilla gorilla (Lowland gorilla), and
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
ON NCBI_TaxID=9595, 9600;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96175151; PubMed=9110929;
RA Alvarez V., Coto E., Setien F., Gonzalez S., Gonzalez-Roces S.,
RA Lopez-Larrea C.;
RT "Characterization of interleukin-8 receptors in non-human primates.";
RL Immunogenetics 43:261-267(1996).
CC -1- FUNCTION: RECEPTOR TO INTERLEUKIN-8, WHICH IS A POWERFUL
CC NEUTROPHILS CHEMOTACTIC FACTOR. BINDING OF IL-8 TO THE RECEPTOR
CC CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA A
CC G-PROTEIN THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND
CC MESSENGER SYSTEM. THIS RECEPTOR BINDS TO IL-8 WITH A HIGH AFFINITY
CC AND TO MSGA (GRO) WITH A LOW AFFINITY.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; X91110; CAB37671.1; -
CC HSPSP; P34996; IIDD.
CC InterPro; IPR000174; -
CC InterPro; IPR000276; -
CC InterPro; IPR001355; -
CC Pfam; PF00001; 7tm.1; 1.
CC PRINTS; PR00237; GPCRHHODOPSN.
CC PRINTS; PR00427; INTRLEUKIN8R.
CC PRINTS; PR00572; INTRLEUKIN8R.
CC PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
CC PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein;
CC Chemotaxis.
CC
CC DOMAIN 1 39 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 40 66 1 (POTENTIAL).
CC DOMAIN 67 75 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 76 96 2 (POTENTIAL).
CC DOMAIN 97 111 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 112 133 3 (POTENTIAL).
CC DOMAIN 134 154 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 155 174 4 (POTENTIAL).
CC DOMAIN 175 199 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 200 220 5 (POTENTIAL).
CC DOMAIN 221 242 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 243 264 6 (POTENTIAL).
CC DOMAIN 265 285 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 286 308 7 (POTENTIAL).
CC DOMAIN 309 350 CYTOPLASMIC (POTENTIAL).
CC CARBOHYD 3 3 N-LINKED (GLCNAC. . .) (POTENTIAL).
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Db 243 VIFAVLFLCWLPLYNVLL 263

RESULT 6
IL8A_PANTR
ID IL8A_PANTR STANDARD; PRT; 350 AA.
AC P55920;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE HIGH AFFINITY INTERLEUKIN-8 RECEPTOR A (IL-8R A) (IL-8 RECEPTOR TYPE
DE 1) (CXCR-1) (CDW128).
GN IL8RA OR CXCR1.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96175151; PubMed=9110929;
RA Alvarez V., Coto E., Setien F., Gonzalez S., Gonzalez-Roces S.,
RA Lopez-Larrea C.;
RT "Characterization of interleukin-8 receptors in non-human primates.";
RL Immunogenetics 43:261-267(1996).
CC -!- FUNCTION: Receptor to interleukin-8, which is a powerful
CC NEUTROPHILS CHEMOTACTIC FACTOR. BINDING OF IL-8 TO THE RECEPTOR
CC CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA A
CC G-PROTEIN THAT ACTIVATES A PHOSPHATIDYLINOSITOL-CALCIUM SECOND
CC MESSENGER SYSTEM. THIS RECEPTOR BINDS TO IL-8 WITH A HIGH AFFINITY
CC AND TO MGSA (GRO) WITH A LOW AFFINITY.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; X91109; ; NOT_ANNOTATED_CDS.
CC HSSP; P34996; 1DDO.
CC InterPro; IPR000174; ;
CC InterPro; IPR000276; ;
CC InterPro; IPR001355; ;
CC Pfam; PF00001; 7tm_1; 1.
CC PRINTS; PR00237; GPCRHHODOPSN.
CC PRINTS; PR00427; INTRLEUKIN8R.
CC PRINTS; PR00572; INTRLEUKIN8R.
CC PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
CC PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein;
CC Chemotaxis.
KW DOMAIN 1 39 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 40 66 1 (POTENTIAL).
FT DOMAIN 67 75 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 76 96 2 (POTENTIAL).
FT DOMAIN 97 111 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 112 133 3 (POTENTIAL).
FT DOMAIN 134 154 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 155 174 4 (POTENTIAL).
FT DOMAIN 175 199 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 200 220 5 (POTENTIAL).
FT DOMAIN 221 242 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 243 264 6 (POTENTIAL).
FT DOMAIN 265 285 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 286 308 7 (POTENTIAL).
FT DOMAIN 309 350 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 3 3 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 16 16 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 110 187 BY SIMILARITY.

SQ SEQUENCE 350 AA; 39818 MW; A56FD0246E1D440 CRC64;

Query Match 62.2%; Score 74; DB 1; Length 350;
Best Local Similarity 66.7%; Pred. No. 0.0017;
Matches 14; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 VITAVLVFLACQIPHNVL 21
II IIII:II I :I:IIII
Db 243 VIFAVLFLCWLPLYNVLL 263

RESULT 7
IL8B_GORGO
ID IL8B_GORGO STANDARD; PRT; 353 AA.
AC O28472;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE HIGH AFFINITY INTERLEUKIN-8 RECEPTOR B (IL-8R B) (CXCR-2) (FRAGMENT).
GN IL8RB OR CXCR2.
OS Gorilla gorilla gorilla (Lowland gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
OX NCBI_TaxID=9595;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96175151; PubMed=9110929;
RA Alvarez V., Coto E., Setien F., Gonzalez S., Gonzalez-Roces S.,
RA Lopez-Larrea C.;
RT "Characterization of interleukin-8 receptors in non-human primates.";
RL Immunogenetics 43:261-267(1996).
CC -!- FUNCTION: RECEPTOR TO INTERLEUKIN-8, WHICH IS A POWERFUL
CC NEUTROPHILS CHEMOTACTIC FACTOR. BINDING OF IL-8 TO THE RECEPTOR
CC CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA A
CC G-PROTEIN THAT ACTIVATES A PHOSPHATIDYLINOSITOL-CALCIUM SECOND
CC MESSENGER SYSTEM. THIS RECEPTOR BINDS TO IL-8 WITH A HIGH AFFINITY
CC AND TO GRO/MGSA AND NAP-2 ALSO WITH A HIGH AFFINITY.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; X91114; CAA62564.1; ;
CC HSSP; P34996; 1DDO.
CC InterPro; IPR000276; ;
CC Pfam; PF00001; 7tm_1; 1.
CC PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
CC PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein;
CC Chemotaxis.
KW DOMAIN 1 1 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM <1 45 1 (POTENTIAL).
FT DOMAIN 46 72 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 73 81 2 (POTENTIAL).
FT TRANSMEM 82 102 3 (POTENTIAL).
FT DOMAIN 103 117 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 118 139 4 (POTENTIAL).
FT DOMAIN 140 160 5 (POTENTIAL).
FT TRANSMEM 161 180 6 (POTENTIAL).
FT DOMAIN 181 205 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 206 228 7 (POTENTIAL).
FT DOMAIN 229 248 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 249 270 8 (POTENTIAL).
FT DOMAIN 271 291 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 292 312 9 (POTENTIAL).
FT DOMAIN 313 >353 CYTOPLASMIC (POTENTIAL).
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FT DISULFID 116 193 BY SIMILARITY.
 FT CARBOHYD 19 19 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT NON_TER 353 353
 SQ SEQUENCE 353 AA; 39919 MW; 1FF04E31A7E825E4 CRC64;
 Query Match 62.2%; Score 74; DB 1; Length 353;
 Best Local Similarity 66.7%; Pred. No. 0.0017;
 Matches 14; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
 QY 1 VIIAVLVFLACOIPHNWLL 21
 || ||||| || | : | : ||||
 Db 249 VIFAVVLFLCWLPLYNLVL 269
 RESULT 8
 IL8B_PANTR STANDARD; PRT; 353 AA.
 AC Q28807;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE HIGH AFFINITY INTERLEUKIN-8 RECEPTOR B (IL-8R B) (CXCR-2) (FRAGMENT).
 GN IL8RB OR CXCR2.
 OS Pan troglodytes (Chimpanzee).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
 OX NCBI_TaxID=9598;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96175151; PubMed=9110929;
 RA Alvarez V., Coto E., Setien F., Gonzalez-Roces S.,
 RA Lopez-Larrea C.;
 RT "Characterization of interleukin-8 receptors in non-human primates.";
 RL Immunogenetics 43:261-267(1996).
 CC -!- FUNCTION: RECEPTOR TO INTERLEUKIN-8, WHICH IS A POWERFUL
 CC NEUTROPHILS CHEMOTACTIC FACTOR. BINDING OF IL-8 TO THE RECEPTOR
 CC CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA A
 CC G-PROTEIN THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND
 CC MESSENGER SYSTEM. THIS RECEPTOR BINDS TO IL-8 WITH A HIGH AFFINITY
 CC AND TO GRO/MGSA AND NAP-2 ALSO WITH A HIGH AFFINITY.
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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 CC -----
 CC EMBL; X91113; CAA62563.1; -
 DR HSSP; P34996; IDDD.
 DR InterPro; IPR000276; -
 DR Pfam; PF00001; 7tm1.1;
 DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL1; 1.
 DR PROSITE; PS00262; G-PROTEIN RECEPTOR FL2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 FT NON_TER 1 1
 FT DOMAIN <1 45 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 46 72 1 (POTENTIAL).
 FT DOMAIN 73 81 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 82 102 2 (POTENTIAL).
 FT DOMAIN 103 117 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 118 139 3 (POTENTIAL).
 FT DOMAIN 140 160 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 161 180 4 (POTENTIAL).
 FT DOMAIN 181 205 5 (POTENTIAL).
 FT TRANSMEM 206 228 6 (POTENTIAL).
 FT DOMAIN 229 248
 FT TRANSMEM 249 270

FT DOMAIN 271 291 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 292 312 7 (POTENTIAL).
 FT DOMAIN 313 >353 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 116 193 BY SIMILARITY.
 FT CARBOHYD 19 19 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT NON_TER 353 353
 SQ SEQUENCE 353 AA; 39998 MW; E745ACD9EC10C1E2 CRC64;
 Query Match 62.2%; Score 74; DB 1; Length 353;
 Best Local Similarity 66.7%; Pred. No. 0.0017;
 Matches 14; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
 QY 1 VIIAVLVFLACOIPHNWLL 21
 || ||||| || | : | : ||||
 Db 249 VIFAVVLFLCWLPLYNLVL 269
 RESULT 9
 IL8A_RABIT STANDARD; PRT; 355 AA.
 AC P21109;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE HIGH AFFINITY INTERLEUKIN-8 RECEPTOR A (IL-8R A) (CXCR-1).
 GN IL8RA OR CXCR1.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91378994; PubMed=1898400;
 RA Beckmann M.P., Munger W.E., Kozlosky C., Vandenbos T., Price V.,
 RA Lyman S., Gerard N.P., Gerard C., Cerretti D.P.;
 RT "Molecular characterization of the interleukin-8 receptor.";
 RL Biochem. Biophys. Res. Commun. 179:784-789(1991).
 CC [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ALBINO; TISSUE=Neutrophils;
 RX MEDLINE=91056034; PubMed=1700779;
 RA Thomas K.M., Pyun H.Y., Navarro J.;
 RT "Molecular cloning of the fmet-Leu-Phe receptor from neutrophils.";
 RL J. Biol. Chem. 265:20061-20064(1990).
 CC [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Neutrophils;
 RX MEDLINE=92148149; PubMed=1737938;
 RA Lee J., Kuang W.-J., Rice G.C., Wood W.I.;
 RT "Characterization of complementary DNA clones encoding the rabbit
 RT IL-8 receptor.";
 RL J. Immunol. 148:1261-1264(1992).
 CC -!- FUNCTION: RECEPTOR TO INTERLEUKIN-8, WHICH IS A POWERFUL
 CC NEUTROPHILS CHEMOTACTIC FACTOR. BINDING OF IL-8 TO THE RECEPTOR
 CC CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA A
 CC G-PROTEIN THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND
 CC MESSENGER SYSTEM.
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -!- TISSUE SPECIFICITY: NEUTROPHILS.
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -!- CAUTION: WAS ORIGINALLY (REF.2) THOUGHT TO BE THE RECEPTOR FOR
 CC FMET-LEU-PHE (N-FORMYL PEPTIDE RECEPTOR).
 CC -----
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 CC -----
 CC EMBL; M74240; AAA31375.1; -

EMBL; M58021; AAA31377.1; -
EMBL; M82873; AAA31376.1; -
PIR; A23669; A23669.
PIR; A46483; A46483.
PIR; JQ1231; JQ1231.
GCRDB; GCR_0107; -
GCRDB; GCR_0108; -
GCRDB; GCR_0298; -
InterPro; IPR0001174; -
InterPro; IPR000276; -
InterPro; IPR001355; -
Pfam; PF00001; 7tm.1; 1.
PRINTS; PR00237; GPCRHDOPSN.
PRINTS; PR00427; INTRLEUKIN8R.
PRINTS; PR00572; INTRLEUKIN8R.
PROSITE; PS00237; G-PROTEIN_RECEP_FL1; 1.
PROSITE; PS0262; G-PROTEIN_RECEP_FL2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein;
Chemoaxis.
DOMAIN 1 40 EXTRACELLULAR (POTENTIAL).
TRANSMEM 41 67 1 (POTENTIAL).
DOMAIN 68 73 CYTOPLASMIC (POTENTIAL).
TRANSMEM 74 92 2 (POTENTIAL).
DOMAIN 93 114 EXTRACELLULAR (POTENTIAL).
TRANSMEM 115 138 3 (POTENTIAL).
DOMAIN 139 159 CYTOPLASMIC (POTENTIAL).
TRANSMEM 160 184 4 (POTENTIAL).
DOMAIN 185 204 EXTRACELLULAR (POTENTIAL).
TRANSMEM 205 232 5 (POTENTIAL).
DOMAIN 233 247 CYTOPLASMIC (POTENTIAL).
TRANSMEM 248 270 6 (POTENTIAL).
DOMAIN 271 290 EXTRACELLULAR (POTENTIAL).
TRANSMEM 291 313 7 (POTENTIAL).
DOMAIN 314 355 CYTOPLASMIC (POTENTIAL).
CARBOHYD 21 21 N-LINKED (GLCNAC. . .) (POTENTIAL).
CARBOHYD 115 192 N-LINKED (GLCNAC. . .) (POTENTIAL).
DISULFID 90 111 BY SIMILARITY.
CONFLICT 146 147 DLFAITMPWVSKSGKGIWG ->
CONFLICT 204 204 HA -> QS (IN REF. 2).
CONFLICT 246 247 R -> C (IN REF. 2).
CONFLICT 287 288 DI -> EL (IN REF. 2).
SEQUENCE 355 AA; 40622 MW; EFE49ACB9D1E0F21 CRC64;

Query Match 62.2%; Score 74; DB 1; Length 355;
Best Local Similarity 66.7%; Pred. No. 0.0018;
Matches 14; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 VIIAVLVFLACQIPHNVL 21
II IIII:II I :I:IIII
Db 248 VIFAVLFLCWLPLYNLVLL 268

RESULT 10
IL8B_RABIT STANDARD; PRT; 358 AA.
ID IL8B_RABIT
AC P35344;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE HIGH AFFINITY INTERLEUKIN-8 RECEPTOR B (IL-8R B) (CXCR-2) (GRO/MGSA DE RECEPTOR).
GN IL8RB OR CXCR2.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ALBINO; TISSUE=Blood;
RX MEDLINE=94230294; PubMed=8175642;
RA Prado G.N., Thomas K.M., Suzuki H., Larosa G.J., Wilkinson N.C.,

Folco E., Navarro J.;
"Molecular characterization of a novel rabbit interleukin-8 receptor isotype";
J. Biol. Chem. 269:12391-12394(1994).
-!- FUNCTION: RECEPTOR TO INTERLEUKIN-8, WHICH IS A POWERFUL NEUTROPHILS CHEMOTACTIC FACTOR. BINDING OF IL-8 TO THE RECEPTOR CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA A G-PROTEIN THAT ACTIVATES A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM. THE AFFINITY OF THIS RECEPTOR IS IL-8 >> NAP-2 > MSGA (GRO).
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-!- TISSUE SPECIFICITY: EXPRESSED PREFERENTIALLY IN NEUTROPHILS.
-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

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EMBL; L24445; AAA31378.1; -
PIR; A53752; A53752.
GCRDB; GCR_0861; -
InterPro; IPR0000057; -
InterPro; IPR000174; -
InterPro; IPR000276; -
Pfam; PF00001; 7tm.1; 1.
PRINTS; PR00237; GPCRHDOPSN.
PRINTS; PR00427; INTRLEUKIN8R.
PRINTS; PR00573; INTRLEUKIN8R.
PROSITE; PS00237; G-PROTEIN_RECEP_FL1; 1.
PROSITE; PS0262; G-PROTEIN_RECEP_FL2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein;
Chemoaxis.
DOMAIN 1 46 EXTRACELLULAR (POTENTIAL).
TRANSMEM 47 73 1 (POTENTIAL).
DOMAIN 74 82 CYTOPLASMIC (POTENTIAL).
TRANSMEM 83 103 2 (POTENTIAL).
DOMAIN 104 118 EXTRACELLULAR (POTENTIAL).
TRANSMEM 119 140 3 (POTENTIAL).
DOMAIN 141 161 CYTOPLASMIC (POTENTIAL).
TRANSMEM 162 181 4 (POTENTIAL).
DOMAIN 182 206 EXTRACELLULAR (POTENTIAL).
TRANSMEM 207 229 5 (POTENTIAL).
DOMAIN 230 249 CYTOPLASMIC (POTENTIAL).
TRANSMEM 250 271 6 (POTENTIAL).
DOMAIN 272 292 EXTRACELLULAR (POTENTIAL).
TRANSMEM 293 313 7 (POTENTIAL).
DOMAIN 314 358 CYTOPLASMIC (POTENTIAL).
CARBOHYD 8 8 N-LINKED (GLCNAC. . .) (POTENTIAL).
CARBOHYD 20 20 N-LINKED (GLCNAC. . .) (POTENTIAL).
DISULFID 117 194 BY SIMILARITY.
SEQUENCE 358 AA; 40632 MW; 6899716944D6126A CRC64;

Query Match 62.2%; Score 74; DB 1; Length 358;
Best Local Similarity 66.7%; Pred. No. 0.0018;
Matches 14; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 VIIAVLVFLACQIPHNVL 21
II IIII:II I :I:IIII
Db 250 VIFAVLFLCWLPLYNLVLL 270

RESULT 11
IL8B_HUMAN
ID IL8B_HUMAN STANDARD; PRT; 360 AA.
AC P25025;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)

DE HIGH AFFINITY INTERLEUKIN-8 RECEPTOR B (IL-8R B) (CXCR-2) (GRO/MGSA
DE RECEPTOR) (IL-8 RECEPTOR TYPE 2) (CDW128B).
GN IL8RB OR CXCR2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91368200; PubMed=1891716;
RA Murphy P.M., Tiffany H.L.;
RT "Cloning of complementary DNA encoding a functional human
interleukin-8 receptor.";
RT Science 253:1280-1283(1991).
RN [2]
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
RX MEDLINE=93205012; PubMed=8384312;
RA Cerretti D.P., Kozlosky C.J., Vanden Bos T., Nelson N., Gearing D.P.,
RA Beckmann M.P.;
RT "Molecular characterization of receptors for human interleukin-8,
RT GRO/melanoma growth-stimulatory activity and neutrophil activating
RT peptide-2.";
RN Mol. Immunol. 30:359-367(1993).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=94209273; PubMed=7512557;
RA Sprenger H., Lloyd A.R., Lautens L.L., Bonner T.I., Kelvin D.J.;
RT "Structure, genomic organization, and expression of the human
interleukin-8 receptor B gene.";
RN J. Biol. Chem. 269:11065-11072(1994).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=95014476; PubMed=7929358;
RA Ahuja S.K., Shetty A., Tiffany H.L., Murphy P.M.;
RT "Comparison of the genomic organization and promoter function for
RT human interleukin-8 receptors A and B.";
RN J. Biol. Chem. 269:26381-26389(1994).
RN [5]
RP CHARACTERIZATION.
RX MEDLINE=92355587; PubMed=1379593;
RA Lee J., Horuk R., Rice G.C., Bennett G.L., Camerato T., Wood W.I.;
RT "Characterization of two high affinity human interleukin-8
RT receptors.";
RN J. Biol. Chem. 267:16283-16287(1992).
CC -!- FUNCTION: RECEPTOR TO INTERLEUKIN-8, WHICH IS A POWERFUL
CC NEUTROPHILS CHEMOTACTIC FACTOR. BINDING OF IL-8 TO THE RECEPTOR
CC CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA A
CC G-PROTEIN THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND
CC MESSENGER SYSTEM. THIS RECEPTOR BINDS TO IL-8 WITH A HIGH AFFINITY
CC AND TO GRO/MGSA AND NAP-2 ALSO WITH A HIGH AFFINITY.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -!- DATABASE: NAME=PROW; NOTE=CD guide Cdw128b entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cdw128b.htm".
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M73969; AAA83148.1; -
CC EMBL; M94582; AAA36108.1; -
CC EMBL; M99412; AAC14460.1; -
CC EMBL; L19593; AAB59437.1; -
CC EMBL; U11869; AAB60656.1; -
CC PIR; A39446; A39446.
CC PIR; A53611; A53611.
CC HSP; P34996; 1DD0.
CC GCRDb; GCR_0077; -

DR GCRDb; GCR_0610; -
DR GCRDb; GCR_1001; -
DR GCRDb; GCR_1339; -
DR GCRDb; GCR_1831; -
DR MIM; 146928; -
DR InterPro; IPR000057; -
DR InterPro; IPR000174; -
DR InterPro; IPR000276; -
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PRINTS; PR00427; INTRLEUKIN8R.
DR PRINTS; PR00573; INTRLEUKIN8R.
DR PROSITE; PS00237; G_PROTEIN_RECF_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECF_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Chemotaxis.
FT DOMAIN 1 48 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 49 75 1 (POTENTIAL).
FT DOMAIN 76 84 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 85 105 2 (POTENTIAL).
FT DOMAIN 106 120 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 121 142 3 (POTENTIAL).
FT DOMAIN 143 163 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 164 183 4 (POTENTIAL).
FT DOMAIN 184 208 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 209 231 5 (POTENTIAL).
FT DOMAIN 232 251 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 252 273 6 (POTENTIAL).
FT DOMAIN 274 294 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 295 315 7 (POTENTIAL).
FT DOMAIN 316 360 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 22 22 N-LINKED (GLCNAC. .) (POTENTIAL).
FT DISULFID 119 196 BY SIMILARITY.
SQ SEQUENCE 360 AA; 40759 MW; 564F04A8BCC0A197 CRC64;
Query Match 62.2%; Score 74; DB 1; Length 360;
Best Local Similarity 66.7%; Pred. No. 0.0018;
Matches 14; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
QY 1 VIIAVLVFLACQIPHNVL 21
DB 252 VIFAVLVFLCWLPLNVL 272
RESULT 12
IL8B_BOVIN STANDARD; PRT; 360 AA.
ID IL8B_BOVIN
AC Q28003;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE HIGH AFFINITY INTERLEUKIN-8 RECEPTOR B (IL-8R B) (CXCR-2).
GN IL8RB OR CXCR2.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_Taxid=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Li Y., Feng J., Templeton J.W.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: RECEPTOR TO INTERLEUKIN-8, WHICH IS A POWERFUL
CC NEUTROPHILS CHEMOTACTIC FACTOR. BINDING OF IL-8 TO THE RECEPTOR
CC CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA A
CC G-PROTEIN THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND
CC MESSENGER SYSTEM. THIS RECEPTOR BINDS TO IL-8 WITH A HIGH AFFINITY
CC AND TO GRO/MGSA AND NAP-2 ALSO WITH A HIGH AFFINITY (BY
CC SIMILARITY).
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
CC

RN [3]

SEQUENCE FROM N.A.
STRAIN-129/SV;
MEDLINE=95363183; PubMed=7636264;
Lee J., Cacalano G., Camerato T., Toy K., Moore M.W., Wood W.I.;
"Chemokine binding and activities mediated by the mouse IL-8
receptor";
J. Immunol. 155:2158-2164(1995).
(4)
SEQUENCE FROM N.A.
MEDLINE=94252584; PubMed=8194768;
Harada A., Kuno K., Nomura H., Mukaida N., Murakami S., Matsushima K.;
"Cloning of a cDNA encoding a mouse homolog of the interleukin-8
receptor";
Gene 142:297-300(1994).
(5)
SEQUENCE OF 145-258 FROM N.A.
TISSUE=Testis;
MEDLINE=94116980; PubMed=8288218;
Wilkie T.M., Chen Y., Gilbert D.J., Moore K.J., Yu L., Simon M.I.,
Copeland N.G., Jenkins N.A.;
"Identification, chromosomal location, and genome organization of
mammalian G-protein-coupled receptors";
Genomics 18:175-184(1993).
-!- FUNCTION: RECEPTOR TO INTERLEUKIN-8, WHICH IS A POWERFUL
NEUTROPHILS CHEMOTACTIC FACTOR. BINDING OF IL-8 TO THE RECEPTOR
CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA A
G-PROTEIN THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND
MESSENGER SYSTEM. THIS RECEPTOR BINDS TO IL-8 WITH A HIGH AFFINITY
AND TO GRO/MGSA AND NAP-2 ALSO WITH A HIGH AFFINITY.

[illegible]

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	EMLB; L23637; AAA39305.1;	-
DR	EMBL; I13239; AAA62109.1;	-
DR	EMBL; U31207; AAC52239.1;	-
DR	EMBL; D17630; BAA04536.1;	-
DR	EMBL; L20337; BAA16853.1;	-
DR	PIR; A53677; AS3677.	-
DR	GCRdb; GCR_0550;	--
DR	GCRdb; GCR_0812;	--
DR	GCRdb; GCR_0838;	--
DR	GCRdb; GCR_1027;	--
DR	GCRdb; GCR_1670;	--
DR	MGI; MGI-105303; Cmkar2.	-
DR	InterPro; IPRO00057;	-
DR	InterPro; IPRO00174;	-
DR	InterPro; IPRO00276;	-
DR	pfam; PF00001; 7tm_l; 1.	-
DR	PRINTS; PR00237; GPCRHHODOPSN.	-
DR	PRINTS; PR00427; INTRLEUKIN8R.	-
DR	PRINTS; PR00573; INTRLEUKN8BR.	-
DR	PROSITE; PS00237; G_PROTEIN_RECEP_Fl_1; 1.	-
DR	PROSITE; PSS0262; G_PROTEIN_RECEP_Fl_2; 1.	-
KW	G-protein coupled receptor; Transmembrane; Glycoprotein;	-
KW	Chemotaxis.	-
FT	DOMAIN 1 47	EXTRACELLULAR (POTENTIAL)

FT TRANSMEM 48 74 1 (POTENTIAL).
 FT DOMAIN 75 83 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 84 104 2 (POTENTIAL).
 FT DOMAIN 105 119 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 120 141 3 (POTENTIAL).
 FT DOMAIN 142 162 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 163 182 4 (POTENTIAL).
 FT DOMAIN 183 207 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 208 230 5 (POTENTIAL).
 FT DOMAIN 231 250 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 251 272 6 (POTENTIAL).
 FT DOMAIN 273 293 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 294 314 7 (POTENTIAL).
 FT DOMAIN 315 359 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 23 23 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT DISULFID 118 195 BY SIMILARITY.
 SQ SEQUENCE 359 AA; 40425 MW; 74BD166E9B679F88 CRC64;

Query Match 59.7%; Score 71; DB 1; Length 359;
 Best Local Similarity 70.0%; Pred. No. 0.0047;
 Matches 14; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 VIIAVLVFLACQIPHNVL 20
 || ||||| | :|:|
 Db 251 VIFAVLVFLCWPYNVL 270

RESULT 14
 IL8B_RAT STANDARD; PRT; 359 AA.
 AC P35407;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE HIGH AFFINITY INTERLEUKIN-8 RECEPTOR B (IL-8R B) (CXCR-2) (GRO/MGSA RECEPTOR).
 GN IL8RB OR CXCR2.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 [1]
 SEQUENCE FROM N.A.
 RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Lung;
 RX MEDLINE=97361587; PubMed=9218548;
 RA Gobl A.E., Huang M.R., Wang S., Zhou Y., Oberg K.;
 RT "Molecular cloning and characterization of a cDNA encoding the rat interleukin-8 receptor.";
 RL Biochim. Biophys. Acta 1326:171-177(1997).
 [2]
 SEQUENCE FROM N.A.
 RC STRAIN=Wistar; TISSUE=Liver;
 RA Konishi K., Shibata F., Watanabe K., Tsurufuji S., Nakagawa H.,
 RA Fujioka M.;
 RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
 [3]
 SEQUENCE FROM N.A.
 RC STRAIN=Wistar; TISSUE=Spleen, and Lung;
 RX MEDLINE=97115810; PubMed=8955112;
 RA Dunstan C.A.N., Salafra M.N., Adhikari S., Xia Y., Feng L.,
 RA Harrison J.K.;
 RT "Identification of two rat genes orthologous to the human interleukin-8 receptors.";
 RL J. Biol. Chem. 271:32770-32776(1996).
 CC -!- FUNCTION: RECEPTOR TO INTERLEUKIN-8, WHICH IS A POWERFUL NEUTROPHILS CHEMOTACTIC FACTOR. BINDING OF IL-8 TO THE RECEPTOR CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA A G-PROTEIN THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM. THIS RECEPTOR BINDS TO IL-8 WITH A HIGH AFFINITY AND TO GRO/MGSA AND NAP-2 ALSO WITH A HIGH AFFINITY.
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

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 CC -----
 DR EMBL; X77797; CAA54824.1; -
 DR EMBL; D63584; BAA09797.1; -
 DR EMBL; U70988; AAC52961.1; -
 DR PIR; S42096; S42096.
 DR GCRDB; GCR.0913; -
 DR GCRDB; GCR.1405; -
 DR GCRDB; GCR.1524; -
 DR InterPro; IPR000057; -
 DR InterPro; IPR000174; -
 DR InterPro; IPR000276; -
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRHHODOPSN.
 DR PRINTS; PR00427; INTRLEUKIN8R.
 DR PRINTS; PR00573; INTRLEUKIN8R.
 DR PROSITE; PS00237; G-PROTEIN_RECEPT_F1_1; 1.
 DR PROSITE; PS0262; G-PROTEIN_RECEPT_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Chemotaxis.
 FT DOMAIN 1 47 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 48 74 1 (POTENTIAL).
 FT DOMAIN 75 83 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 84 104 2 (POTENTIAL).
 FT DOMAIN 105 119 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 120 141 3 (POTENTIAL).
 FT DOMAIN 142 162 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 163 182 4 (POTENTIAL).
 FT DOMAIN 183 207 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 208 230 5 (POTENTIAL).
 FT DOMAIN 231 250 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 251 272 6 (POTENTIAL).
 FT DOMAIN 273 296 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 297 314 7 (POTENTIAL).
 FT DOMAIN 315 359 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 8 8 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 23 23 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 202 202 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT DISULFID 118 195 BY SIMILARITY.
 SQ SEQUENCE 359 AA; 40532 MW; EF547326A074ABDD CRC64;
 Query Match 58.8%; Score 70; DB 1; Length 359;
 Best Local Similarity 70.0%; Pred. No. 0.0064;
 Matches 14; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 QY 1 VIIAVLVFLACQIPHNVL 20
 || ||||| | :|:|
 Db 251 VIFAVLVFLCWPYNVL 270
 RESULT 15
 IL8B_MACMU STANDARD; PRT; 353 AA.
 ID IL8B_MACMU
 AC Q28519;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE HIGH AFFINITY INTERLEUKIN-8 RECEPTOR B (IL-8R B) (CXCR-2) (FRAGMENT).
 GN IL8RB OR CXCR2.
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Macaca.
 OX NCBI_TaxID=9544;

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RN SEQUENCE FROM N.A.
RP MEDLINE=96175151; PubMed=9110929;
RA Alvarez V., Coto E., Setien F., Gonzalez S., Gonzalez-Roces S.,
RA Lopez-Larrea C.;
RL "Characterization of interleukin-8 receptors in non-human primates.";
CC Immunogenetics 43:261-267(1996).
CC -!- FUNCTION: RECEPTOR TO INTERLEUKIN-8, WHICH IS A POWERFUL
CC NEUTROPHILS CHEMOTACTIC FACTOR. BINDING OF IL-8 TO THE RECEPTOR
CC CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA A
CC G-PROTEIN THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND
CC MESSENGER SYSTEM. THIS RECEPTOR BINDS TO IL-8 WITH A HIGH AFFINITY
CC AND TO GRO/MGSA AND NAP-2 ALSO WITH A HIGH AFFINITY.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CC -----
DR EMBL; X91116; CAA62565.1; -.
DR HSSP; P34996; 1DDD.
DR InterPro: IPR000276; -.
DR Pfam; PF00001; 7tm_1; 1.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR_F1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECEPTOR_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Chemotaxis.
FT NON_TER 1 45
FT DOMAIN <1 45 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 46 72 1 (POTENTIAL).
FT DOMAIN 73 81 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 82 102 2 (POTENTIAL).
FT DOMAIN 103 117 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 118 139 3 (POTENTIAL).
FT DOMAIN 140 160 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 161 180 4 (POTENTIAL).
FT DOMAIN 181 205 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 206 228 5 (POTENTIAL).
FT DOMAIN 229 248 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 249 270 6 (POTENTIAL).
FT DOMAIN 271 291 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 292 312 7 (POTENTIAL).
FT DOMAIN 313 >353 CYTOPLASMIC (POTENTIAL).
FT DISULFID 116 193 BY SIMILARITY.
FT CARBOHYD 19 19 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT NON_TER 353 353
SQ SEQUENCE 353 AA; 39947 MW; EC8B38130657C713 CRC64;

Query Match 58.0%; Score 69; DB 1; Length 353;
Best Local Similarity 61.9%; Pred. No. 0.0088;
Matches 13; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 1 VIIAVLVFLACQIPHNMVLL 21
|||:|:|:|:|:|:|:|:|
Db 249 VIFAVVLIQLCWLPYSVLVLL 269

Search completed: May 23, 2001, 15:36:20
Job time: 651 sec
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OM protein - protein search, using sw model

Run on: May 23, 2001, 15:35:16 ; Search time 189.03 Seconds
(without alignments)
15.501 Million cell updates/sec

Title: US-08-887-977-10_COPY_246_270

Perfect score: 119

Sequence: 1 VIIAVLVFLACQIPHNNVLLVTA 25

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_15:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phase:*

10: sp_plant:*

11: sp_rodent:*

12: sp_unclassified:*

13: sp_vertebrate:*

14: sp_virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	114	95.8	367	11	Q9R1V0	Q9R1V0 mus musculus
2	74	62.2	79	4	Q9P2U2	Q9P2U2 homo sapien
3	74	62.2	111	4	Q9P2T6	Q9P2T6 homo sapien
4	70	58.8	380	4	Q9UNW8	Q9UNW8 homo sapien
5	68	57.1	174	6	Q9TU48	Q9TU48 bos taurus
6	68	57.1	174	6	Q9TQ57	Q9TQ57 bos taurus
7	67	56.3	382	11	Q9Z282	Q9Z282 mus musculus
8	61	51.3	361	6	O46685	O46685 bos taurus
9	60	50.4	368	13	O42444	O42444 oncorhynch
10	59	49.6	375	4	O43494	O43494 homo sapien
11	58	48.7	342	13	Q93239	Q93239 cyprinus ca
12	57	47.9	360	11	Q9JL20	Q9JL20 mus musculus
13	57	47.9	362	11	Q9JL21	Q9JL21 mus musculus
14	57	47.9	362	11	Q9JIP1	Q9JIP1 mus musculus
15	56	47.1	350	4	Q9NPB9	Q9NPB9 homo sapien
16	55	46.2	346	13	Q9PUA9	Q9PUA9 bufo japoni
17	55	46.2	354	14	Q9IP69	Q9IP69 human cytom
18	55	46.2	354	14	Q9IP68	Q9IP68 human cytom
19	55	46.2	354	14	Q9IP67	Q9IP67 human cytom

20	55	46.2	354	14	Q9IP66	Q9IP66 human cytom
21	55	46.2	354	14	Q9IP65	Q9IP65 human cytom
22	55	46.2	361	4	Q9NZG2	Q9NZG2 homo sapien
23	55	46.2	362	11	O89039	O89039 rattus norv
24	55	46.2	362	11	Q9JLZ0	Q9JLZ0 rattus norv
25	54	45.4	336	5	Q9Y073	Q9Y073 lymnaea sta
26	54	45.4	369	4	Q9UQ06	Q9UQ06 homo sapien
27	53	44.5	385	11	Q9JK40	Q9JK40 mus musculu
28	52	43.7	296	6	Q9TTY6	Q9TTY6 canis famil
29	52	43.7	367	11	Q9JII9	Q9JII9 rattus norv
30	51	42.9	336	14	Q9J5H4	Q9J5H4 fowlpox vir
31	51	42.9	415	4	O15185	O15185 homo sapien
32	51	42.9	678	5	Q94736	Q94736 stomoxys ca
33	50	42.0	106	5	O9W4R0	O9W4R0 drosophila
34	50	42.0	263	5	O76873	O76873 drosophila
35	50	42.0	351	6	Q9MYJ9	Q9MYJ9 oryctolagus
36	50	42.0	367	11	O88410	O88410 mus musculu
37	50	42.0	367	11	Q9QWN6	Q9QWN6 mus musculu
38	50	42.0	394	5	O9U721	O9U721 drosophila
39	50	42.0	521	5	O9VAD2	O9VAD2 drosophila
40	49	41.2	343	6	Q9XT45	Q9XT45 macaca mula
41	49	41.2	343	6	Q9N0Z0	Q9N0Z0 cercopithec
42	49	41.2	359	13	Q9PVY7	Q9PVY7 anguilla an
43	49	41.2	360	4	Q9ULY7	Q9ULY7 homo sapien
44	49	41.2	360	4	Q9ULY6	Q9ULY6 homo sapien
45	49	41.2	384	13	Q9PUQ8	Q9PUQ8 fugu rubrip

ALIGNMENTS

RESULT 1						
Q9R1V0						
ID	Q9R1V0	PRELIMINARY;	PRT;	367	AA.	
AC	Q9R1V0					
DT	01-MAY-2000 (Tremblrel. 13, Created)					
DT	01-MAY-2000 (Tremblrel. 13, Last sequence update)					
DT	01-JUN-2000 (Tremblrel. 14, Last annotation update)					
DE	CC CHEMOKINE LARC SPECIFIC RECEPTOR.					
GN	MCCR6.					
OS	Mus musculus (Mouse).					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OX	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.					
OC	NCBI_TaxID=10090;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RA	Tanaka Y.;					
RT	"Molecular Cloning of Murine Homologue of CCR6, the Specific Receptor for CC Chemokine LARC."					
RL	Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.					
DR	EMBL; AB016031; BAA82443.1;					
DR	INTERPRO; IPR000190;					
DR	INTERPRO; IPR000276;					
DR	INTERPRO; IPR000355;					
DR	PFAM; PF00001; 7tm.1; 1.					
DR	PRINTS; PR00237; GPCRHHODOPSN.					
DR	PRINTS; PR00635; ANGIOTENSINR.					
DR	PRINTS; PR00657; CCEMOKINER.					
DR	PROSITE; PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.					
KW	Receptor.					
SQ	SEQUENCE 367 AA; 42082 MW; 207FD98B2F7A6DD3 CRC64;					

Query Match	95.8%	Score 114;	DB 11;	Length 367;
Best Local Similarity	95.8%	Pred. No. 6.5e-09;		
Matches 23;	Conservative 1;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1 VIIAVLVFLACQIPHNNVLLVTA 24			
	1:			
Db	247 VIIAVLVFLACQIPHNNVLLVTA 270			
RESULT 2				

Q9P2U2
ID Q9P2U2 PRELIMINARY; PRT; 79 AA.
AC Q9P2U2;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DE IL-8 RECEPTOR TYPE A (FRAGMENT).
GN CXCR1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kato H., Tsuchiya N., Tokunaga K.;
RT "Detection of single nucleotide polymorphisms in the coding region of
human CXCR1-chemokine receptor CXCR1, CXCR2, and CXCR3."
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB032728; BAA92290.1; -
KW Receptor.
FT NON_TER 1 1
FT NON_TER 79 79
SQ SEQUENCE 79 AA; 9103 MW; D9393C53AA651564 CRC64;

Query Match 62.2%; Score 74; DB 4; Length 79;
Best Local Similarity 66.7%; Pred. No. 0.0011;
Matches 14; Conservative 4; Mismatches 4; Indels 3; Gaps 0;
QY 1 VTIIVLVFLACQIPHNMLVLL 21
II IIII I I I I I I I I
DB 21 VIFAVLVFLCWLPLYNVLVLL 41

RESULT 3
Q9P2T6
ID Q9P2T6 PRELIMINARY; PRT; 111 AA.
AC Q9P2T6;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DE IL-8 RECEPTOR TYPE B (FRAGMENT).
GN CXCR2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kato H., Tsuchiya N., Tokunaga K.;
RT "Detection of single nucleotide polymorphisms in the coding region of
human CXCR1-chemokine receptor CXCR1, CXCR2, and CXCR3."
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB032734; BAA92296.1; -
KW Receptor.
FT NON_TER 1 1
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12947 MW; 1425DC123439A1BB CRC64;

Query Match 62.2%; Score 74; DB 4; Length 111;
Best Local Similarity 66.7%; Pred. No. 0.0014;
Matches 14; Conservative 4; Mismatches 4; Indels 3; Gaps 0;
QY 1 VTIIVLVFLACQIPHNMLVLL 21
II IIII I I I I I I I I
DB 62 VIFAVLVFLCWLPLYNVLVLL 82

RESULT 4
Q9UNW8
ID Q9UNW8 PRELIMINARY; PRT; 380 AA.
AC Q9UNW8;

DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE G PROTEIN-COUPLED RECEPTOR.
GN G2A.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Weng Z., Witte O.N.;
RT "A DNA damage and stress inducible G protein-coupled receptor blocks
cells in G2/M."
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF083955; AAD47380.1; -
DR INTERPRO; IPR000276; -
DR PFAM; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
KW Receptor.
SQ SEQUENCE 380 AA; 42499 MW; 6DE63D17275ECD74 CRC64;

Query Match 58.8%; Score 70; DB 4; Length 380;
Best Local Similarity 60.9%; Pred. No. 0.015;
Matches 14; Conservative 5; Mismatches 5; Indels 4; Gaps 0;
QY 3 IAVLVFLACQIPHNMLVLTAA 25
II IIII I I I I I I I I
DB 245 IAVVFLVCFAPYHLLVLAKAA 267

RESULT 5
Q9TU48
ID Q9TU48 PRELIMINARY; PRT; 174 AA.
AC Q9TU48;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE INTERLEUKIN 8 RECEPTOR-LIKE PROTEIN (FRAGMENT).
GN IL8R.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Grosche W.M., Kappes S.M., Laegreid W.W., Keele J.W.,
Chitko-McKown C.G., Heaton M.P.;
RT "Single Nucleotide Polymorphism (SNP) Discovery and Linkage Mapping of
Bovine Cytokine Genes."
RL Mamm. Genome 10:1062-1069(1999).
DR EMBL; AF140650; AAF07867.1; -
DR INTERPRO; IPR000174; -
DR INTERPRO; IPR000276; -
DR PFAM; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PRINTS; PR00427; INTRLEUKIN8R.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 174 174
SQ SEQUENCE 174 AA; 20107 MW; D20E223B0FEFEB836 CRC64;

Query Match 57.1%; Score 68; DB 6; Length 174;
Best Local Similarity 61.9%; Pred. No. 0.015;
Matches 13; Conservative 4; Mismatches 4; Indels 4; Gaps 0;
QY 1 VTIIVLVFLACQIPHNMLVLL 21
II IIII I I I I I I I I
DB 100 VIFAVLVFLCWLPLYNVLVLI 120

```
RESULT 6
Q9TQ57 ID Q9TQ57 PRELIMINARY; PRT; 174 AA.
AC OQ57; 2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE INTERLEUKIN 8 RECEPTOR-LIKE PROTEIN (FRAGMENT).
GN IL8R.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Grosse W.M., Kappes S.M., Laegreid W.W., Keele J.W.,
RA Chitko-McKown C.G., Heaton M.P.;
RT "Single Nucleotide Polymorphism (SNP) Discovery and Linkage Mapping of
RT Bovine Cytokine Genes.";
RL Mamm. Genome 10:1062-1069(1999).
DR EMBL; AF140652; AAF07869.1; -
DR EMBL; AF140648; AAF07865.1; -
DR EMBL; AF140649; AAF07866.1; -
DR EMBL; AF140651; AAF07868.1; -
DR INTERPRO; IPR000174; -
DR INTERPRO; IPR000276; -
DR PFAM; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPS.
DR PRINTS; PR00427; INTRLEUKIN8R.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 174 174
SQ SEQUENCE 174 AA; 20116 MW; D21C87CE5BAFC6 CRC64;

Query Match 57.1%; Score 68; DB 6; Length 174;
Best Local Similarity 61.9%; Pred. No. 0.015;
Matches 13; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 VIIAVLVFLACQIPHNMVLL 21
Db 100 VIFAVLVFLXCLWLPYNLVI 120

RESULT 7
Q9Z282 ID Q9Z282 PRELIMINARY; PRT; 382 AA.
AC Q9Z282;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE G PROTEIN-COUPLED RECEPTOR G2A.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE-98445372; PubMed-9770487;
RA Weng Z., Fluckiger A.C., Nisitani S., Wahl M.I., Le L.Q., Hunter C.A.,
RA Fernal A.A., Le Beau M.M., Witte O.N.;
RT "A DNA damage and stress inducible G protein-coupled receptor blocks
RT cells in G2/M.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:12334-12339(1998).
DR EMBL; AF083442; AAC67542.1; -
DR INTERPRO; IPR000276; -
DR PFAM; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
KW Receptor.
```

```
SQ SEQUENCE 382 AA; 42652 MW; D4F8CE0370CCD610 CRC64;

Query Match 56.3%; Score 67; DB 11; Length 382;
Best Local Similarity 60.9%; Pred. No. 0.041;
Matches 14; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 3 IAVVLVFLACQIPHNMVLLVTAA 25
Db 243 IAVVTIFLVCFAPYHVLLVTKAA 265

RESULT 8
O46685 ID O46685 PRELIMINARY; PRT; 361 AA.
AC O46685;
DT 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE ORPHAN G PROTEIN-COUPLED RECEPTOR BRGRIB.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Ferrer-Martinez A., Felipe A., Casado J., Pastor-Anglada M.;
RA Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; U88367; AAC05612.1; -
DR EMBL; U88366; AAC05611.1; -
DR INTERPRO; IPR000276; -
DR PFAM; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
SQ SEQUENCE 361 AA; 40905 MW; 4802E77C9A45DEE1 CRC64;

Query Match 51.3%; Score 61; DB 6; Length 361;
Best Local Similarity 40.9%; Pred. No. 0.29;
Matches 9; Conservative 11; Mismatches 2; Indels 0; Gaps 0;

QY 1 VIIAVLVFLACQIPHNMVLLV 22
Db 229 LVLSVVIFLACFLPYHVLLIV 250

RESULT 9
O42444 ID O42444 PRELIMINARY; PRT; 368 AA.
AC O42444;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE INTERLEUKIN-8-LIKE RECEPTOR.
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE FROM N.A.
RA Zou J., Daniels G.D., Cunningham C., Secombes C.J.;
RA Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ003159; CAA05917.1; -
DR INTERPRO; IPR000276; -
DR PFAM; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
```

SQ SEQUENCE 368 AA; 41523 MW; BE28E2D4C47E821A CRC64;

Query Match 50.4%; Score 60; DB 13; Length 368;
Best Local Similarity 50.0%; Pred. No. 0.4;
Matches 12; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

OY 1 VIIAVLVFLACQIPHNMVLLVTA 24
II:IIIIII I:I:I I:I:I I

Db 255 VILVAVVFLVQLPYNVLMVEA 278

RESULT 10

O43494 PRELIMINARY; PRT; 375 AA.

AC O43494;

DT 01-JUN-1998 (TREMBlrel. 06, Created)

DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)

DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)

DE G PROTEIN-COUPLED RECEPTOR.

GN GPR30.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=98140132; PubMed=9479505;

RA O'dowd B.E., Nguyen T., Marchese A., Cheng R., Lynch K.R.,

RA Heng H.H.Q., Kolakowski L.F. Jr., George S.R.;

RT "Discovery of three novel G-protein-coupled receptor genes.";

RL Genomics 47:310-313(1998).

CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).

CC EMBL: AF027956; AAC52027.1; -

DR INTERPRO: IPR000276; -

DR PFAM: PF00001; 7tm_1; 1.

DR PRINTS: PR00237; GPCRHHODPSN.

DR PROSITE: PS00237; G-PROTEIN RECEPTOR; 1.

KW G-protein coupled receptor; Transmembrane; Glycoprotein.

SQ SEQUENCE 375 AA; 42230 MW; 619CFLEAE65A912 CRC64;

Query Match 49.6%; Score 59; DB 4; Length 375;
Best Local Similarity 50.0%; Pred. No. 0.57;
Matches 11; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

OY 1 VIIAVLVFLACQIPHNMVLLV 22

II:IIIIII I:I:I I:I:I I

Db 260 MILAVLVVFFVCLPENVFISV 281

RESULT 11

O93239 PRELIMINARY; PRT; 342 AA.

AC O93239;

DT 01-NOV-1998 (TREMBlrel. 08, Created)

DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)

DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)

DE CXC CHEMOKINE RECEPTOR-2.

OS Cyprinus carpio (Common carp).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;

OC Cypriniformes; Cyprinidae; Cyprininae; Cyprinus.

OX NCBI_TaxID=7962;

RN [1]

RP SEQUENCE FROM N.A.

RA Fujiki K., Nakao M., Shin D., Yano T.;

RT "cDNA cloning of a carp homologue-2 of mammalian interleukin-8

RT receptors.";

RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.

DR EMBL: AB010713; BAA31470.1; -

DR INTERPRO: IPR000276; -

DR PFAM: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCRHHODPSN.
DR PROSITE: PS00237; G-PROTEIN RECEPTOR; UNKNOWN.1.
SQ SEQUENCE 342 AA; 38481 MW; 8946E5E534B39 CRC64;

Query Match 48.7%; Score 58; DB 13; Length 342;
Best Local Similarity 45.5%; Pred. No. 0.74;
Matches 10; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

OY 1 VIIAVLVFLACQIPHNMVLLV 22

II:IIIIII I:I:I I:I:I I

Db 233 VILSVLAFIVCLPFIILELI 254

RESULT 12

O9JL20

AC O9JL20 PRELIMINARY; PRT; 360 AA.

DT 01-OCT-2000 (TREMBlrel. 15, Created)

DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)

DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)

DE CC CHEMOKINE RECEPTOR 10B (FRAGMENT).

GN CCR10.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RX STRAIN=BALB/C;

RX MEDLINE=20191997; PubMed=10725696;

RA Jarmin D.I., Rits M., Bota D., Gerard N.P., Graham G.J.,

RA Clark-Lewis I., Gerard C.;

RT "Cutting edge: identification of the orphan receptor G-protein-coupled

RT receptor 2 as CCR10, a specific receptor for the chemokine ESKine.";

RL J. Immunol. 164:3460-3464(2000).

DR EMBL: AF215983; AAF63711.1; -

KW NON-TER.

FT NON-TER.

SQ SEQUENCE 360 AA; 38738 MW; 16CBEF69F785BA23 CRC64;

Query Match 47.9%; Score 57; DB 11; Length 360;
Best Local Similarity 36.0%; Pred. No. 1.1;
Matches 9; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

OY 1 VIIAVLVFLACQIPHNMVLLVTA 25

II:IIIIII I:I:I I:I:I I

Db 246 VVALVAVFVVLQPLYSIALLLDTA 270

RESULT 13

O9JL21

AC O9JL21 PRELIMINARY; PRT; 362 AA.

DT 01-OCT-2000 (TREMBlrel. 15, Created)

DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)

DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)

DE CC CHEMOKINE RECEPTOR 10A.

GN CCR10.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RX STRAIN=BALB/C;

RX MEDLINE=20191997; PubMed=10725696;

RA Jarmin D.I., Rits M., Bota D., Gerard N.P., Graham G.J.,

RA Clark-Lewis I., Gerard C.;

RT "Cutting edge: identification of the orphan receptor G-protein-coupled

RT receptor 2 as CCR10, a specific receptor for the chemokine ESKine.";

RESULT	15	
Q9NPB9		
ID	Q9NPB9	PRELIMINARY; PRT; 350 AA.
AC	Q9NPB9;	
DT	01-OCT-2000 (TReMBLrel. 15, Created)	
DT	01-OCT-2000 (TReMBLrel. 15, Last sequence update)	
DT	01-OCT-2000 (TReMBLrel. 15, Last annotation update)	
DE	OC KINE RECEPTOR (CC CHEMOKINE RECEPTOR) (ORPHAN SEVEN-TRANSMEMBRANE RECEPTOR).	
GN	CCR11 OR CCBP2 OR VSHK1.	
OS	Homo sapiens (Human).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.	
OX	NCBI_TaxID=9606;	
RP	[1]	
RP	SEQUENCE FROM N.A.	
RP	Schweickart V.L., Epp A., Raport C.J., Gray P.W.;	
RT	"CCR11 Is a Functional Receptor for the Monocyte Chemoattractant	
RT	Protein Family of Chemokines.";	
RL	J. Biol. Chem. 275:9550-9556(2000).	
RL	[2]	
RP	SEQUENCE FROM N.A.	
RP	MEDLINE=20171478; PubMed=10706668;	
RX		

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 23, 2001, 15:28:32 ; Search time 184.73 Seconds
(without alignments)
6.189 Million cell updates/sec

Title: US-08-887-977-10_COPY_271_290

Perfect score: 105

Sequence: 1 NLGKNRSCQSEKLGITYTKT 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 390729 seqs, 57163235 residues

Total number of hits satisfying chosen parameters: 390729

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	105	100.0	365	19 W48086	Human dendritic ce
2	105	100.0	365	21 Y97077	Primate (human) ch
3	46	43.8	202	21 G07214	Arabidopsis thalia
4	46	43.8	202	21 G51812	Arabidopsis thalia
5	46	43.8	218	21 G31193	Arabidopsis thalia
6	46	43.8	250	21 G07213	Arabidopsis thalia
7	46	43.8	250	21 G51811	Arabidopsis thalia
8	46	43.8	266	21 G31192	Arabidopsis thalia
9	46	43.8	379	22 B49209	V.cholerae VPI pha
10	44	41.9	49	18 Y11212	S. pneumoniae 3-ox
11	44	41.9	140	21 B41413	Human ORFX ORF1177

12	44	41.9	186	19 W38474	S. pneumoniae 3-ox
13	44	41.9	243	19 W80670	S. pneumoniae fatt
14	44	41.9	243	21 B15706	Streptococcus pneu
15	42	40.0	349	21 G31207	Arabidopsis thalia
16	42	40.0	1198	20 Y29248	Amino acid sequenc
17	41	39.0	610	11 R05494	Endothelial leukoc
18	41	39.0	610	11 R05538	Endothelial-leukoc
19	41	39.0	610	11 R08116	Endothelial cell-1
20	41	39.0	610	18 W18839	E-selectin. Homo
21	41	39.0	610	19 W46733	Amino acid sequenc
22	41	39.0	610	21 Y94504	Human E-selectin p
23	41	39.0	610	21 Y59500	Human ELAM-1 prote
24	41	39.0	694	19 W56539	Chicken hedgehog i
25	41	39.0	700	19 W56537	Mouse hedgehog int
26	41	39.0	700	19 W56538	Human hedgehog int
27	40.5	38.6	727	17 R88390	Human neurotransmi
28	40	38.1	25	17 R99674	RHAMM gene exon 2A
29	40	38.1	38	17 R99676	RHAMM gene exon 2A
30	40	38.1	84	21 G02646	Human secreted pro
31	40	38.1	204	21 G28778	Arabidopsis thalia
32	40	38.1	258	21 G28777	Arabidopsis thalia
33	40	38.1	304	21 G28776	Arabidopsis thalia
34	40	38.1	315	17 R89323	Rape leaf beta-ket
35	40	38.1	315	17 R89322	Rape seed beta-ket
36	40	38.1	343	21 B43598	Human cancer assoc
37	40	38.1	368	20 Y60520	Human normal bladd
38	40	38.1	426	18 W09821	Mouse interleukin-
39	40	38.1	630	18 W39166	Mouse RHAMM protei
40	40	38.1	631	17 R99675	RHAMM 1-2a isoform
41	39	37.1	31	20 Y02849	Fragment of human
42	39	37.1	101	20 W98976	Alcaligenes sp. pr
43	39	37.1	187	20 Y02844	Fragment of human
44	39	37.1	235	21 G22781	Arabidopsis thalia
45	39	37.1	235	21 G50473	Arabidopsis thalia

ALIGNMENTS

RESULT 1
W48086
ID W48086 standard; Protein; 365 AA.
XX
AC W48086;
XX
DT 11-JUN-1998 (first entry)
XX
DE Human dendritic cell chemokine receptor.
DE
KW Human; thymus expressed chemokine; TECK; MIP-3alpha; MIP-3beta;
KW receptor; dendritic cell; macrophage; inflammation; asthma.
XX
OS Homo sapiens.
OS
XX
FH Key Location/Qualifiers
FT Misc-difference 193
FT /note= "encoded by CAN"
FT
PN WO9801557-A2.
XX
XX 15-JAN-1998.
XX
PF 02-JUL-1997; 97WO-US10819.
XX
PR 04-JUN-1997; 97US-0048593.
PR 05-JUL-1996; 96US-0675814.
PR 11-OCT-1996; 96US-0028329.
XX
XX (SCHE) SCHERING CORP.
PA
XX
PI Gish KC, Schall TJ, Vicari A, Wang W, Zlotnik A;
XX
XX WPI; 1998-101054/09.
DR

DR N-PSDB; V15418.
XX Novel chemokines, e.g. thymus expressed chemokine - used for
PT treating inflammatory conditions including asthma.
XX
XX Claim 3; Page 94-95; 202pp; English.
XX
CC The present sequence represents human dendritic cell chemokine receptor.
CC Antibodies which bind to the protein can be used in detecting or
CC diagnosing various immunological conditions related to expression
CC of the protein. The nucleic acid can be used for screening and
CC isolating DNA clones for the chemokines, especially from other
CC species. The chemokine can be used in the treatment of conditions
CC associated with abnormal physiology or development, including
CC inflammatory conditions such as asthma.
XX
XX Sequence 365 AA;
SQ

Query Match 100.0%; Score 105; DB 19; Length 365;
Best Local Similarity 100.0%; Pred. No. 3.5e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NLGKNRSCQSEKLIQYTKT 20
Db 271 nlgkmrscqsekligytk 290
|||||

RESULT 2
Y97077
ID Y97077 standard; Protein; 365 AA.
XX
XX Y97077;
XX
XX 04-DEC-2000 (first entry)
XX
XX Primate (human) chemokine receptor CCR6.
XX
XX MIP-3-alpha; chemokine; CCR6 receptor; ligand; cytostatic; agonist;
KW antagonist; anti-psoriatic; dermatological; immunosuppressive;
KW anti-inflammatory.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH Misc-difference 193 /note="Encoded by CAN#"
FT
XX
XX WO2000046248-A1.
XX
XX 10-AUG-2000.
XX
XX 02-FEB-2000; 2000WO-US00511.
XX
XX 03-FEB-1999; 99US-0244281.
XX
XX (SCHE) SCHERING CORP.
XX
XX Oldham ER, Honey B, Dieu-Nosjean M, Caux C, Zlotnik A;
XX
XX WPI; 2000-543477/49.
XX
XX N-PSDB; A51971.
XX
XX Novel methods for modulating the migration of cells within or to the
PT skin using MIP-3-alpha or CCR6 agonists or antagonists, useful for
PT treating skin disorders, e.g. cancer
XX
XX Disclosure; Page 53-54; 61pp; English.
XX
XX The MIP-3-alpha chemokine is expressed in inflamed skin cells. This
CC chemokine is the ligand for the CCR6 receptor. MIP-3-alpha or CCR6
CC agonists or antagonists can be used to modulate the migration of a cell
CC within or to the skin of a mammal. MIP-3-alpha can be used to purify a

CC population of cells expressing a MIP-3-alpha receptor. The methods are
CC useful for treating a mammalian subject with a skin disease or condition,
CC e.g. cancer, metastasis, psoriasis, atopic or contact dermatitis,
CC systemic lupus erythematosus and lichen ruber planus, or for treating
CC skin transplants or grafts.
XX
XX Sequence 365 AA;
SQ

Query Match 100.0%; Score 105; DB 21; Length 365;
Best Local Similarity 100.0%; Pred. No. 3.5e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NLGKNRSCQSEKLIQYTKT 20
Db 271 nlgkmrscqsekligytk 290
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RESULT 3
G07214
ID G07214 standard; Protein; 202 AA.
XX
XX G07214;
XX
XX 17-OCT-2000 (first entry)
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XX Arabidopsis thaliana protein fragment SEQ ID NO: 4283.
XX
XX Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
XX Arabidopsis thaliana.
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XX EP1033405-A2.
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XX 06-SEP-2000.
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XX 25-FEB-2000; 2000EP-0301439.
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XX 25-FEB-1999; 99US-0121825.
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XX 05-MAR-1999; 99US-0123180.
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RESULT 4										
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DT		18-OCT-2000 (first entry)								
XX		XX								
DE		Arabidopsis thaliana protein fragment SEQ ID NO: 65796.								
XX		XX								
KW		Protein identification; signal transduction pathway; metabolic pathway;								
KW		hybridisation assay; genetic mapping; gene expression control; promoter;								
KW		termination sequence.								
XX		XX								
OS		Arabidopsis thaliana.								
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PR		25-MAY-1999; 99US-0135629.								
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PR		28-MAY-1999; 99US-0136392.								
PR		01-JUN-1999; 99US-0136782.								

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PR 09-AUG-1999; 99US-0147935.
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Query Match 43.8%; Score 46; DB 21; Length 202;
Best Local Similarity 50.0%; Pred. No. 7.1;
Matches 9; Conservative 1; Mismatches 8; Indels 0; Gaps 0;
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DT 17-OCT-2000 (first entry)
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KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
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PD 06-SEP-2000.
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PF 25-FEB-2000; 2000EP-0301439.
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PR 09-MAR-1999; 99US-0123548.
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Query Match 43.8%; Score 46; DB 21; Length 218;

Best Local Similarity 50.0%;

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G07213

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Query Match 43.8%; Score 46; DB 21; Length 250;
Best Local Similarity 50.0%; Pred. No. 9;
Matches 9; Conservative 1; Mismatches 8; Indels 0; Gaps 0;
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XX AC G51811;
XX 18-OCT-2000 (first entry)
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KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
OS Arabidopsis thaliana.
PN EPI033405-A2.
XX
PD
XX
XX 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
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PR 25-MAY-1999; 99US-0136021.
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PR 01-SEP-1999; 99US-0151930.
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PR 10-SEP-1999; 99US-0153070.
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PR 28-OCT-1999; 99US-0161992.
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PR 29-OCT-1999; 99US-0162142.

Query Match 43.8%; Score 46; DB 21; Length 250;
Best Local Similarity 50.0%; Pred. No. 9;
Matches 9; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 3 GKMNRSCQSEKLCIGYTKT 20
Db 85 gsinnlqlnkqygltkt 102

RESULT 8
G31192
ID G31192 standard; Protein; 266 AA.
XX
AC G31192;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 37418.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
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XX 06-SEP-2000. 99US-0142055.
PD 06-JUL-1999; PR 02-JUL-1999;
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PF 08-JUL-1999; PR 08-JUL-1999;
XX 09-MAR-1999; PR 09-MAR-1999;
XX 25-FEB-2000; 2000EP-0301439. PR 09-JUL-1999;
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PR 29-OCT-1999; 99US-0162142.

Query Match 43.8%; Score 46; DB 21; Length 266;

Best Local Similarity 50.0%; Pred. No. 9.6;

Matches 9; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

Qy 3 CKMNRSCQSEKLGITYTKT 20
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Db 85 gslnnlcqlnkqyltkt 102

RESULT 9

B49209
ID B49209 standard; Protein; 379 AA.

XX AC B49209;

XX DT 12-MAR-2001 (first entry)

XX DE V.cholerae VPI phage VPI orf3 protien.

XX KW Bacteriophage; pathogenicity island; vaccine; allergy.

XX OS Unidentified.

XX PN WO200067784-A1.

XX PD 16-NOV-2000.

XX PF 10-MAY-2000; 2000WO-US12580.

XX PR 10-MAY-1999; 99US-0133373.

XX PA (UYMA-) UNIV MARYLAND BALTIMORE.

XX

PI Karaolis DKR;
XX WPI; 2001-122703/13.
XX
XX Isolated bacteriophage encoded by a pathogenicity island of a
PT pathogenic bacterium, useful for generating bacteriophage-base vaccines
PT or vectors, e.g. to treat allergies -
XX
PS Disclosure; Fig 5; 59pp; English.
XX
CC The present invention relates to an isolated bacteriophage encoded by
CC a pathogenicity island of a pathogenic bacterium. The bacteriophage may
CC be used in pharmaceuticals e.g. for generating an immune response,
CC especially to produce antibodies, as a bacteriophage-based vaccine
CC against pathogenic bacteria expressing virulence factors, as a
CC vaccine vector, e.g. to prevent or treat allergies, diseases or
CC other pathological conditions.
XX
SQ Sequence 379 AA;

Query Match 43.8%; Score 46; DB 22; Length 379;

Best Local Similarity 45.0%; Pred. No. 14;

Matches 9; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

Qy 1 NLGKMNRSCQSEKLGITYTKT 20
| : | | | | | | | |
Db 198 nkgksneslnrkiigtnt 217

RESULT 10

Y11212

ID Y11212 standard; Protein; 49 AA.

XX AC Y11212;

XX DT 20-MAY-1999 (first entry)

XX DE S. pneumoniae 3-oxoacyl-(acyl carrier protein) reductase.

XX KW Streptococcus pneumoniae strain 0100993; vaccine; immune response;

KW streptococcal infection; pneumococcal.

XX OS Streptococcus pneumoniae.

XX PN WO9737026-A1.

XX PD 09-OCT-1997.

XX PF 01-APR-1997; 97WO-US05306.

XX PR 22-AUG-1996; 96US-0025788.

XX PR 02-APR-1996; 96US-0014690.

XX PA (SMIK) SMITHKLINE BEECHAM CORP.

XX PA (SMIK) SMITHKLINE BEECHAM PLC.

XX PI Black MT, Hodgson JE, Knowles DJC, Nicholas RO;

XX PI Stodola RK;

XX DR WPI; 1997-503111/46.

XX DR N-PSDB; X30801.

XX PT Nucleic acids encoding pneumococcal polypeptide(s) - useful in
XX vaccines, drug screening, etc

XX PS Claim 6; Page 253; 354pp; English.

XX CC X30724 to X30946 represent genomic DNA sequences isolated from
XX Streptococcus pneumoniae strain 0100993. These genomic DNA sequences
CC encode the novel proteins given in Y11114 to Y11367. The proteins, against
CC isolated from Streptococcus pneumoniae, can be used in vaccines against
CC streptococcal infections and in assays for identifying compounds that

CC inhibit or activate the activity of the proteins. The antagonists can
 CC be used to treat an individual having need to inhibit a bacterial
 CC protein. Vectors expressing the proteins can be used to induce a
 CC protective immune response in mammals.

XX Sequence 49 AA;

Query Match 41.9%; Score 44; DB 18; Length 49;

Best Local Similarity 40.0%; Pred. No. 3-2;

Matches 8; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 1 NLGKMNRCQSEKLGITYKT 20

I: I: I: |||: ||:

Db 10 nigqanyaaskagligftks 29

RESULT 11

B41413

ID B41413 standard; Protein: 140 AA.

XX AC

XX B41413;

XX DT

08-FEB-2001 (first entry)

XX DE

Human ORFX ORF1177 polypeptide sequence SEQ ID NO:2354.

XX KW

Human: open reading frame; ORFX: detection; cytostatic; hepatotropic;
 KW vulnary; antiparotatic; antiparkinsonian; nootropic; neuroprotective;
 KW anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;
 KW immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
 KW hypotensive; dermatological; immunosuppressive; antiinflammatory;
 KW antiviral; antibacterial; antifungal; antirheumatic; antithyroid;
 KW antianemic; gene therapy; cancer; proliferative disorder; hypertension;
 KW neurodegenerative disorder; osteoarthritis; graft vs host disease;
 KW cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
 KW cholesterol ester storage; systemic lupus erythematosus; infection;
 KW severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
 KW allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
 KW bone damage; cartilage damage; antiinflammatory disease; coagulation;
 KW thrombosis; contraceptive.

XX OS Homo sapiens.

XX PN WO200058473-A2.

XX PD 05-OCT-2000.

XX PF 31-MAR-2000; 2000WO-US08621.

XX PR 31-MAR-1999; 99US-0127607.

XX PR 02-APR-1999; 99US-0127636.

XX PR 05-APR-1999; 99US-0127728.

XX PR 30-MAR-2000; 2000US-0540763.

XX PA (CURA-) CURAGEN CORP.

XX PI Shimkets RA, Leach M;

XX DR WPI; 2000-60362/57.

XX DR N-PSDB; C75622.

XX PT Novel nucleic acids and peptides derived from open reading frame X,
 PT useful for treating e.g. cancers, proliferative disorders,
 PT neurodegenerative disorders and cardiovascular disease -

XX PS Claim 11; Page 1718; 5507pp; English.

XX CC

C74446 to C77606 encode the proteins given in B40237 to B43397, which
 CC represent the human ORFX open reading frames 1 to 3161. The ORFX
 CC sequences have activities such as: cytostatic; hepatotropic; vulnary;
 CC antiparotatic; antiparkinsonian; nootropic; neuroprotective; osteopathic;
 CC anticonvulsant; antiarthritic; immunosuppressant; immunostimulant;

CC cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive;
 CC dermatological; immunosuppressive; antiinflammatory; antibacterial;
 CC antiviral; antifungal; antirheumatic; antithyroid; and antianemic. The
 CC sequences can be used for determining the presence of or predisposition
 CC to, or preventing or treating pathological conditions associated with an
 CC ORFX-associated disorder. The nucleic acids can be used to express ORFX
 CC proteins in gene therapy vectors. The proteins and nucleic acids may be
 CC used to treat cancers, proliferative disorders, neurodegenerative
 CC disorders, osteoarthritis, graft vs host disease, cardiovascular disease,
 CC diabetes mellitus, hypertension, hypothyroidism, cholesterol ester
 CC storage, systemic lupus erythematosus, severe combined immunodeficiency
 CC (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune
 CC disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and
 CC cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to
 CC enhance coagulation; to inhibit thrombosis; and as a contraceptive.

XX Sequence 140 AA;

Query Match 41.9%; Score 44; DB 21; Length 140;

Best Local Similarity 40.0%; Pred. No. 10;

Matches 8; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 1 NLGKMNRCQSEKLGITYKT 20

I: I: I: |||: ||:

Db 110 nigqanyaaskagligftks 129

RESULT 12

W38474

ID W38474 standard; Protein: 186 AA.

XX AC

XX W38474;

XX DT

06-NOV-1998 (first entry)

XX DE

S. pneumoniae 3-oxoacyl reductase precursor protein.

XX KW

Streptococcus pneumoniae protein; genetic immunisation; antagonist;
 KW immunological response; inoculation; antibody production; inhibitor;
 KW T cell immune response; antimicrobial compound; bacterial adhesion;
 KW extracellular matrix protein; protein-mediated cell invasion; wound;
 KW pathogenesis.

XX OS Streptococcus pneumoniae.

XX PN WO9743303-A1.

XX PD 20-NOV-1997.

XX PF 14-MAY-1997; 97WO-US07950.

XX PR 14-MAY-1996; 96US-0017670.

XX PA (SMIK) SMITHKLINE BEECHAM CORP.

XX PA (SMIK) SMITHKLINE BEECHAM PLC.

XX PI Black MT, Hodgson JE, Knowles DJC, Nicholas RO;

XX DR Stodola RK;

XX DR WPI; 1998-008793/01.

XX DR N-PSDB; T98542.

XX PT Novel Streptococcus pneumoniae proteins and related DNA - useful for
 PT diagnosing anti-microbial agents for treatment of bacterial
 PT infections

XX PS Claim 12; Page 268; 483pp; English.

XX CC

This sequence represents a Streptococcus pneumoniae protein that, based
 CC on homology with a Cuphea lanceolata protein is a 3-oxoacyl reductase
 CC precursor protein, and is encoded by a DNA sequence of the invention.
 CC The DNA sequences were isolated from Streptococcus pneumoniae strain

CC 0100993 (NCIMB 40794). The Streptococcus pneumoniae proteins of the
 CC invention can be used to identify compounds which interact with and
 CC inhibit or activate the activity of the proteins. Antagonists can be
 CC used to treat diseases caused by S. pneumoniae proteins, through genetic
 CC immunisation. They can also be used to induce an immunological response
 CC in a mammal by inoculation with the S. pneumoniae proteins or delivery
 CC of the encoding nucleic acids in a vector adequate to produce antibody
 CC and/or T cell immune responses to protect the animal from disease. The
 CC proteins can also be used to identify antimicrobial compounds which are
 CC capable of inhibiting their bioactivity. In particular the proteins of
 CC the invention can be used to prevent adhesion of bacteria to mammalian
 CC extracellular matrix proteins on in-dwelling devices or in wounds, to
 CC block protein-mediated mammalian cell invasion, and to block the normal
 CC progression of pathogenesis in infections initiated other than by the
 CC implantation of in-dwelling devices or other surgical techniques.

XX Sequence 186 AA;

Query Match 41.9%; Score 44; DB 19; Length 186;
 Best Local Similarity 40.0%; Pred. No. 14;
 Matches 8; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 1 NLGNRSCQSEKLGITYTKT 20
 I:|:|:|:|:|:|:
 Db 147 niganyaaskagligftks 166

RESULT 13

W80670
 ID W80670 standard; Protein; 243 AA.

XX W80670;

DT 24-DEC-1998 (first entry)

DE S. pneumoniae fatty acid biosynthesis protein.

XX Streptococcus pneumoniae protein; recombinant; gene expression; DNA chip;
 KW virulence; antibody; infection; detection; treatment; hypothetical;
 KW cell wall biosynthetic, external target; minimal gene set protein.

XX Streptococcus pneumoniae.

OS W09826072-A1.

PN 18-JUN-1998.

XX 09-DEC-1997; 97WO-US22578.

XX 13-DEC-1996; 96US-0036281.

XX (ELIL) LILLY & CO ELI.

XX Baltz RH, Burgett SG, Dehoff BS, Hoskins JA, Jaskunas SR;

PI Mills BJ, Norris FH, Peery RB, Rockey PK, Rostock PR;

PI Skatrud PL, Smith MC, Solenberg PJ, Treadway PJ;

PI Young Bellido ML;

XX WPI; 1998-348529/30.

XX Streptococcus pneumoniae nucleic acid sequences - used in DNA chips
 PT for evaluating gene expression, and identification of virulence
 PT genes

PS Claim 3; Page 270; 333pp; English.

XX This sequence represents a S. pneumoniae fatty acid biosynthesis
 CC protein. The invention provides DNA sequences (V65201 to V65304) from
 CC the Streptococcus pneumoniae genome and corresponding protein sequences
 CC (W80605 to W80728). The protein sequences are classified as hypothetical,
 CC cell wall biosynthetic, external target, or minimal gene set proteins. A
 CC recombinant host containing a vector comprising any of the above nucleic

CC acids can be used for the recombinant expression of the proteins. The
 CC invention also provides a DNA chip having arrayed on it at least 15 base
 CC pair fragment of any one or more of these DNA sequences. The DNA chip can
 CC be used methods for evaluating gene expression in S. pneumoniae and for
 CC identifying virulence genes in S. pneumoniae. Antibodies that selectively
 CC bind to the above proteins or peptide fragments can be used to treat
 CC S. pneumoniae infection. The antibodies can also be used to detect
 CC S. pneumoniae cells.

XX Sequence 243 AA;

Query Match 41.9%; Score 44; DB 19; Length 243;
 Best Local Similarity 40.0%; Pred. No. 18;
 Matches 8; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 1 NLGNRSCQSEKLGITYTKT 20
 I:|:|:|:|:|:|:
 Db 147 niganyaaskagligftks 166

RESULT 14

B15706
 ID B15706 standard; Protein; 243 AA.

XX B15706;

DT 07-DEC-2000 (first entry)

DE Streptococcus pneumoniae FabG polypeptide.

XX Streptococcus pneumoniae; FabG; 3-oxoacyl-acyl carrier protein reductase;
 KW antibacterial; cytostatic; antiulcer; cancer; gastric ulcer; gastritis;
 KW Helicobacter pylori infection; microbial infection.

XX Streptococcus pneumoniae.

PN W0200044885-A1.

XX 03-AUG-2000.

XX 19-JAN-2000; 2000WO-US01131.

XX 27-JAN-1999; 99US-0239052.

XX (SMIK) SMITHKLINE BEECHAM CORP.

XX Holmes DJ, Mooney J, Zhong YY, Debouck C, Jaworski DD, Wang M;
 PI Warren RL, Kosmatka AL, Mcdevitt D, Ingraham KA, Chaliker AF;
 PI So CY, Wallis NG, Pearson SC;

XX WPI; 2000-482971/42.
 DR N-PSDB; A74684.

XX FabG polypeptide, isolated from Streptococcus pneumoniae, is used to
 PT treat microbial diseases, identify agonists and antagonists for
 PT treating microbial infections and to detect diseases associated with
 PT microbial infections -

XX Claim 1; Page 3; 40pp; English.

XX The present sequence is a FabG (2-oxoacyl-acyl carrier protein
 CC reductase) polypeptide. A full length FabG gene was isolated from a
 CC Streptococcus pneumoniae 0100993 DNA library in E. coli. FabG
 CC polynucleotides and polypeptides are used for detection and treatment of
 CC microbial diseases. They may also be used to identify antagonists and
 CC agonists which can then be used to treat microbial diseases. Compounds
 CC that interfere with the initial physical interaction between a pathogen
 CC and a host have been identified. The compounds are able to prevent the
 CC adhesion of bacteria to mammalian extracellular proteins in wounds,
 CC prevent adhesion between mammalian extracellular proteins and bacterial
 CC FabG proteins which mediate tissue damage and/or to block normal
 CC progression of pathogenesis in infections mediated by implantation of

CC in-dwelling devices or other surgical techniques. The Fabg
CC polypeptides, polynucleotides, antagonists and agonists are especially
CC useful in the treatment of Helicobacter pylori infection. They may be
CC used to decrease H. pylori-induced cancers and to prevent, inhibit
CC and/or cure gastric ulcers and gastritis.

XX Sequence 243 AA;

Query Match 41.9%; Score 44; DB 21; Length 243;
Best Local Similarity 40.0%; Pred. No. 18;
Matches 8; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 1 NLGKMNRCSQSEKLIGYTKT 20
I::I:: I::I::
Db 147 niganyaaskagligftks 166

RESULT 15

G31207
ID G31207 standard; Protein; 349 AA.

XX AC G31207;

XX DT 17-OCT-2000 (first entry)

XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 37438.

XX KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.

XX OS Arabidopsis thaliana.

XX PN EP1033405-A2.

XX PD 06-SEP-2000.

XX PF 25-FEB-2000; 2000EP-0301439.

XX PR 25-FEB-1999; 99US-0121825.

XX PR 05-MAR-1999; 99US-0123180.

XX PR 09-MAR-1999; 99US-0123548.

XX PR 23-MAR-1999; 99US-0125788.

XX PR 25-MAR-1999; 99US-0126264.

XX PR 29-MAR-1999; 99US-0126785.

XX PR 01-APR-1999; 99US-0127462.

XX PR 06-APR-1999; 99US-0128234.

XX PR 08-APR-1999; 99US-0128714.

XX PR 16-APR-1999; 99US-0128714.

XX PR 19-APR-1999; 99US-0129845.

XX PR 21-APR-1999; 99US-0130077.

XX PR 23-APR-1999; 99US-0130449.

XX PR 23-APR-1999; 99US-0130510.

XX PR 23-APR-1999; 99US-0130891.

XX PR 28-APR-1999; 99US-0131449.

XX PR 30-APR-1999; 99US-0132048.

XX PR 30-APR-1999; 99US-0132407.

XX PR 04-MAY-1999; 99US-0132484.

XX PR 05-MAY-1999; 99US-0132485.

XX PR 06-MAY-1999; 99US-0132486.

XX PR 06-MAY-1999; 99US-0132487.

XX PR 07-MAY-1999; 99US-0132863.

XX PR 11-MAY-1999; 99US-0134256.

XX PR 14-MAY-1999; 99US-0134218.

XX PR 14-MAY-1999; 99US-0134221.

XX PR 14-MAY-1999; 99US-0134221.

XX PR 18-MAY-1999; 99US-0134370.

XX PR 18-MAY-1999; 99US-0134768.

XX PR 19-MAY-1999; 99US-0134941.

XX PR 20-MAY-1999; 99US-0135124.

XX PR 21-MAY-1999; 99US-0135353.

XX PR 24-MAY-1999; 99US-0135629.

XX PR 25-MAY-1999; 99US-0136021.

PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
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PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
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PR 04-OCT-1999; 99US-0157117.
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PR 21-OCT-1999; 99US-0160814.
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PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
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PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.

PR 29-OCT-1999; 99US-0162142.

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Best Local Similarity 64.3%; Pred. No. 58;
Matches 9; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 23, 2001, 15:30:08 ; Search time 95.91 seconds
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Title: US-08-887-977-10_COPY_271_290

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Searched: 185757 seqs, 19210857 residues

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Post-processing: Minimum Match 0%

Maximum Match 100%

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SUMMARIES

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2	41	39.0	610	4	US-09-209-668-19
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5	40.5	38.6	727	5	PCT-US94-05363A-2
6	40	38.1	315	3	US-08-793-035-9
7	40	38.1	315	3	US-08-793-035-10
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10	37	35.2	338	3	US-08-988-876-8
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22	36	34.3	31	3	US-09-071-090-8
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27	36	34.3	306	4	US-09-082-593-2

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ALIGNMENTS

RESULT 1

US-08-365-470-3

; Sequence 3, Application US/08365470

; Patent No. 5632991

; GENERAL INFORMATION:

; APPLICANT: Gimbrone, Jr., Michael A.

; TITLE OF INVENTION: Antibodies Specific For E-selectin And The Uses

; TITLE OF INVENTION: Thereof

; NUMBER OF SEQUENCES: 3

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX

; STREET: 1100 New York Ave., NW

; CITY: Washington

; STATE: DC

; COUNTRY: USA

; ZIP: 20005

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/365,470

; FILING DATE: herewith

; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/102,510

; FILING DATE: 05-AUG-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/850,802

; FILING DATE: 13-MAR-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Markowicz, Karen R.

; REGISTRATION NUMBER: 36,351

; REFERENCE/DOCKET NUMBER: 0627.1350003

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-371-2600

; TELEFAX: 202-371-2540

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 610 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; US-08-365-470-3

Query Match 39.0%; Score 41; DB 1; Length 610;

Best Local Similarity 50.0%; Pred. No. 49;

Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

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Db 500 GKNMSCGEPVFG 513

RESULT 2
US-09-209-668-19
; Sequence 19, Application US/09209668A
; Patent No. 6114517
; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P.
; APPLICANT: Xu, Xiaoxing S.
; TITLE OF INVENTION: METHODS OF MODULATING TUMOR NECROSIS FACTOR
; FILE REFERENCE: ISPH-0336
; CURRENT FILING DATE: 1998-12-10
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 19
; LENGTH: 610
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-209-668-19

Query Match 39.0%; Score 41; DB 4; Length 610;
Best Local Similarity 50.0%; Pred. No. 49;
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RESULT 3
5217870-2
; Patent No. 5217870
; APPLICANT: HESSION, CATHERINE A.; LOBB, ROY R.; GOELZ, SUSAN E.
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES AGAINST CDX
; NUMBER OF SEQUENCES: 4
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/345,151
; FILING DATE: 28-APR-1989
; SEQ ID NO: 2;
; LENGTH: 610
5217870-2

Query Match 39.0%; Score 41; DB 6; Length 610;
Best Local Similarity 50.0%; Pred. No. 49;
Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

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RESULT 4
US-08-424-424B-2
; Sequence 2, Application US/08424424B
; Patent No. 5759854
; GENERAL INFORMATION:
; APPLICANT: LI, ET AL.
; TITLE OF INVENTION: Neurotransmitter Transporter
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA

QY 3 GKNRSCQSEKLG 16
    ||:| || |.:|
Db 500 GKNMSCGEPVFG 513

RESULT 5
PCT-US94-05363A-2
; Sequence 2, Application PC/TUS9405363A
; GENERAL INFORMATION:
; APPLICANT: LI, ET AL.
; TITLE OF INVENTION: Neurotransmitter Transporter
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/05363A
FILING DATE: SUBMITTED HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-118
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744

QY 5 MNRSC---QSEKLGTYKT 20
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Db 362 MNEKCVVNAEKILGYLNT 380

Query Match 38.6%; Score 40.5; DB 1; Length 727;
Best Local Similarity 42.1%; Pred. No. 71;
Matches 8; Conservative 3; Mismatches 5; Indels 3; Gaps 1;

QY 5 MNRSC---QSEKLGTYKT 20
    || | |.:| |
Db 362 MNEKCVVNAEKILGYLNT 380

RESULT 5
PCT-US94-05363A-2
; Sequence 2, Application PC/TUS9405363A
; GENERAL INFORMATION:
; APPLICANT: LI, ET AL.
; TITLE OF INVENTION: Neurotransmitter Transporter
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/05363A
FILING DATE: SUBMITTED HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-118
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
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ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/424,424B
FILING DATE: APRIL 21, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/05363
FILING DATE: MAY 25, 1996
ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 325800-308
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 727 AMINO ACIDS
TYPE: AMINO ACID
STRANDEDNESS:
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
US-08-424-424B-2

Query Match 38.6%; Score 40.5; DB 1; Length 727;
Best Local Similarity 42.1%; Pred. No. 71;
Matches 8; Conservative 3; Mismatches 5; Indels 3; Gaps 1;

QY 5 MNRSC---QSEKLGTYKT 20
    || | |.:| |
Db 362 MNEKCVVNAEKILGYLNT 380

RESULT 5
PCT-US94-05363A-2
; Sequence 2, Application PC/TUS9405363A
; GENERAL INFORMATION:
; APPLICANT: LI, ET AL.
; TITLE OF INVENTION: Neurotransmitter Transporter
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/05363A
FILING DATE: SUBMITTED HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-118
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
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;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 727 AMINO ACIDS
;; TYPE: AMINO ACID
;; STRANDEDNESS:
;; TOPOLOGY: LINEAR
;; MOLECULE TYPE: PROTEIN
PCT-US94-05363A-2

Query Match 38.6%; Score 40.5; DB 5; Length 727;
Best Local Similarity 42.1%; Pred. No. 71;
Matches 8; Conservative 3; Mismatches 5; Indels 3; Gaps 1;

Qy 5 MNRSC---QSEKLGITYKT 20
||| :||:| |
Db 362 MNEKCVVNAEKILGYLNT 380

RESULT 6
US-08-793-035-9
; Sequence 9, Application US/08793035
; Patent No. 6011201

;; GENERAL INFORMATION:
;; APPLICANT: Slabas, Antoni R.
;; APPLICANT: White, Andrew
;; APPLICANT: Chase, Dianne
;; APPLICANT: Elborough, Keiran
;; APPLICANT: Pentem, Phillip A.
;; TITLE OF INVENTION: B-Ketoacyl ACP Reductase Genes From
;; TITLE OF INVENTION: Brassica Napus
;; NUMBER OF SEQUENCES: 10
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Arnold White & Durkee
;; STREET: P.O. Box 4433
;; CITY: Houston
;; STATE: TX
;; COUNTRY: US
;; ZIP: 77210-4433

;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/793,035
;; FILING DATE: 28-JUL-1997
;; CLASSIFICATION: 800
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: GB 9414622.2
;; FILING DATE: 20-JUL-1994

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: GB95/01678
;; FILING DATE: 17-JUL-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Kammerer, Patricia A.
;; REGISTRATION NUMBER: 29,775
;; REFERENCE/DOCKET NUMBER: MOBT:132
;; TELEPHONE: 713.787.1400
;; TELEFAX: 713.787.1440

;; INFORMATION FOR SEQ ID NO: 9:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 315 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear

US-08-793-035-9

Query Match 38.1%; Score 40; DB 3; Length 315;
Best Local Similarity 35.0%; Pred. No. 36;
Matches 7; Conservative 6; Mismatches 7; Indels 7; Gaps 0;

Qy 1 NLGKMNRSQCSEKLGITYKT 20
|:|:| :||:| |
Db 216 NIGQANYAAKAGVIGFSKT 235

RESULT 7
US-08-793-035-10
; Sequence 10, Application US/08793035
; Patent No. 6011201

;; GENERAL INFORMATION:
;; APPLICANT: Slabas, Antoni R.
;; APPLICANT: White, Andrew
;; APPLICANT: Chase, Dianne
;; APPLICANT: Elborough, Keiran
;; APPLICANT: Pentem, Phillip A.
;; TITLE OF INVENTION: B-Ketoacyl ACP Reductase Genes From
;; TITLE OF INVENTION: Brassica Napus
;; NUMBER OF SEQUENCES: 10
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Arnold White & Durkee
;; STREET: P.O. Box 4433
;; CITY: Houston
;; STATE: TX
;; COUNTRY: US
;; ZIP: 77210-4433

;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/793,035
;; FILING DATE: 28-JUL-1997
;; CLASSIFICATION: 800
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: GB 9414622.2
;; FILING DATE: 20-JUL-1994

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: GB95/01678
;; FILING DATE: 17-JUL-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Kammerer, Patricia A.
;; REGISTRATION NUMBER: 29,775
;; REFERENCE/DOCKET NUMBER: MOBT:132
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 713.787.1400
;; TELEFAX: 713.787.1440

;; INFORMATION FOR SEQ ID NO: 10:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 315 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear

US-08-793-035-10

Query Match 38.1%; Score 40; DB 3; Length 315;
Best Local Similarity 35.0%; Pred. No. 36;
Matches 7; Conservative 6; Mismatches 7; Indels 7; Gaps 0;

Qy 1 NLGKMNRSQCSEKLGITYKT 20
|:|:| :||:| |
Db 216 NIGQANYAAKAGVIGFSKT 235

RESULT 8
US-08-467-948A-29
; Sequence 29, Application US/08467948A
; Patent No. 5998164

;; GENERAL INFORMATION:
;; APPLICANT: Li, Yi
;; APPLICANT: CAO, LIANG

APPLICANT: NI, JIAN
APPLICANT: GENTZ, REINER
APPLICANT: BULT, CAROL J.
APPLICANT: SUTTON III, GRANGER G.
APPLICANT: ROSEN, CRAIG A.
TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein
TITLE OF INVENTION: Coupled Receptor GPR2
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVE., NW, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,948A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04079
FILING DATE: 30-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.1140003/EKS/KLM
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 325 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-08-467-948A-29

Query Match 35.2%; Score 37; DB 2; Length 325;
Best Local Similarity 50.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 8 SCQSEKLIQYTK 19
|||||: |
Db 265 SCQSEILRYMK 276

RESULT 9
US-08-467-947A-29
Sequence 29, Application US/08467947A
Patent No. 6090575
GENERAL INFORMATION:
APPLICANT: LI, YI
APPLICANT: CAO, LIANG
APPLICANT: NI, JIAN
APPLICANT: GENTZ, REINER
APPLICANT: BULT, CAROL J.
APPLICANT: SUTTON III, GRANGER G.
APPLICANT: ROSEN, CRAIG A.
TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein
TITLE OF INVENTION: Coupled Receptor GPR1
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVE., NW, SUITE 600
CITY: WASHINGTON
STATE: DC

COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,947A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04079
FILING DATE: 30-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.1140002/EKS/KLM
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 325 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-08-467-947A-29

Query Match 35.2%; Score 37; DB 3; Length 325;
Best Local Similarity 50.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 8 SCQSEKLIQYTK 19
|||||: |
Db 265 SCQSEILRYMK 276

RESULT 10
US-08-988-876-8
Sequence 8, Application US/08988876
Patent No. 6063596
GENERAL INFORMATION:
APPLICANT: Lal, Preeti
APPLICANT: Bandman, Olga
APPLICANT: Hillman, Jennifer L.
APPLICANT: Yue, Henry
TITLE OF INVENTION: G PROTEIN COUPLED RECEPTORS ASSOCIATED
TITLE OF INVENTION: WITH IMMUNE RESPONSE
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/988,876
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.

NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 South Wacker Drive, Seventh Floor
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/847,007A
FILING DATE: 01-MAY-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: No. 6083480nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 97,209
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
TELEFAX: 312-913-0002
TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
TYPE: amino acid
TOPOLOGY: circular
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1..6
OTHER INFORMATION: /label= Cyclic
OTHER INFORMATION: /note= "The amino terminus and the side chain sulfur
OTHER INFORMATION: atom of homomocysteine are covalently linked via
OTHER INFORMATION: a acetyl group."
FEATURE:
NAME/KEY: Modified-site
LOCATION: 6
OTHER INFORMATION: /label= Variant residues
OTHER INFORMATION: /note= "The residue is homomocysteine."
FEATURE:
NAME/KEY: Modified-site
LOCATION: 13
OTHER INFORMATION: /label= BAT
OTHER INFORMATION: /note= "The side chain sulfur atom of the cysteine is
OTHER INFORMATION: covalently linked to a BAT chelating moiety."
FEATURE:
NAME/KEY: Modified-site
LOCATION: 31
OTHER INFORMATION: /label= Amide
OTHER INFORMATION: /note= "The carboxyl terminus is modified to an
OTHER INFORMATION: amide"
US-08-847-007A-4

Query Match 34.3%; Score 36; DB 3; Length 31;
Best Local Similarity 47.4%; Pred. NO. 15;
Matches 9; Conservative 3; Mismatches 5; Indels 2; Gaps 1;

QY 2 LGKMNRCQSEKLGITYTKT 20
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Db 8 LGKL--SCELHKLQTYPRT 24

RESULT 14
US-08-847-007A-5
; Sequence 5, Application US/08847007A
; Patent No. 6083480
; GENERAL INFORMATION:
; APPLICANT: Dean, Richard T

APPLICANT: Bush, Larry R
APPLICANT: Pearson, Daniel P
APPLICANT: Lister-James, John
TITLE OF INVENTION: Radiolabeled peptides
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 South Wacker Drive, Seventh Floor
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/847,007A
FILING DATE: 01-MAY-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: No. 6083480nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 97,209
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
TELEFAX: 312-913-0002
TELEX:
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
TYPE: amino acid
TOPOLOGY: circular
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1..6
OTHER INFORMATION: /label= Cyclic
OTHER INFORMATION: /note= "The amino terminus and the side chain sulfur
OTHER INFORMATION: atom of homomocysteine are covalently linked via
OTHER INFORMATION: a acetyl group."
FEATURE:
NAME/KEY: Modified-site
LOCATION: 6
OTHER INFORMATION: /label= Variant residues
OTHER INFORMATION: /note= "The residue is homomocysteine."
FEATURE:
NAME/KEY: Modified-site
LOCATION: 31
OTHER INFORMATION: /label= Amide
OTHER INFORMATION: /note= "The carboxyl terminus is modified to an
OTHER INFORMATION: amide"
US-08-847-007A-5

Query Match 34.3%; Score 36; DB 3; Length 31;
Best Local Similarity 47.4%; Pred. NO. 15;
Matches 9; Conservative 3; Mismatches 5; Indels 2; Gaps 1;

QY 2 LGKMNRCQSEKLGITYTKT 20
||| ||| | | | | |
Db 8 LGKL--SCELHKLQTYPRT 24

RESULT 15
US-08-847-007A-6
; Sequence 6, Application US/08847007A
; Patent No. 6083480
; GENERAL INFORMATION:
; APPLICANT: Dean, Richard T
; APPLICANT: Bush, Larry R
; APPLICANT: Pearson, Daniel P

APPLICANT: Lister-James, John
 TITLE OF INVENTION: Radiolabeled Peptides
 NUMBER OF SEQUENCES: 8
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: McDonnell Boenhen Hulbert & Berghoff
 STREET: 300 South Wacker Drive, Seventh Floor
 CITY: Chicago
 STATE: IL
 COUNTRY: USA
 ZIP: 60606
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/847,007A
 FILING DATE: 01-MAY-1997
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: No. 6083480nan, Kevin E
 REGISTRATION NUMBER: 35,303
 REFERENCE/DOCKET NUMBER: 97,209
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312-913-0001
 TELEFAX: 312-913-0002
 TELEX:

INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 31 amino acids
 TYPE: amino acid
 TOPOLOGY: circular
 MOLECULE TYPE: peptide
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 1..6
 OTHER INFORMATION: /label= Cyclic
 OTHER INFORMATION: /note= "The amino terminus and the side chain sulfur
 OTHER INFORMATION: atom of homohomocysteine are covalently linked via
 OTHER INFORMATION: a acetyl group."
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 6
 OTHER INFORMATION: /label= Variant residues
 OTHER INFORMATION: /note= "The residue is homohomocysteine."
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 31
 OTHER INFORMATION: /label= Amide
 OTHER INFORMATION: /note= "The carboxyl terminus is modified to an
 OTHER INFORMATION: amide"

US-08-847-007A-6

Query Match 34.3%; Score 36; DB 3; Length 31;
 Best Local Similarity 47.4%; Pred. No. 15;
 Matches 9; Conservative 3; Mismatches 5; Indels 2; Gaps 1;
 QY 2 LGKMRSCQSEKLGTYTKT 20
 ||| ||| |||
 Db 8 LGKL--SCELHKLQTYPRT 24

Search completed: May 23, 2001, 15:30:08
 Job time: 415 sec

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OM protein - protein search, using sw model

Run on: May 23, 2001, 15:32:02 ; Search time 110.15 Seconds
(without alignments)
12.478 Million cell updates/sec

Title: US-08-887-977-10_COPY_271_290

Perfect score: 105

Sequence: 1 NLGKMRSCQSEKLGIVTKT 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 198801 seqs, 68722935 residues

Total number of hits satisfying chosen parameters: 198801

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_67:*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	105	100.0	369	2 JC5068	G protein-coupled
2	52	49.5	1123	2 T22608	hypothetical prote
3	46	43.8	248	2 H70447	3-oxoacyl-lacyl-ca
4	46	43.8	266	2 T08937	hypothetical prote
5	46	43.8	379	2 T09439	hypothetical prote
6	45	42.9	3071	2 T45584	hypothetical prote
7	44	41.9	320	2 S22450	3-oxoacyl-lacyl-ca
8	43	41.0	350	2 C36769	13R protein - huma
9	43	41.0	353	2 T44027	hypothetical prote
10	42	40.0	102	2 T49479	hypothetical prote
11	42	40.0	247	2 S77280	3-oxoacyl-lacyl-ca
12	42	40.0	307	2 C83188	probable ATP-bind
13	42	40.0	349	2 T04549	hypothetical prote
14	42	40.0	538	2 S22472	cell fusion protei
15	42	40.0	608	1 S28313	hypothetical prote
16	42	40.0	858	2 T00258	hypothetical prote
17	41.5	39.5	399	2 A60088	postsynaptic membr
18	41	39.0	164	2 S57074	H1T1 protein - yea
19	41	39.0	485	2 S36772	E-selectin - bovin
20	41	39.0	551	2 I46709	endothelial leukoc
21	41	39.0	556	2 T28960	hypothetical prote
22	41	39.0	610	2 A35046	E-selectin precurs
23	40	38.1	139	2 S22417	3-oxoacyl-lacyl-ca
24	40	38.1	208	2 T75427	mazG protein - Dei
25	40	38.1	247	2 T43015	hypothetical prote
26	40	38.1	363	2 T51992	MAP kinase kinase
27	40	38.1	363	2 T51294	MAP kinase kinase
28	40	38.1	631	2 JC2345	kexin-like protein
29	40	38.1	631	2 JC4298	hyaluronan recepto

30	40	38.1	644	2 JC2346	kexin-like protein
31	40	38.1	865	2 A47282	calcium-binding pr
32	40	38.1	873	2 A47283	calphotin - fruit
33	40	38.1	908	2 A83424	assimilatory nitra
34	40	38.1	932	2 I52527	PACE4A - mouse (fir
35	40	38.1	937	2 I53282	gene PACE4 protein
36	40	38.1	1149	2 T30869	probable adenosine
37	40	38.1	1307	2 T30887	146D nuclear prote
38	39.5	37.6	362	2 F64070	hISB bifunctional
39	39.5	37.6	412	2 A31995	nicotinic acetylch
40	39.5	37.6	412	2 S45064	nicotinic acetylch
41	39.5	37.6	1322	2 T15689	hypothetical prote
42	39	37.1	153	2 S63228	hypothetical prote
43	39	37.1	279	1 I40494	thymidylate syntha
44	39	37.1	279	1 SYBP3T	thymidylate syntha
45	39	37.1	296	2 T26723	hypothetical prote

ALIGNMENTS

RESULT 1

JC5068

G protein-coupled receptor CKR-L3 - human

C:Species: Homo sapiens (man)

C:Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 21-Jul-2000

C:Accession: JC5068

R:Zaballos, A.; Varona, R.; Gutierrez, J.; Lind, P.; Marquez, G.

Biochem. Biophys. Res. Commun. 227, 846-853, 1996

A:Title: Molecular cloning and RNA expression of two new human chemokine receptor-lik

A:Reference number: JC5067; MUID:97040707

A:Accession: JC5068

A:Molecule type: DNA

A:Residues: 1-369 <ZAB>

A:Cross-references: EMBL:Z79784; NID:gl668737; PIDN:CAB02144.1; PID:gl668738

C:Comment: This protein belongs to the family of alpha chemokine receptors.

C:Genetics:

A:Gene: GDB:CMK9R6; STRL22; GPR29; CCR6; CKR-L3; GPR-CY4

A:Cross-references: GDB:5370639; OMIM:601835

A:Map position: 6q27-6q27

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor; transmembrane protein

F:42-68/Domain: transmembrane #status predicted <TM1>

F:79-99/Domain: transmembrane #status predicted <TM2>

F:115-136/Domain: transmembrane #status predicted <TM3>

F:160-180/Domain: transmembrane #status predicted <TM4>

F:212-233/Domain: transmembrane #status predicted <TM5>

F:250-271/Domain: transmembrane #status predicted <TM6>

F:292-315/Domain: transmembrane #status predicted <TM7>

Query Match 100.0%; Score 105; DB 2; Length 369;
Best Local Similarity 100.0%; Pred. No. 9.4e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLGKMRSCQSEKLGIVTKT 20

Db 275 NLGKMRSCQSEKLGIVTKT 294

RESULT 2

T22608

hypothetical protein F54B11.3 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000

C:Accession: T22608

R:Swinnburne, J.

submitted to the EMBL Data Library, March 1996

A:Reference number: Z19588

A:Accession: T22608

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-1123 <WIL>

RESULT 5
T094.39

hypocnematal protein Ocr27 VC0821 [imported] - vibrio cholerae (group O1 strain N1696)
C.Species: Vibrio cholerae
C.Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 02-Sep-2000
C.Accession: T09439. C82276

Proc. Natl. Acad. Sci. U.S.A. 95, 3134-3139, 1998
A:Title: A *Vibrio cholerae* pathogenicity island associated with epidemic and pandemic
A:Reference number: 216672; MUID:98169509
A:Accession: T09439
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-379 <map>

A; Cross-references: EMBL:AF034434; NID:g3004923; PIDN:AAC1275.1; PID:g3004927
R; Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.
l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
A; Cross-references: EMBL:AF034434; NID:g3004923; PIDN:AAC1275.1; PID:g3004927
R; Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.
l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.

Nature 406, 477-483, 2000
A:Title: DNA Sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.
A:Reference number: A82035; MUID:20406833

A;Accession: C82276
A;Status: preliminary
A;Molecule type: DNA

A:Residues: 1-379 <HEI>
A:Cross-references: GB:AE003852; NID:9655268; PIDN:AAF93984.1; GSPDB:GN
A:Experimental source: serogroup O1; strain N16961; biotype El Tor
C:Genetics:
A:Gene: VC0821
A:Map position: 1
A:Note: part of the pathogenicity island (VPI); associated with epidemic and pandemic

Query Match	Score 46;	DB 2;	Length 379;
Best Local	Similarity	43.8%;	
Matches	9;	Conservative	45.0%;
	Pred. No. 6.1;		
	Mismatches	2;	
	Indels	9;	
	Gaps	0;	

QY 1 NLGKMNRSCQSEKLGITYKT 20
| | | : | | | |
DB 198 NKGKSGNESLNRKIIGYTNT 217

RESULT 6
 T45584
 hypothetical protein FilC1.220 - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 18-Feb-2000
 C:Accession: T45584
 R:Barques, M.; Collado, M.C.; Navarro, P.; Terol, J.; Perez-Alonso, M.; Mewes, H.W.;
 submitted to the Protein Sequence Database, December 1999
 A:Reference number: Z23007
 A:Accession: T45584

A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-3071 <BAR>
A; Cross-references: EMBL:AL132976
A; Experimental source: cultivar Columbia; BAC clone F11C1

C; Genetics:
A; Map position: 3
A; Introns: 94/2; 125/3; 865/2; 896/3; 1144/3; 1228/1; 1385/3; 1428/1; 1468/3; 1680/2;
419/1; 2525/3; 2564/3; 2620/3; 2662/3; 2692/3; 2728/2; 2778/1; 2805/3; 2837/3; 2878/3

A; Note: F1lC1.220
C; Superfamily: Arabidopsis thaliana hypothetical protein F1lC1.220

Query Match 42.9%; Score 45; DB 2; Length 3071;
Best Local Similarity 53.3%; Pred. No. 63;
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 NLGKNRSCQSEKLI 15
||||:| |||
Db 473 NLGKLSVTCYPEKII 487

RESULT 7

S22450
3-oxoacyl-[acyl-carrier-protein] reductase (EC 1.1.1.100) precursor, NADPH-dependent [va
N:Alternate names: beta-ketoacyl-ACP reductase
C:Species: Cuphea lanceolata
C:Date: 16-Feb-1995 #sequence_revision 23-Feb-1996 #text_change 17-Mar-2000
C:Accession: S22450; S19832
R:Klein, B.; Pawlowski, K.; Hoerick-Grandpierre, C.; Schell, J.; Toepfer, R.
Mol. Gen. Genet. 233, 122-128, 1992
A:Title: Isolation and characterization of a cDNA from Cuphea lanceolata encoding a beta
A:Reference number: S22450; MUID:92293104
A:Accession: S22450
A:Molecule type: mRNA
A:Residues: 1-320 <KLE>
A:Cross-references: EMBL:X64566; NID:g18045; PIDN:CAA45866.1; PID:g18046
A:Experimental source: immature embryo
C:Genetics:
A:Gene: Ckr27
A:Genome: nuclear
C:Function:
A:Description: EC 1.1.1.100 [validated; MUID:92293104]
A:Pathway: fatty acid biosynthesis
A:Note: integral part of the fatty acid synthase type II
C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
C:Keywords: chloroplast; fatty acid biosynthesis; NADP; oxidoreductase
F:1-63/Domain: transit peptide (chloroplast) #status predicted <TNP>
F:64-320/Product: 3-oxoacyl-[acyl-carrier-protein] reductase #status predicted <MAT>
F:78-258/Domain: short-chain alcohol dehydrogenase homology <SADH>
F:227/Active site: Tyr #status predicted

Query Match 41.9%; Score 44; DB 2; Length 320;
Best Local Similarity 45.0%; Pred. No. 11;
Matches 9; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

Qy 1 NLGKNRSCQSEKLIQYTKT 20
| | | | : | | | | |
Db 221 NAGQANYSAKAGVIGFTKT 240

RESULT 8

C36769
13R protein - human herpesvirus 6 (strain Uganda-1102)
C:Species: human herpesvirus 6
C:Date: 26-Jul-1991 #sequence_revision 26-Jul-1991 #text_change 02-Jun-2000
C:Accession: C36769
R:Lawrence, G.L.; Chee, M.; Craxton, M.A.; Gompels, U.A.; Honess, R.W.; Barrrell, B.G.
J. Virol. 64, 287-299, 1990
A:Title: Human herpesvirus 6 is closely related to human cytomegalovirus.
A:Reference number: A33560; MUID:90080132
A:Accession: C36769
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-350 <LAW>
A:Cross-references: GB:M28243
C:Superfamily: human herpesvirus 4 BGLF3 protein

Query Match 41.0%; Score 43; DB 2; Length 350;
Best Local Similarity 58.3%; Pred. No. 18;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 9 CQSEKLIQYTKT 20
| | | : | | | |
Db 181 CQSDSCFGYSKT 192

RESULT 9

T44027
hypothetical protein U67 [imported] - human herpesvirus 6
C:Species: human herpesvirus 6
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
C:Accession: T44027; T44212
R:Isegawa, Y.; Mukai, T.; Nakano, K.; Kagawa, M.; Chen, J.; Mori, Y.; Sunagawa, T.; K
J. Virol. 73, 8053-8063, 1999
A:Title: Comparison of the complete DNA sequences of human herpesvirus 6 variants A a
A:Reference number: 222732; MUID:99412319
A:Accession: T44027
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-353 <ISE>
A:Cross-references: EMBL:AB021506; NID:g4995977; PIDN:BAA78288.1; PID:g4996055
A:Experimental source: strain HST; pop. variant B
R:Dominguez, G.; Dambaugh, T.R.; Stamey, F.R.; Dewhurst, S.; Inoue, N.; Pellett, P.E.
J. Virol. 73, 8040-8052, 1999
A:Title: Human herpesvirus 6B genome sequence: coding content and comparison with hum
A:Reference number: 222734; MUID:99412318
A:Accession: T44212
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-353 <DOM>
A:Cross-references: EMBL:AF157706; PIDN:AAD49668.1
A:Experimental source: strain 429; variant B
C:Genetics:
A:Gene: U67
C:Superfamily: human herpesvirus 4 BGLF3 protein

Query Match 41.0%; Score 43; DB 2; Length 353;
Best Local Similarity 58.3%; Pred. No. 18;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 9 CQSEKLIQYTKT 20
| | | : | | | |
Db 184 CQSDSCFGYSKT 195

RESULT 10

T49479
hypothetical protein B14D6.310 [imported] - Neurospora crassa
C:Species: Neurospora crassa
C:Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 18-Aug-2000
C:Accession: T49479
R:Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatu
submitted to the Protein Sequence Database, May 2000
A:Reference number: 225022
A:Accession: T49479
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-102 <SCH>
A:Cross-references: EMBL:AL356173; GSPDB:GN00116; NCSP:B14D6.310
A:Experimental source: BAC clone B14D6; strain OR74A
C:Genetics:
A:Gene: NCSP:B14D6.310
A:Map position: 6
C:Superfamily: Neurospora crassa hypothetical protein B14D6.310

Query Match 40.0%; Score 42; DB 2; Length 102;
Best Local Similarity 53.8%; Pred. No. 8.2;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 6 NRSCQSEKLIQYTKT 18
| | | | : | | | |
Db 5 NRSCNSQLISFT 17

RESULT 11
S77280
3-oxoacyl-[acyl-carrier-protein] reductase (EC 1.1.1.100) - *Synechocystis* sp. (strain PC
N/Alternate names: protein sir0886
C:Species: *Synechocystis* sp.
A:Variety: PC 5803
C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
C:Accession: S77280
R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis*
S.
A:Reference number: S74322; MUID:97061201
A:Accession: S77280
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-247 <KAN>
A:Cross-references: EMBL:D90907; GB:AB001339; NID:g1652618; PIDN:BAAL7614.1; PID:g165269
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C:Genetics:
A:Gene: fabG
C:Function:
A:Pathway: fatty acid biosynthesis
C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
C:Keywords: fatty acid biosynthesis; NADP; oxidoreductase
F:7-187/Domain: short-chain alcohol dehydrogenase homology <SADH>
F:156/Active site: Tyr #status predicted

Query Match 40.0%; Score 42; DB 2; Length 247;
Best Local Similarity 45.0%; Pred. No. 19;
Matches 9; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 1 NLGKNRSCQSEKLIYTKT 20
| | | | | | | | | |
DB 150 NPGQANYSAKAGVIGFTKT 169

RESULT 12
C83188
Probable ATP-binding component of ABC transporter PA3672 [imported] - *Pseudomonas aerugi*
C:Species: *Pseudomonas aeruginosa*
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: C83188
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic patho
A:Reference number: A82950; MUID:20437337
A:Accession: C83188
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-307 <STO>
A:Cross-references: GB:AE004786; GB:AE004091; NID:g9949822; PIDN:AAG07060.1; GSPDB:GN001
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA3672
C:Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homology

Query Match 40.0%; Score 42; DB 2; Length 307;
Best Local Similarity 58.3%; Pred. No. 23;
Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 6 NRSCQSEKLIY 17
| | | | | | | | | |
DB 67 NRTLQAQRILY 78

RESULT 13
T04549
hypothetical protein F28J12.190 - *Arabidopsis thaliana*
C:Species: *Arabidopsis thaliana* (mouse-ear cress)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 15-Sep-2000
C:Accession: T04549
R:Bevan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; Bancro
submitted to the Protein Sequence Database, February 1998
A:Reference number: 215377
A:Accession: T04549
A:Molecule type: DNA
A:Residues: 1-349 <BEV>
A:Cross-references: EMBL:AL021710
A:Experimental source: cultivar Columbia; BAC clone F28J12
C:Genetics:
A:Map position: 4
A:Introns: 27/3; 62/3; 90/3; 118/3; 224/2; 246/3; 264/3; 306/3
A:Note: F28J12.190
C:Superfamily: *Arabidopsis thaliana* hypothetical protein T20K18.190

Query Match 40.0%; Score 42; DB 2; Length 349;
Best Local Similarity 64.3%; Pred. No. 26;
Matches 9; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 LGKNRSCQSEKLI 15
| | | | | | | | | |
DB 27 LGSNRSCLCSVLI 40

RESULT 14
S52472
cell fusion protein precursor - mumps virus
C:Species: mumps virus
C:Date: 08-May-1995 #sequence_revision 21-Jul-1995 #text_change 24-Nov-1999
C:Accession: S52472
R:Cusi, M.G.
submitted to the EMBL Data Library, November 1994
A:Reference number: S52472
A:Accession: S52472
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-538 <CUS>
A:Cross-references: EMBL:X82887; NID:g683483; PIDN:CAA58060.1; PID:g683484
C:Superfamily: parainfluenza virus cell fusion protein

Query Match 40.0%; Score 42; DB 2; Length 538;
Best Local Similarity 35.0%; Pred. No. 39;
Matches 7; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 NLGKNRSCQSEKLIYTKT 20
| | | | | | | | | |
DB 56 NIQPIDNSCKSVTQYNTK 75

RESULT 15
S28313
hypothetical protein F02A9.5 - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: S28313
R:Barks, M.
submitted to the EMBL Data Library, December 1992
A:Reference number: S28296
A:Accession: S28313
A:Molecule type: DNA
A:Residues: 1-608 <BER>
A:Cross-references: EMBL:Z19555; NID:g6705; PID:g6711
C:Genetics:
A:Introns: 19/1; 55/2; 152/3; 352/1; 453/3; 505/2; 584/3
C:Superfamily: propionyl-CoA carboxylase beta chain

Query Match 40.0%; Score 42; DB 1; Length 608;
 Best Local Similarity 44.0%; Pred. NO. 44;
 Matches 11; Conservative 2; Mismatches 6; Indels 6; Gaps 1;

Qy 1 NLGKMNRSQSEKLI-----GYTK 19
 Db 8 NLGSRNTSIQSYVLLRLTRWERYLK 32

Search completed: May 23, 2001, 15:32:03
 Job time: 510 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 23, 2001, 15:36:20 ; Search time 62.39 Seconds
(without alignments)
10.981 Million cell updates/sec

Title: US-08-887-977-10_COPY_271_290
Perfect score: 105
Sequence: 1 NLGKNRSCQSEKLGTYTKT 20

Scoring table: BLOSUM62

Searched: Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	105	100.0	374	1 CKR6_HUMAN	P51684 homo sapien
2	63	60.0	367	1 CKR6_MOUSE	O54689 mus musculus
3	46	43.8	248	1 FABG_AOUAE	O67610 aquifex aeo
4	44	41.9	320	1 FABG_CUPLA	P28643 cuphea lanc
5	43	41.0	353	1 UL95_HSV6U	P24444 human herpe
6	42.5	40.5	730	1 KDGA_MOUSE	O88673 mus musculus
7	42	40.0	247	1 FAG1_SYNY3	P73574 synechocyst
8	42	40.0	414	1 YLPC_CAEEL	P34384 caenorhabdi
9	42	40.0	608	1 YLPC_CAEEL	P34385 caenorhabdi
10	41.5	39.5	411	1 RAPS_CHICK	O42393 gallus gall
11	41	39.0	164	1 HIT1_YEAST	P46973 saccharomyc
12	41	39.0	485	1 LEM2_BOVIN	P98107 bos taurus
13	41	39.0	551	1 LEM2_RABIT	P27113 oryctolagus
14	41	39.0	610	1 LEM2_HUMAN	P16581 homo sapien
15	40	38.1	201	1 FABG_BRANA	P27582 brassica na
16	40	38.1	340	1 ENDR_PAEPO	P27871 paenibacill
17	40	38.1	424	1 I131_MOUSE	O09030 mus musculus
18	40	38.1	794	1 HMNR_MOUSE	Q00547 mus musculus
19	40	38.1	865	1 CPN_DROME	Q02910 drosophila
20	40	38.1	937	1 PAC4_RAT	O63415 rattus norv
21	40	38.1	1149	1 AT1A_MOUSE	P07004 mus musculus
22	40	38.1	1164	1 AT1A_HUMAN	Q9Y290 homo sapien
23	39.5	37.6	362	1 HIS7_HAEIN	P44327 haemophilus
24	39.5	37.6	411	1 RAPS_HUMAN	Q13702 homo sapien
25	39.5	37.6	411	1 RAPS_MOUSE	P12672 mus musculus
26	39.5	37.6	745	1 NSF1_DROME	P46461 drosophila
27	39	37.1	153	1 YNZ5_YEAST	P53849 saccharomyc
28	39	37.1	227	1 TYSA_BACAT	O30394 bacillus at
29	39	37.1	230	1 TYSA_BACAM	O30397 bacillus am
30	39	37.1	244	1 FABG_BUCAI	P57432 buchnera ap
31	39	37.1	279	1 TYSA_BACSU	P42326 bacillus su
32	39	37.1	279	1 TYSY_BPHPT	P07606 bacterioph
33	39	37.1	342	1 CGGR_BACME	P35168 bacillus me

34 39 37.1 1 VAC1_YEAST P32609 saccharomyc
35 39 37.1 1 LEM2_RAT P98105 rattus norv
36 39 37.1 1 LEM2_MOUSE Q00590 mus musculus
37 39 37.1 1 YD64_MYCPN P75417 mycoplasma
38 39 37.1 1 MP10_HUMAN O00566 homo sapien
39 39 37.1 1 YC84_MYCPN P75493 mycoplasma
40 39 37.1 1 FOX2_NEUCR Q01373 neurospora
41 38.5 36.7 212 1 MAD2_PETHY Q07474 petunia hyb
42 38.5 36.7 419 1 PFTB_PEA Q04903 pismum sativ
43 38 36.2 102 1 YNI2_METTL P05410 methanococc
44 38 36.2 266 1 CD82_MOUSE P40237 mus musculus
45 38 36.2 314 1 MIAA_BACHD Q9KAC3 bacillus ha

ALIGNMENTS

RESULT 1
CKR6_HUMAN STANDARD; PRT; 374 AA.
ID CKR6_HUMAN STANDARD; PRT; 374 AA.
AC P51684; Q92846 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 40, Last annotation update)
DE 01-OCT-2000 (Rel. 40, Last annotation update)
DE C-C CHEMOKINE RECEPTOR TYPE 6 (C-C CKR-6) (CCR-6) (LARC
DE RECEPTOR) (GPR-CY4) (GPCY4) (CHEMOKINE RECEPTOR-LIKE 3) (CKR-L3)
DE (DRY6).
GN CKR6 OR CMKBR6 OR STRL22 OR GPR29 OR CKRL3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID:9606;
RN [1]
RP SEQUENCE FROM N.A., AND FUNCTION.
RX MEDLINE=973113465; PubMed=9169459;
RA Baba M., Imai T., Nishimura M., Kakizaki M., Takagi S., Hieshima K.,
RA Nomiyama H., Yoshie O.;
RT Identification of CKR6, the specific receptor for a novel
RT lymphocyte-directed CC chemokine LARC.;
RL J. Biol. Chem. 272:14893-14898(1997).
RN [2]
RP SEQUENCE FROM N.A.
RA Lautens L.L., Modi W., Bonner T.I.;
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=97040707; PubMed=8886020;
RA Zaballo A., Varona R., Gutierrez J., Lind P., Marquez G.;
RT Molecular cloning and RNA expression of two new human chemokine
RT receptor-like genes.;
RL Biochem. Biophys. Res. Commun. 227:846-853(1996).
RN [4]
RP SEQUENCE FROM N.A.
RA McCoy R., Perlmutter D.H.;
RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=97224503; PubMed=9070937;
RA Liao F., Lee H.-H., Farber J.M.;
RT Cloning of STRL22, a new human gene encoding a G-protein-coupled
RT receptor related to chemokine receptors and located on chromosome
RT 6q27.;
RL Genomics 40:175-180(1997).
CC -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-3-
CC ALPHA/LARC AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE
CC INTRACELLULAR CALCIUM IONS LEVELS.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- TISSUE SPECIFICITY: SPLEEN, LYMPH NODES, APPENDIX, AND FETAL
CC NATURAL KILLER CELLS, MONOCYTES, OR GRANULOCYTES.
CC -!- INDUCTION: INTERLEUKIN-2.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -!- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-6 IS THE INITIATOR.

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EMBL; U45984; AAB62714.1; -
EMBL; 279784; CAB02144.1; ALT_INIT.
EMBL; U60000; AAB06949.1; -
EMBL; U68030; AAC51124.1; -
EMBL; U68032; AAC51125.1; -
HSP; P34996; IDDD.
GCRDB; GCR_1037; -
GCRDB; GCR_1075; -
GCRDB; GCR_1906; -
GCRDB; GCR_1919; -
GCRDB; GCR_1941; -
GCRDB; GCR_2110; -
MIM; 601835; -
InterPro: IPR000276; -
Pfam: PF00001; 7tm1.1;
PRINTS; PR00237; GPCRHHODPSN.
PROSITE; PS00237; G_PROTEIN_RECP_FL_1; 1.
PROSITE; PS0262; G_PROTEIN_RECP_FL_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein.
DOMAIN 1 47 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 48 74 1 (POTENTIAL).
FT DOMAIN 75 83 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 84 104 2 (POTENTIAL).
FT DOMAIN 105 119 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 120 141 3 (POTENTIAL).
FT DOMAIN 142 159 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 160 180 4 (POTENTIAL).
FT DOMAIN 181 211 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 212 238 5 (POTENTIAL).
FT DOMAIN 239 254 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 255 279 6 (POTENTIAL).
FT DOMAIN 280 303 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 304 321 7 (POTENTIAL).
FT DOMAIN 322 374 CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
7 7
CARBOHYD 23 23 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 74 74 L -> V (IN REF. 4).
FT CONFLICT 86 86 L -> V (IN REF. 4).
FT CONFLICT 164 164 S -> T (IN REF. 5).
FT CONFLICT 182 182 T -> S (IN REF. 4).
FT CONFLICT 192 192 Q -> L (IN REF. 4).
FT CONFLICT 206 206 E -> V (IN REF. 4).
FT CONFLICT 225 225 I -> F (IN REF. 4).
FT CONFLICT 370 374 SFSMT -> VVLHYVIES (IN REF. 4).
SEQUENCE 374 AA; 42494 MW; D7F9633545990BC4 CRG64;

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RESULT 3
FABG_AQUAE
ID FABG_AQUAE STANDARD; PRT; 248 AA.
AC O67610;
DT 15-DEC-1998 (Rel. 37, Created)
DT 13-DEC-1998 (Rel. 37, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE 3-OXOACYL-[ACYL-CARRIER PROTEIN] REDUCTASE (EC 1.1.1.100) (3-KETOACYL-
DE ACYL CARRIER PROTEIN REDUCTASE).
GN FABG OR AQ_1716.
OS Aquifex aeolicus.
OC Bacteria; Aquificales; Aquificaceae; Aquifex.
OX NCBI_TaxID=63363;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=VF5;
RX MEDLINE=98196666; PubMed=9537320;
RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
RA Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber R.,
RA Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
RA "The complete genome of the hyperthermophilic bacterium Aquifex
RA aeolicus.";
RL Nature 392:353-358(1998).
CC -1- CATALYTIC ACTIVITY: (3R)-3-HYDROXYACYL-[ACYL-CARRIER PROTEIN] +
CC NADP(+) = 3-OXOACYL-[ACYL-CARRIER PROTEIN] + NADPH.
CC -1- PATHWAY: FIRST REDUCTION STEP IN THE FATTY ACID BIOSYNTHESIS
CC PATHWAY.
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.
CC -----
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CC -----
EMBL: AE000752; AAC07575.1;
DR InterPro: IPR002198;
DR InterPro: IPR002347;
DR Pfam: PF00106; adh_short; 1.
DR Pfam: PF00678; adh_short_C2; 1.
DR PRINTS: PR00080; SDRFAMILY.
DR PRINTS: PR00081; GDRDH.
DR PROSITE: PS00061; ADH_SHORT; 1.
KW Fatty acid biosynthesis; Oxidoreductase; NADP.
FT NP_BIND 12 36 NADP (BY SIMILARITY).
FT ACT_SITE 157 157 BY SIMILARITY.
SQ SEQUENCE 248 AA; 26867 MW; 5CFD9B9AD83F2C5 CRC64;

Query Match 43.8%; Score 46; DB 1; Length 248;
Best Local Similarity 45.0%; Pred. No. 1.6;
Matches 9; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 NLGKNRSCQSEKLGITYTKT 20
|:|:| | | | | | | | | | |
DQ 151 NVGQVNTTKAGLIGFTKS 170

RESULT 4
FABG_CUPLA
ID FABG_CUPLA STANDARD; PRT; 320 AA.
AC P28643;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE 3-OXOACYL-[ACYL-CARRIER PROTEIN] REDUCTASE PRECURSOR (EC 1.1.1.100)
DE (3-KETOACYL-ACYL CARRIER PROTEIN REDUCTASE).
GN CLKR27.
OS Cuphea lanceolata.

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OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
OC Myrtales; Lythraceae; Cuphea.
OX NCBI_TaxID=3930;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92293104; PubMed=1376402;
RA Klein B., Pawlowski K., Hoerick-Grandpierre C., Schell J.,
RA Toepfer R.;
RA "Isolation and characterization of a cDNA from Cuphea lanceolata
RA encoding a beta-ketoacyl-ACP reductase.";
RL Mol. Gen. Genet. 233:122-128(1992).
CC -1- CATALYTIC ACTIVITY: (3R)-3-HYDROXYACYL-[ACYL-CARRIER PROTEIN] +
CC NADP(+) = 3-OXOACYL-[ACYL-CARRIER PROTEIN] + NADPH.
CC -1- PATHWAY: FIRST REDUCTION STEP IN THE FATTY ACID BIOSYNTHESIS
CC PATHWAY.
CC -1- SUBUNIT: HOMOTETRAMER (PROBABLE).
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST AND NON-PHOTOSYNTHETIC
CC PLASTIDS.
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.
CC -----
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CC -----
EMBL: X64566; CAA45866.1;
DR PIR: S19832; S19832.
DR HSP: Q12634.1YBV.
DR InterPro: IPR002198;
DR InterPro: IPR002347;
DR Pfam: PF00106; adh_short; 1.
DR Pfam: PF00678; adh_short_C2; 1.
DR PRINTS: PR00080; SDRFAMILY.
DR PRINTS: PR00081; GDRDH.
DR PROSITE: PS00061; ADH_SHORT; 1.
KW Fatty acid biosynthesis; Oxidoreductase; NADP; Chloroplast;
KW Transit peptide.
FT TRANSIT 1 61 CHLOROPLAST (BY SIMILARITY).
FT CHAIN 62 320 3-OXOACYL-[ACYL-CARRIER PROTEIN]
FT NP_BIND 82 106 REDUCTASE.
FT ACT_SITE 227 227 NADP (BY SIMILARITY).
FT ACT_SITE 227 227 BY SIMILARITY.
SQ SEQUENCE 320 AA; 33103 MW; 06BAF0522B2B8C87 CRC64;

Query Match 41.9%; Score 44; DB 1; Length 320;
Best Local Similarity 45.0%; Pred. No. 4.3;
Matches 9; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 1 NLGKNRSCQSEKLGITYTKT 20
|:|:| | | | | | | | | | |
DQ 221 NAGQANYSAKAGVIGFTKT 240

RESULT 5
UL95_HSV6U
ID UL95_HSV6U STANDARD; PRT; 353 AA.
AC P24444;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE PROTEIN U67.
GN U67 OR 13R.
OS Human herpesvirus (type 6 / strain Uganda-1102) (HHV6).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Betaherpesvirinae; Roseolovirus.
OX NCBI_TaxID=10370;
RN [1]

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RP SEQUENCE FROM N.A.
 RX MEDLINE=90080132; PubMed=2152817;
 RA Lawrence G.L., Chee M., Craxton M.A., Gompels U.A., Honess R.W.,
 RA Barrall B.G.;
 RT "Human herpesvirus 6 is closely related to human cytomegalovirus.";
 RL J. Virol. 64:287-299(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95266321; PubMed=7747482;
 RA Gompels U.A., Nicholas J., Lawrence G., Jones M., Thomson B.J.,
 RA Martin M.E., Efstathiou S., Craxton M., Macaulay H.A.;
 RT "The DNA sequence of human herpesvirus-6: structure, coding content,
 RT and genome evolution.";
 RL Virology 209:29-51(1995).
 CC -!- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS TOGETHER EBV BGLF3,
 CC HVS-1 34, HSV-6 U67, AND HCMV UL95.
 CC -----
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 CC -----
 DR EMBL; M68963; AAA65575.1; -;
 DR EMBL; X83413; CAA58359.1; -;
 DR PIR; C36769; C36769.
 SQ SEQUENCE 353 AA; 39531 MW; E30E73D5D0ACEBA7 CRC64;

 Query Match 41.0%; Score 43; DB 1; Length 353;
 Best Local Similarity 58.3%; Pred. No. 7;
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 9 CQSEKLIYTKT 20
 |||: ||||
 DB 184 CQSDSCFGYSKT 195

 RESULT 6
 KDGA_MOUSE STANDARD; PRT; 730 AA.
 ID AC 088673;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE DIACYLGLYCEROL KINASE, ALPHA (EC 2.7.1.107) (DIGLYCERIDE KINASE) (DGK-
 DE ALPHA) (DAG KINASE ALPHA) (80 KDA DIACYLGLYCEROL KINASE).
 GN DGKA OR DAGK1.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 [1]
 RP SEQUENCE FROM N.A.
 RA Sanjuan M.A., Carrera A.C., Merida I.;
 RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: UPON CELL STIMULATION CONVERTS THE SECOND MESSENGER
 CC DIACYLGLYCEROL INTO PHOSPHATIDATE, INITIATING THE RESYNTHESIS
 CC OF PHOSPHATIDYLINOSITOLS AND ATTENUATING PROTEIN KINASE C
 CC ACTIVITY (BY SIMILARITY).
 CC -!- CATALYTIC ACTIVITY: ATP + 1,2-DIACYLGLYCEROL = ADP +
 CC 1,2-DIACYLGLYCEROL 3-PHOSPHATE.
 CC -!- ENZYME REGULATION: STIMULATED BY CALCIUM AND PHOSPHATIDYL SERINE.
 CC PHOSPHORYLATED BY PROTEIN KINASE C (BY SIMILARITY).
 CC -!- SUBUNIT: MONOMER (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE EUKARYOTIC DIACYLGLYCEROL KINASE
 CC FAMILY.
 CC -!- SIMILARITY: CONTAINS 2 ZINC-DEPENDENT PHORBOL-ESTER AND DAG
 CC BINDING DOMAINS.
 CC -!- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
 CC -----

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 CC -----
 DR EMBL; AF085219; AAC33483.1; -;
 DR MGD; MGI:102952; Dagk1.
 DR InterPro; IPR000756; -;
 DR InterPro; IPR001206; -;
 DR InterPro; IPR002048; -;
 DR InterPro; IPR002219; -;
 DR Pfam; PF00609; DAGKA; 1.
 DR Pfam; PF00781; DAGKC; 1.
 DR Pfam; PF00130; DAG-PE-bind; 2.
 DR Pfam; PF00036; ehand; 2.
 DR PROSITE; PS00479; DAG-PE_BIND_DOM_1; 2.
 DR PROSITE; PS00081; DAG-PE_BIND_DOM_2; 2.
 DR PROSITE; PS00018; EF_HAND; 2.
 KW Transferase; Kinase; Calcium-binding; Phorbol-ester binding;
 KW Multigene family.
 FT CA_BIND 124 135 SITE 1 (PROBABLE).
 FT CA_BIND 169 180 SITE 2 (PROBABLE).
 FT DOMAIN 207 254 PHORBOL-ESTER AND DAG BINDING (BY
 FT SIMILARITY).
 FT DOMAIN 271 320 PHORBOL-ESTER AND DAG BINDING (BY
 FT SIMILARITY).
 FT DOMAIN 370 495 CATALYTIC-A (POTENTIAL).
 FT DOMAIN 515 696 CATALYTIC-B (POTENTIAL).
 SQ SEQUENCE 730 AA; 82791 MW; 277D8975961599DE CRC64;

 Query Match 40.5%; Score 42.5; DB 1; Length 730;
 Best Local Similarity 60.0%; Pred. No. 17;
 Matches 9; Conservative 2; Mismatches 3; Indels 1; Gaps 1;
 QY 3 GRMNRSCQSEKLIGY 17
 |::|: ||: |||
 DB 37 GEMNREFCQGD-AIGY 50

 RESULT 7
 FAGL_SYNY3 STANDARD; PRT; 247 AA.
 ID FAGL_SYNY3
 AC P73574;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE 3-OXOACYL-[ACYL-CARRIER PROTEIN] REDUCTASE 1 (EC 1.1.1.100) (3-
 DE KETOACYL-ACYL CARRIER PROTEIN REDUCTASE 1).
 GN FAGB1 OR SILR0886.
 OS Synechocystis sp. (strain PCC 6803).
 CC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
 OX NCBI_TaxID=11148;
 [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97061201; PubMed=8905231;
 RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
 RA Miyajima N., Hirose M., Sugita M., Sasamoto S., Kimura T.,
 RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,
 RA Shimpou S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
 RA Tabata S.;
 RT "Sequence analysis of the genome of the unicellular cyanobacterium
 RT Synechocystis sp. strain PCC6803. II. Sequence determination of the
 RT entire genome and assignment of potential protein-coding regions.";
 RL DNA Res. 3:109-136(1996).
 CC -!- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 CC (SDR) FAMILY.
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CC -----

DR EMBL; D90907; BAA17614.1; -
DR InterPro; IPR002198; -
DR InterPro; IPR002347; -
DR Pfam; PF00106; adh_short; 1.
DR Pfam; PF00678; adh_short_C2; 1.
DR PRINTS; PR00080; SDRFAMILY.
DR PRINTS; PR00081; GDRHDH.
DR PROSITE; PS00061; ADH_SHORT; 1.
KW Fatty acid biosynthesis; Oxidoreductase; NADP.
FT NP_BIND 11 35 NADP (BY SIMILARITY).
FT ACT_SITE 156 156 BY SIMILARITY.
SQ SEQUENCE 247 AA; 25724 MW; 91EBF9409C777F20 CRC64;

Query Match 40.0%; Score 42; DB 1; Length 247;
Best Local Similarity 45.0%; Pred. No. 7.4;
Matches 9; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 1 NLGKMRSCQSEKLIGYTKT 20
| | | | | :|||
Db 150 NPGQANYSAKAGVIGTKT 169

RESULT 8
YLPD_CAEEL STANDARD; PRT; 414 AA.
AC P34384;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE HYPOTHETICAL 46.8 KDA PROTEIN F02A9.4B IN CHROMOSOME III.
GN F02A9.4.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_Taxid=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RX MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Ainscough R., Anderson K., Baynes C., Copsey T., Cooper J., Coulson A.,
RA Bonfield J., Burton J., Connell M., Copsey T., Favello A., Fraser A.,
RA Craxton M., Dear S., Du Z., Durbin R., Hawkins T., Hillier L., Jier M.,
RA Fulton L., Gardner A., Green P., Kershaw J., Kirsten J., Laister N.,
RA Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Showkneen R.,
RA Sims M., Smalton N., Smith A., Smith M., Sonhammer E., Staden K.,
RA Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
RA Watson R., Watson A., Weinstock L., Wilkinson-Sproat J.,
RA Wohldman P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
elegans";
RL Nature 368:32-38(1994).

CC -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; F02A9.4B (SHOWN HERE) AND
CC F02A9.4B (P34384); MAY BE PRODUCED BY ALTERNATIVE SPLICING.
CC -!- SIMILARITY: BELONGS TO THE ACID / PCOB FAMILY.
CC -----
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CC -----
CC EMBL; Z19555; CAA79618.1; -
CC PIR; S28313; S28313.
DR WormPep; F02A9.4A; CE00136.
DR InterPro; IPR000022; -
DR Pfam; PF01039; Carboxyl_trans; 1.
KW Hypothetical protein; Alternative splicing.
SQ SEQUENCE 608 AA; 66524 MW; 2502FB70D987B6E0 CRC64;

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CC -----

DR EMBL; Z19555; CAA79619.1; -
DR PIR; S28312; S28312.
DR WormPep; F02A9.4B; CE20652.
KW Hypothetical protein; Alternative splicing.
SQ SEQUENCE 414 AA; 46765 MW; 1BFD5BA193D14368 CRC64;

Query Match 40.0%; Score 42; DB 1; Length 414;
Best Local Similarity 44.0%; Pred. No. 12;
Matches 11; Conservative 2; Mismatches 6; Indels 6; Gaps 1;

QY 1 NLGKMRSCQSEKLI-----GYTK 19
| | | | | :|||
Db 8 NLGSRNTSIQSYRLLRTRWERYLK 32

RESULT 9
YLPD_CAEEL STANDARD; PRT; 608 AA.
AC P34385;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE HYPOTHETICAL 66.5 KDA PROTEIN F02A9.4A IN CHROMOSOME III.
GN F02A9.4.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_Taxid=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RX MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Ainscough R., Anderson K., Baynes C., Copsey T., Cooper J., Coulson A.,
RA Bonfield J., Burton J., Connell M., Copsey T., Favello A., Fraser A.,
RA Craxton M., Dear S., Du Z., Durbin R., Hawkins T., Hillier L., Jier M.,
RA Fulton L., Gardner A., Green P., Kershaw J., Kirsten J., Laister N.,
RA Latreille P., Lightening J., Lloyd C., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Showkneen R.,
RA Sims M., Smalton N., Smith A., Smith M., Sonhammer E., Staden K.,
RA Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
RA Watson R., Watson A., Weinstock L., Wilkinson-Sproat J.,
RA Wohldman P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
elegans";
RL Nature 368:32-38(1994).

CC -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; F02A9.4A (SHOWN HERE) AND
CC F02A9.4B (P34384); MAY BE PRODUCED BY ALTERNATIVE SPLICING.
CC -!- SIMILARITY: BELONGS TO THE ACID / PCOB FAMILY.
CC -----
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CC -----
CC EMBL; Z19555; CAA79618.1; -
CC PIR; S28313; S28313.
DR WormPep; F02A9.4A; CE00136.
DR InterPro; IPR000022; -
DR Pfam; PF01039; Carboxyl_trans; 1.
KW Hypothetical protein; Alternative splicing.
SQ SEQUENCE 608 AA; 66524 MW; 2502FB70D987B6E0 CRC64;

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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; Z19555; CAA79618.1; -
CC PIR; S28313; S28313.
DR WormPep; F02A9.4A; CE00136.
DR InterPro; IPR000022; -
DR Pfam; PF01039; Carboxyl_trans; 1.
KW Hypothetical protein; Alternative splicing.
SQ SEQUENCE 608 AA; 66524 MW; 2502FB70D987B6E0 CRC64;

Query Match 40.0%; Score 42; DB 1; Length 608;
Best Local Similarity 44.0%; Pred. No. 17;

QY 1 NLGMN-RSCQSEKLIYYTKT 20
 || : | : | : | : ||
Dd 87 NLA RSNCKLCEFOKTISYCKT 107

OC Eukary

aniata; Verte

leostomi;

OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Adrenal gland;
 RX MEDLINE=93382537; PubMed=7690465;
 RA Nguyen M., Strubel N.A., Bischoff J.;
 RT "A role for sialyl Lewis-X/A glycoconjugates in capillary
 RT morphogenesis";
 RL Nature 365:267-269(1993).
 CC -!- FUNCTION: EXPRESSED ON CYTOKINE INDUCED ENDOTHELIAL CELLS AND
 CC MEDIATES THEIR BINDING TO LEUKOCYTES. THE LIGAND RECOGNIZED BY
 CC ELAM-1 IS SIALYL-LEWIS X (ALPHA(1->3)FUCOSYLATED DERIVATIVES OF
 CC POLYLACTOSAMINE THAT ARE FOUND AT THE NONREDUCING TERMINI OF
 CC GLYCOLIPIDS).
 CC -!- FUNCTION: INVOLVED IN CAPILLARY MORPHOGENESIS BY BINDING TO A
 CC BOVINE CAPILLARY ENDOTHELIAL (BCE) CELL SIALYL LEWIS-X AND/OR
 CC SIALYL LEWIS A-CONTAINING LIGAND (PROBABLY).
 CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -!- SIMILARITY: TO OTHER SELECTINS/LECAMS.
 CC -!- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
 CC -!- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
 CC -!- SIMILARITY: CONTAINS 4 SUSHI (SCR) REPEATS; BOVINE E-LECTIN LACKS
 CC THE HUMAN SUSHI-4 AND 5 EQUIVALENTS.
 CC -----
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 CC -----
 CC EMBL; L12039; AAA02991.1; -
 DR HSP; P16581; IESL.
 DR InterPro: IPR000436; -
 DR InterPro: IPR000561; -
 DR InterPro: IPR001304; -
 DR InterPro: IPR002396; -
 DR Pfam; PF00008; EGF; 1.
 DR Pfam; PF00059; lectin_c; 1.
 DR Pfam; PF00084; sushi; 4.
 DR PRINTS; PR00343; SELECTIN.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS01186; EGF_2; 1.
 DR PROSITE; PS00615; C-TYPE LECTIN_1; 1.
 DR PROSITE; PS50041; C-TYPE LECTIN_2; 1.
 DR Cell adhesion; Transmembrane; Glycoprotein; EGF-like domain; Lectin;
 KW Selectin; Signal; Sushi; Repeat.
 FT SIGNAL 1 22 BY SIMILARITY.
 FT CHAIN 1 485
 FT DOMAIN 23 430
 FT TRANSMEM 431 453
 FT DOMAIN 454 485
 FT DOMAIN 39 139
 FT DOMAIN 140 176
 FT DOMAIN 180 422
 FT DOMAIN 180 238
 FT DOMAIN 241 300
 FT DOMAIN 303 363
 FT DOMAIN 366 422
 FT DISULFID 41 139
 FT DISULFID 112 131
 FT DISULFID 144 155
 FT DISULFID 149 164
 FT DISULFID 166 175
 FT DISULFID 181 224
 FT DISULFID 210 237
 FT DISULFID 242 286
 FT DISULFID 272 299
 FT DISULFID 304 349
 FT DISULFID 335 362
 FT DISULFID 367 408
 FT DISULFID 367 408

FT DISULFID 394 421 BY SIMILARITY.
 FT CARBOHYD 61 61 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 79 79 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 88 88 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 161 161 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 203 203 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 265 265 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 312 312 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 316 316 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 379 379 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 401 401 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 485 AA; 53200 MW; AE931C9B521E3904 CRC64;
 Query Match 39.08; Score 41; DB 1; Length 485;
 Best Local Similarity 42.98; Pred. No. 21;
 Matches 6; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
 QY 3 GKNRSCQSEKLG 16
 ||:|:| |::|
 Db 374 KLANNCSEGPVLG 387
 ||:|:| |::|
 RESULT 13
 LEM2_RABIT
 ID LEM2_RABIT STANDARD; PRT; 551 AA.
 AC P27113;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE E-SELECTIN PRECURSOR (ENDOTHELIAL LEUKOCYTE ADHESION MOLECULE 1)
 DE (ELAM-1) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 2) (LECAM2)
 DE (CD62E).
 GN SELE.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Heart;
 RX MEDLINE=92189729; PubMed=1372169;
 RA Larian J.D., Tsang T.C., Rumberger J.M., Burns D.K.;
 RT "Characterization of cDNA and genomic sequences encoding rabbit
 RT ELAM-1: conservation of structure and functional interactions with
 RT leukocytes";
 RL DNA Cell Biol. 11:149-162(1992).
 CC -!- FUNCTION: EXPRESSED ON CYTOKINE INDUCED ENDOTHELIAL CELLS AND
 CC MEDIATES THEIR BINDING TO LEUKOCYTES. THE LIGAND RECOGNIZED BY
 CC ELAM-1 IS SIALYL-LEWIS X (ALPHA(1->3)FUCOSYLATED DERIVATIVES OF
 CC POLYLACTOSAMINE THAT ARE FOUND AT THE NONREDUCING TERMINI OF
 CC GLYCOLIPIDS).
 CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -!- INDUCTION: BY CYTOKINES.
 CC -!- SIMILARITY: TO OTHER SELECTINS/LECAMS.
 CC -!- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
 CC -!- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
 CC -!- SIMILARITY: CONTAINS 5 SUSHI (SCR) REPEATS.
 CC -----
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 CC -----
 CC EMBL; M91004; AAA31243.1; -
 DR EMBL; M91005; AAA31244.1; -
 DR HSP; P16581; IKJA.
 DR InterPro: IPR000436; -
 DR InterPro: IPR000561; -
 DR InterPro: IPR001304; -

CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- POLYMORPHISM: A POLYMORPHISM IN POSITION 149 IS ASSOCIATED WITH A
 CC HIGHER RISK OF CORONARY ARTERY DISEASE (CAD). A SIGNIFICANTLY
 CC HIGHER MUTATION FREQUENCY (ARG-149) IS OBSERVED IN PATIENTS WITH
 CC ANGIOGRAPHICALLY PROVEN SEVERE ATHEROSCLEROSIS COMPARED WITH AN
 CC UNSELECTED POPULATION (SER-149).
 CC -1- SIMILARITY: TO OTHER SELECTINS/LECTINS.
 CC -1- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
 CC -1- SIMILARITY: CONTAINS 6 SUSHI (SCR) REPEATS.
 CC -1- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
 CC -1- DATABASE: NAME=PROW; NOTE=CD guide CD62e entry;
 CC WWW:"http://www.ncbi.nlm.nih.gov/prov/cd/cd62e.htm".
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; M30640; AAA52377.1; -;
 CC EMBL; M61893; AAA52375.1; -;
 CC EMBL; M61895; AAA52375.1; JOINED.
 CC EMBL; M61887; AAA52375.1; JOINED.
 CC EMBL; M61888; AAA52375.1; JOINED.
 CC EMBL; M61890; AAA52375.1; JOINED.
 CC EMBL; M61891; AAA52375.1; JOINED.
 CC EMBL; M61892; AAA52375.1; JOINED.
 CC EMBL; M24736; AAA52376.1; -;
 CC PIR; A32606; A32606.
 CC PIR; A35046; A35046.
 CC PIR; A38615; A38615.
 CC PDB; 1ESL; 31-AUG-94.
 CC PDB; 1KJA; 03-APR-96.
 CC MIM; 131210; -;
 CC InterPro; IPR000436; -;
 CC InterPro; IPR000561; -;
 CC InterPro; IPR001304; -;
 CC InterPro; IPR002396; -;
 CC Pfam; PF00008; EGF_1;
 CC Pfam; PF00059; lectin_c; 1.
 CC Pfam; PF00084; sush1; 6.
 CC PRINTS; PR00343; SELECTIN.
 CC PROSITE; PS00022; EGF_1; 1.
 CC PROSITE; PS01186; EGF_2; 1.
 CC PROSITE; PS00615; C-TYPE LECTIN_1; 1.
 CC PROSITE; PS00641; C-TYPE LECTIN_2; 1.
 CC Cell adhesion; Transmembrane; Glycoprotein; EGF-like domain; Lectin;
 CC Selectin; Signal; Sush1; Repeat; Polymorphism; 3D-structure.
 CC SIGNAL 1 21
 CC CHAIN 22 610
 CC E-SELECTIN.
 CC EXTRACELLULAR (POTENTIAL).
 CC TRANSMEM 557 578
 CC POTENTIAL.
 CC DOMAIN 579 610
 CC CYTOPLASMIC (POTENTIAL).
 CC C-TYPE LECTIN (SHORT FORM).
 CC DOMAIN 139 175
 CC EGF-LIKE.
 CC DOMAIN 179 548
 CC 6 X SUSHI (SCR) REPEATS.
 CC DOMAIN 179 238
 CC SUSHI 1.
 CC DOMAIN 241 300
 CC SUSHI 2.
 CC DOMAIN 303 363
 CC SUSHI 3.
 CC DOMAIN 366 426
 CC SUSHI 4.
 CC DOMAIN 429 489
 CC SUSHI 5.
 CC DOMAIN 492 548
 CC SUSHI 6.
 CC DOMAIN 548 610
 CC SUSHI 6.
 CC DISULFID 40 138
 CC DISULFID 111 130
 CC DISULFID 143 154
 CC DISULFID 148 163
 CC DISULFID 165 174
 CC DISULFID 180 224
 CC DISULFID 210 237
 CC DISULFID 242 286
 CC DISULFID 272 299
 CC BY SIMILARITY.
 CC BY SIMILARITY.
 CC BY SIMILARITY.
 CC BY SIMILARITY.

FT DISULFID 304 349 BY SIMILARITY.
 FT DISULFID 335 362 BY SIMILARITY.
 FT DISULFID 367 412 BY SIMILARITY.
 FT DISULFID 398 425 BY SIMILARITY.
 FT DISULFID 430 475 BY SIMILARITY.
 FT DISULFID 461 488 BY SIMILARITY.
 FT DISULFID 493 534 BY SIMILARITY.
 FT DISULFID 520 547 BY SIMILARITY.
 FT CARBOHYD 25 25 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 145 145 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 160 160 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 179 179 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 199 199 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 203 203 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 265 265 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 312 312 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 332 332 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 503 503 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 527 527 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT VARIANT 149 149 S -> R (ASSOCIATED WITH A RISK FACTOR FOR
 FT CAD).
 FT /FTID=VAR_004191.
 FT H -> Y (IN REF. 2).
 FT CONFLICT 468 468
 FT SEQUENCE 610 AA; 66655 MW; 7D43E3C0D1229229 CRC64;
 SQ
 Query Match 39.0%; Score 41; DB 1; Length 610;
 Best Local Similarity 50.0%; Pred. No. 26;
 Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
 QY 3 GKMNRSCOSEKILIG 16
 ||:||||:
 Db 500 GKINMSCSGEPVFG 513
 RESULT 15
 FABG_BRANA
 ID FABG_BRANA STANDARD; PRT; 201 AA.
 AC P27582;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE 3-OXOACYL-[ACYL-CARRIER PROTEIN] REDUCTASE (EC 1.1.1.100) (3-KETOACYL-
 DE ACYL CARRIER PROTEIN REDUCTASE) (FRAGMENTS).
 OS Brassica napus (rape).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
 OC Brassicales; Brassicaceae; Brassica.
 OX NCBI_TaxID=3708;
 RN [1]
 RP SEQUENCE OF 35-62 AND 81-84.
 RC TISSUE=Seed;
 RX MEDLINE=92223071; PubMed=1562581;
 RA Sheldon P.S., Kekwick R.G.O., Smith C.G., Sidebottom C.M.,
 RA Slabas A.R.;
 RT "3-oxoacyl-[ACP] reductase from oilseed rape (Brassica napus).";
 RL Biochim. Biophys. Acta 1120:151-159(1992).
 RN [2]
 RP SEQUENCE OF 63-201 FROM N.A., AND PARTIAL SEQUENCE.
 RC TISSUE=Seed;
 RX MEDLINE=92246853; PubMed=1575676;
 RA Slabas A.R., Chase D., Nishida I., Murata N., Sidebottom C.,
 RA Safford R., Kekwick R.G., Sheldon P.S., Hardie D.G., Mackintosh R.W.;
 RT "Molecular cloning of higher-plant 3-oxoacyl-(acyl carrier protein)
 RT reductase. Sequence identities with the nodG-gene product of the
 RT nitrogen-fixing soil bacterium Rhizobium meliloti.";
 RL Biochem. J. 283:321-326(1992).
 EC -1- CATALYTIC ACTIVITY: (3R)-3-HYDROXYACYL-[ACYL-CARRIER PROTEIN] +
 CC NADP(+) = 3-OXOACYL-[ACYL-CARRIER PROTEIN] + NADPH.
 CC -1- PATHWAY: FIRST REDUCTION STEP IN THE FATTY ACID BIOSYNTHESIS
 CC PATHWAY.
 CC -1- SUBUNIT: HOMOTETRAMER (PROBABLE).
 CC -1- SUBCELLULAR LOCATION: CHLOROPLAST AND NON-PHOTOSYNTHETIC

CC PLASTIDS.
CC -!- TISSUE SPECIFICITY: EMBRYO AND LEAF TISSUES.
CC -!- MISCELLANEOUS: EXHIBITS A MARKED PREFERENCE FOR ACYL-CARRIER
CC PROTEIN DERIVATIVES OVER COA DERIVATIVES AS SUBSTRATES.
CC -!- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.
CC -----
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CC -----
DR EMBL; X64463; CAA45793.1; -
DR HSSP; P19992; 2HSD.
DR InterPro; IPR002198; -
DR Pfam; PF00106; adh_short; 1.
DR Pfam; PF00678; adh_short_C2; 1.
DR PROSITE; PS00061; ADH_SHORT; 1.
KW Fatty acid biosynthesis; Oxidoreductase; NADP; Chloroplast.
FT NON_CONS 27 28
FT NON_CONS 34 35
FT NON_CONS 62 63
FT ACT_SITE 108 108 BY SIMILARITY.
SQ SEQUENCE 201 AA; 21042 MW; FD51B2E369D2D967 CRC64;

Query Match 38.1%; Score 40; DB 1; Length 201;
Best Local Similarity 35.0%; Pred. No. 13;
Matches 7; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Oy 1 NLGKMNRCQSEKLGITYTKT 20
|.:|.:|.:|.:|
Db 102 NIGQANYAAKAGVIGFSKT 121

Search completed: May 23, 2001, 15:36:21
Job time: 652 sec

Result No.	Score	Query		Length	DB	ID	Description
		Match					
1	58.1	58.1	367	11	Q9R1V0	Q9rlv0 mus musculus	
2	52	49.5	1123	5	Q20745	Q20745 caenorhabdi	
3	46	43.8	266	10	Q9SZS0	Q9szs0 arabidopsiis	
4	46	43.8	379	2	O68336	O68336 vibrio chol	
5	45	42.9	620	10	Q9ZQS4	Q9zqs4 perilla fru	
6	45	42.9	620	10	Q9SLX2	Q9slx2 perilla fru	
7	45	42.9	3071	10	Q9SND0	Q9snd0 arabidopsiis	
8	44	41.9	260	13	Q9YCX9	Q9ycx9 xenopus lae	
9	43	41.0	353	14	Q9WT06	Q9wt06 human herpe	
10	43	41.0	522	5	Q9U9C1	Q9uc1 manduca sex	
11	43	41.0	556	4	Q93000	Q93000 homo sapien	
12	43	41.0	680	4	Q92498	Q92498 homo sapien	
13	43	41.0	734	4	Q92771	Q92771 homo sapien	
14	43	41.0	906	4	Q92770	Q92770 homo sapien	
15	43	41.0	906	4	Q92998	Q92998 homo sapien	
16	42	40.0	102	3	Q9P5F7	Q9p5f7 neurospora	
17	42	40.0	349	10	Q49521	Q49521 arabidopsiis	
18	42	40.0	498	8	O98781	O98781 hypecomm lm	
19	42	40.0	538	14	Q83653	Q83653 mumps virus	


```

Query Match      49.5%   Score 52;   DB 5;   Length 1123;
Best Local Similarity 42.1%   Pred. No. 1.5;
Matches 8;   Conservative 5;   Mismatches 6;   Indels 0;   Gaps 0;

Qy      2  LGMNRSCQSEKLIGYTKT  20
      :||| | | | | | | | | |
Db      671  IGRKENTNCMQSKCVGHTKS  689

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Query Match      43.8%;   Score 46;   DB 2;   Length 379;
Best Local Similarity 45.0%;   Pred. No. 5.5;
Matches 9;   Conservative 2;   Mismatches 9;   Indels 0;   Gaps 0;

Qy 1 NLGKMNRSCQSEKLIQYTKT 20
      ||| : |||||
Db 198 NKGKSGNESLRKLIQYTN 217

```

RA Schnübler C.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP
RN
RA SEQUENCE FROM N.A.
RL EU Arabidopsis sequencing project;
RL Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
RN [3]
RP
RN
RA SEQUENCE FROM N.A.
RL Hilbert H., Braun M., Holzer E., Brandt A., Duesterhoeft A.,
RA Mwes H.W., Lemcke K., Mayer K.F.X.;

```

RESULT 5
Q9ZQS4 PRELIMINARY; PRT; 620 AA.
AC Q9ZQS4;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE MYC-RP.
GN MYC-RP.
OS Perilla frutescens
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I;
OC Lamiales; Lamiales; Perilla.
OX NCBI_TaxID=48386;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LEAF;
RA Gong Z., Yamagishi E., Yamazaki M., Saito K.;
RT "A constitutively expressed myc-like gene is involved in the
RT regulation of anthocyanin biosynthesis in the leaves of Perilla
RT frutescens.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB024050; BAA75513.1; -.
DR HSSP; P25912; 1HLO.
DR INTERPRO; IPR001092; -.
DR INTERPRO; IPR003015; -.
DR PFAM; PF00010; HLH; 1.
DR PROSITE; PS00038; HELIX_LOOP_HELIX; UNKNOWN_1.
SQ SEQUENCE 620 AA; 68702 MW; F9B6EBBD377DCF14 CRC64;

Query Match 42.9%; Score 45; DB 10; Length 620;
Best Local Similarity 44.4%; Pred. NO. 14;
Matches 8; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 2 LGKMRSCQSEKLIGYTK 19
II :|| :|| :||
Db 514 LGNKRKSCDTERMAGENK 531

RESULT 6
Q9SLX2 PRELIMINARY; PRT; 620 AA.
AC Q9SLX2;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE MYC-GP.
GN MYC-GP.
OS Perilla frutescens.
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I;
OC Lamiales; Lamiales; Perilla.
OX NCBI_TaxID=48386;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LEAF OF GREEN P. FRUTESCENS;
RA Gong Z., Yamagishi E., Yamazaki M., Saito K.;
RT "A constitutively expressed Myc-like gene involved in anthocyanin
RT biosynthesis from Perilla frutescens: molecular characterization,
RT heterologous expression in transgenic plants and transactivation in
RT yeast cells.";
RL Plant Mol. Biol. 41:33-44(1999).
DR EMBL; AB024051; BAA75514.1; -.
DR HSSP; P25912; 1HLO.
DR INTERPRO; IPR001092; -.
DR INTERPRO; IPR003015; -.
DR PFAM; PF00010; HLH; 1.
DR PROSITE; PS00038; HELIX_LOOP_HELIX; UNKNOWN_1.
SQ SEQUENCE 620 AA; 68718 MW; B0FD91AA9607D8B5 CRC64;

Query Match 42.9%; Score 45; DB 10; Length 620;

```

```

Best Local Similarity 44.4%; Pred. NO. 14;
Matches 8; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 2 LGKMRSCQSEKLIGYTK 19
II :|| :|| :||
Db 514 LGNKRKSCDTERMAGENK 531

RESULT 7
Q9SND0 PRELIMINARY; PRT; 3071 AA.
AC Q9SND0;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE HYPOTHETICAL 343.7 KDA PROTEIN.
GN FlICI.220.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
OC Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Barchiesi M., Collado M.C., Navarro P., Terol J., Perez-Alonso M.,
RA Mewes H.W., Lemcke K., Mayer K.F.X., Quetier F., Salanoubat M.;
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
DR EMBL; AL132976; CAB62317.1; -.
DR INTERPRO; IPR000005; -.
DR PROSITE; PS00041; HTH_ARAC_FAMILY_1; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 3071 AA; 343689 MW; 4A3F7C9F71C92A25 CRC64;

Query Match 42.9%; Score 45; DB 10; Length 3071;
Best Local Similarity 53.3%; Pred. NO. 69;
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 NLGKMRSCQSEKLI 15
IIII::: :|| :||
Db 473 NLGKLSVTCYPEKII 487

RESULT 8
Q9YCX9 PRELIMINARY; PRT; 260 AA.
AC Q9YCX9;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE CALBINDIN D28K.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=INTESTINE;
RX MEDLINE=98232071; PubMed=9572360;
RA Amano T., Noro N., Kawabata H., Kobayashi Y., Yoshizato K.;
RT "Metamorphosis-associated and region-specific expression of calbindin
RT gene in the posterior intestinal epithelium of Xenopus laevis larva.";
RL Dev. Growth Differ. 40:177-188(1998).
DR EMBL; U76636; AAD00259.1; -.
DR HSSP; P02618; ICDP.
DR INTERPRO; IPR002048; -.
DR PFAM; PF00036; ehand; 4.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_4.

```

```

OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Spingioidea; Spingidae; Spinginae; Manduca.
OC NCBI_TaxID=7130;
RP [1]
RP SEQUENCE FROM N.A.
RA Stevens J.L., Snyder M.J., Koener J.F., Feyerisen R.;
RT "Inducible p450s of the Cyp9 family from larval Manduca sexta
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
RL EMBL: AF172279; AAD51036.1; -
DR INTERPRO: IPR001128; -
DR INTERPRO: IPR002401; -
DR INTERPRO: IPR002402; -
DR INTERPRO: IPR002403; -
DR PFAM: PF00067; p450; 1.
DR PRINTS: PR00385; P450.
DR PRINTS: PR00463; EP450I.
DR PRINTS: PR00464; EP450II.
DR PRINTS: PR00465; EP450IV.
DR PROSITE: PS00086; CYTOCHROME_P450; UNKNOWN_1.
FT NON_TER 1
SQ SEQUENCE 522 AA; 59951 MW; D2951BB872591E29 CRC64;

Query Match 41.0%; Score 43; DB 5; Length 522;
Best Local Similarity 46.7%; Pred. No. 25;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 NLGKNRSCQSEKLI 15
Db |||: |||: :|
398 NLGRANRCKKADFII 412

RESULT 11
Q93000 PRELIMINARY; PRT; 556 AA.
AC Q93000;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-AUG-1998 (TrEMBLrel. 07, Last annotation update)
DE CHL1 PROTEIN (FRAGMENT).
GN CHL1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RP [1]
RP SEQUENCE FROM N.A.
RA Ouellette M.M., Wright W.E., Shay J.W.;
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
RL EMBL: U75969; AAB18751.1; -
FT NON_TER 1
SQ SEQUENCE 556 AA; 61643 MW; 1357F45F750756B2 CRC64;

Query Match 41.0%; Score 43; DB 4; Length 556;
Best Local Similarity 43.5%; Pred. No. 27;
Matches 10; Conservative 4; Mismatches 5; Indels 4; Gaps 1;

QY 1 NLGKNRSCQ----SEKLIYTK 19
Db |||: |||: |||:|
216 NLFKVRQYCEKSMISRKLFQFTE 238

RESULT 12
Q92498 PRELIMINARY; PRT; 680 AA.
AC Q92498;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE CHL1 PROTEIN.
GN HCHL-1/KRG-2.

```


GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 23, 2001, 15:28:33 ; Search time 184.73 Seconds
(without alignments)
8.974 Million cell updates/sec

Title: US-08-887-977-10_COPY_291_319

Perfect score: 158

Sequence: 1 VTEVLAFLHCLNPVLYAFIGKFRNYFL 29

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 390729 seqs, 57163235 residues

Total number of hits satisfying chosen parameters: 390729

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_0401.*
1: /SID56/gcgdata/geneseq/geneseq/AA1980.DAT.*
2: /SID56/gcgdata/geneseq/geneseq/AA1981.DAT.*
3: /SID56/gcgdata/geneseq/geneseq/AA1982.DAT.*
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5: /SID56/gcgdata/geneseq/geneseq/AA1984.DAT.*
6: /SID56/gcgdata/geneseq/geneseq/AA1985.DAT.*
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13: /SID56/gcgdata/geneseq/geneseq/AA1992.DAT.*
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17: /SID56/gcgdata/geneseq/geneseq/AA1996.DAT.*
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20: /SID56/gcgdata/geneseq/geneseq/AA1999.DAT.*
21: /SID56/gcgdata/geneseq/geneseq/AA2000.DAT.*
22: /SID56/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	158	100.0	365	19 W48086	Human dendritic ce
2	158	100.0	365	21 Y97077	Primate (human) ch
3	124	78.5	332	18 W26766	Human chemokine re
4	124	78.5	352	18 W27407	Human CCR5, Homo
5	124	78.5	352	18 W27123	Human chemokine re
6	124	78.5	352	18 W27125	Macaque chemokine
7	124	78.5	352	18 W07602	Human G-protein ch
8	124	78.5	352	19 W23835	Human CC chemokine
9	124	78.5	352	20 W88232	HIV-1 co-receptor
10	124	78.5	352	21 Y80128	Human G-protein ch
11	124	78.5	371	19 W23834	Human CC chemokine

12	124	78.5	439	20 Y41280	Fusion protein con
13	121	76.6	354	15 R53932	Interleukin 8 (IL-
14	121	76.6	355	13 R28272	Sequence in a high
15	121	76.6	355	16 R80950	Recombinant high a
16	121	76.6	360	17 R99274	Chemokine receptor
17	121	76.6	360	21 B07498	A human CCR4 chemo
18	120	75.9	209	21 B58414	Lung cancer associ
19	120	75.9	355	15 R52749	C-C chemokine rece
20	120	75.9	355	17 W03376	CC-chemokine recep
21	120	75.9	355	17 W03377	CC-chemokine recep
22	120	75.9	355	17 W03378	CC-chemokine recep
23	120	75.9	355	18 W31850	Human eosinophil e
24	120	75.9	355	18 W26588	Human MIP-1 alpha/
25	120	75.9	355	18 W27124	Human chemokine re
26	120	75.9	355	18 W25751	Human MIP-lalpha/R
27	120	75.9	355	18 W10100	Human C-C chemokin
28	120	75.9	355	19 W51744	Human C-C chemokin
29	120	75.9	355	19 W51745	Human C-C chemokin
30	120	75.9	355	19 W51746	Human C-C chemokin
31	120	75.9	355	21 B20571	Human CC-chemokine
32	116	73.4	350	13 R27791	Interleukin-8 rece
33	116	73.4	350	16 R68811	Interleukin-8 rece
34	116	73.4	350	16 R80756	Interleukin 8 rece
35	116	73.4	350	16 R80951	Recombinant high a
36	116	73.4	350	17 R09989	Human IL-8 recepto
37	116	73.4	355	15 R53748	Seven transmembran
38	116	73.4	355	19 W48722	Human V28 seven tr
39	116	73.4	355	21 B21692	Human 7TM receptor
40	116	73.4	355	21 B21693	Human 7TM receptor
41	116	73.4	355	21 Y90642	Human G protein-co
42	116	73.4	355	21 Y90677	Human mutant G pro
43	116	73.4	1060	16 R70123	IL8-R type 1-GBP 1
44	115	72.8	355	18 W29179	Rat CC chemokine r
45	115	72.8	359	19 W64778	A murine CXC chemo

ALIGNMENTS

RESULT 1

W48086
ID W48086 standard; Protein; 365 AA.

XX
AC W48086;

DF 11-JUN-1998 (first entry)

XX Human dendritic cell chemokine receptor.

XX Human; thymus expressed chemokine; TECK; MIP-3alpha; MIP-3beta;
KW receptor; dendritic cell; macrophage; inflammation; asthma.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 193 /note= "encoded by CAN"

XX W09801557-A2.

XX 15-JAN-1998.

XX 02-JUL-1997; 97WO-US10819.

XX 04-JUN-1997; 97US-0048593.

XX 05-JUL-1996; 96US-0675814.

XX 11-OCT-1996; 96US-0028329.

XX (SCHE) SCHERING CORP.

XX Gish KC, Schall TJ, Vicari A, Wang W, Zlotnik A;

XX WPI; 1998-101054/09.

DR N-PSDB; V15418.
 XX Novel chemokines, e.g. thymus expressed chemokine - used for
 PT treating inflammatory conditions including asthma.
 XX
 PS Claim 3; Page 94-95; 202pp; English.
 XX
 CC The present sequence represents human dendritic cell chemokine receptor.
 CC Antibodies which bind to the protein can be used in detecting or
 CC diagnosing various immunological conditions related to expression
 CC of the protein. The nucleic acid can be used for screening and
 CC isolating DNA clones for the chemokines, especially from other
 CC species. The chemokine can be used in the treatment of conditions
 CC associated with abnormal physiology or development, including
 CC inflammatory conditions such as asthma.
 XX
 SQ Sequence 365 AA;

Query Match 100.0%; Score 158; DB 19; Length 365;
 Best Local Similarity 100.0%; Pred. No. 7.6e-17;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VTEVLAFLHCCLNPLVLYAFIGQKFRNYFL 29
 |||||
 DB 291 vtevlafhlhcclnplvlyafigqkfrnyfl 319

RESULT 2
 Y97077
 ID Y97077 standard; Protein; 365 AA.
 XX
 AC Y97077;
 XX
 DT 04-DEC-2000 (first entry)
 XX
 DE Primate (human) chemokine receptor CCR6.
 XX
 KW MIP-3-alpha; chemokine; CCR6 receptor; ligand; cytostatic; agonist;
 KW antagonist; anti-psoriatic; dermatological; immunosuppressive;
 KW anti-inflammatory.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 193
 FT Misc-difference 193 /note= "Encoded by CAN#"
 XX
 PN W0200046248-A1.
 XX
 PD 10-AUG-2000.
 XX
 PF 02-FEB-2000; 2000WO-US00511.
 XX
 PR 03-FEB-1999; 99US-0244281.
 XX
 PA (SCHE) SCHERING CORP.
 XX
 PI Oldham ER, Homey B, Dieu-Nosjean M, Caux C, Zlotnik A;
 XX
 DR WPI; 2000-543477/49.
 DR N-PSDB; A51971.
 XX
 PT Novel methods for modulating the migration of cells within or to the
 PT skin using MIP-3-alpha or CCR6 agonists or antagonists, useful for
 PT treating skin disorders, e.g. cancer
 XX
 PS Disclosure; Page 53-54; 61pp; English.
 XX
 CC The MIP-3-alpha chemokine is expressed in inflamed skin cells. This
 CC chemokine is the ligand for the CCR6 receptor. MIP-3-alpha or CCR6
 CC agonists or antagonists can be used to modulate the migration of a cell
 CC within or to the skin of a mammal. MIP-3-alpha can be used to purify a

CC population of cells expressing a MIP-3-alpha receptor. The methods are
 CC useful for treating a mammalian subject with a skin disease or condition,
 CC e.g. cancer, metastasis, psoriasis, atopic or contact dermatitis,
 CC systemic lupus erythematosus and lichen ruber planus, or for treating
 CC skin transplants or grafts.
 XX
 SQ Sequence 365 AA;

Query Match 100.0%; Score 158; DB 21; Length 365;
 Best Local Similarity 100.0%; Pred. No. 7.6e-17;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VTEVLAFLHCCLNPLVLYAFIGQKFRNYFL 29
 |||||
 DB 291 vtevlafhlhcclnplvlyafigqkfrnyfl 319

RESULT 3
 W26766
 ID W26766 standard; Protein; 332 AA.
 XX
 AC W26766;
 XX
 DT 21-MAY-1998 (first entry)
 XX
 DE Human chemokine receptor MMLR-CCR.
 XX
 KW Mammalian mixed lymphocyte receptor; chemokine receptor; MMLR-CCR;
 KW human; monocyte; macrophage; chemotaxis; haematopoiesis; infection;
 KW inflammation; proliferative disease; cardiovascular disease;
 KW tumour; rheumatoid arthritis; alveolitis; atherosclerosis;
 KW chronic granulomatous disease; asthma; myasthenia gravis;
 KW diabetes; inflammatory bowel disease; toxic shock syndrome;
 KW septic shock; Chediak-Higashi syndrome; therapy; diagnosis.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 107..128
 FT /note= "conserved peptide"
 FT Misc-difference 121 /note= "a claimed polypeptide has isoleucine at
 FT residue 121"
 XX
 PN W09741225-A2.
 XX
 PD 06-NOV-1997.
 XX
 PF 25-APR-1997; 97WO-US06993.
 XX
 PR 26-APR-1996; 96US-0638081.
 XX
 PA (INCY-) INCYTE PHARM INC.
 XX
 PI Au-Young J, Bandman O, Coleman R, Wilde CG;
 DR WPI; 1997-549729/50.
 DR N-PSDB; T99542.
 XX
 PT Polynucleotide encoding MMLR-CCR or MPHG-CCR chemokine receptor -
 PT useful to study, diagnose and treat, e.g. infection, inflammation,
 PT solid tumour and proliferative and cardiovascular disease
 XX
 PS Claim 8; Page 37-38; 59pp; English.
 XX
 CC This protein comprises human MMLR-CCR, a novel C-C chemokine
 CC receptor associated with monocyte/macrophage infiltration and
 CC chemotaxis and haematopoiesis. The amino acid sequence was deduced
 CC from a cDNA clone (see T99542) obtained from a cDNA library made
 CC from mononuclear cells collected on day 2 of a mixed lymphocyte
 CC culture, i.e. cells associated with inflammation and
 CC immunomodulation. Another novel chemokine receptor, MPHG-CCR

CC (see W36767), is also claimed. MMLR-CCR contains 7 transmembrane
 CC spanning segments connected by a series of intracellular and
 CC extracellular loops. MMLR-CCR and MHPG-CCR can be used to study,
 CC diagnose and treat disease states in which normal leukocyte
 CC function is perturbed by normal leukopoiesis or inappropriate
 CC activation via chemokine agonists or antagonists, such as infection,
 CC inflammation, proliferative disease, tumorigenesis, autoimmune
 CC disease, abnormal cell proliferation, solid tumours, cardiovascular
 CC disease, rheumatoid arthritis, alveolitis, atherosclerosis, chronic
 CC granulomatous disease, asthma, myasthenia gravis, diabetes,
 CC inflammatory bowel disease, toxic shock syndrome, septic shock and
 CC Chediak-Higashi syndrome.

XX Sequence 332 AA;

Query Match 78.5%; Score 124; DB 18; Length 332;
 Best Local Similarity 65.5%; Pred. No. 1.5e-11;
 Matches 19; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 VTEVLAFLHCCLPVLYAFIGOKERNYFL 29
 ||||| |||||:||||:||||:||||| |
 Db 261 vtetgmthccinpiiyafvgekfnyll 289

RESULT 4

W27407
 ID W27407 standard; Protein; 352 AA.

XX W27407;

XX 14-APR-1998 (first entry)

XX Human CCR5.

XX Human Cys-Cys chemokine receptor 5; CCR5;
 KW human immunodeficiency virus; type 1; type 2; HIV-1; HIV-2;
 KW diagnosis; treatment; prevention;
 KW inflammatory disease; rheumatoid arthritis; glomerulonephritis;
 KW asthma; idiopathic pulmonary fibrosis; psoriasis; viral infection;
 KW cancer; atherosclerosis; autoimmune disorder.

XX Homo sapiens.

XX WO9732019-A2.

XX 04-SEP-1997.

XX 28-FEB-1997; 97WO-BE00023.

XX 06-AUG-1996; 96EP-0870102.

XX 01-MAR-1996; 96EP-0870021.

XX (EURO-) EUROSREEN SA.

XX Libert F, Parmentier M, Samson M, Vassart G;

XX WPI; 1997-479829/44.

XX N-PSDB; T90117.

XX Active and inactive forms of human CC chemokine receptor CCR-5 -
 PT useful to diagnose, prevent and/or treat inflammatory disorders,
 PT autoimmune disease and viral infection

XX Claim 4; Fig 1b-c; 94pp; English.

XX The present sequence is human CC (Cys-Cys) chemokine receptor
 CC 5 (CCR5), which is stimulated by MIP-1 alpha, MIP-1 beta or RANTES
 CC chemokines, but not by monocyte chemoattractant protein 1 (MCP-1),
 CC MCP-3, MCP-3, interleukin-8 (IL-8) or growth related gene product
 CC alpha (GRO alpha) chemokines. Active CCR-5 is also a receptor of
 CC human immunodeficiency virus type 1 or type 2 (HIV-1 or HIV-2).
 CC CCR5 or its cDNA can be used to diagnose, treat and/or prevent

CC inflammatory diseases, e.g. rheumatoid arthritis,
 CC glomerulonephritis, asthma, idiopathic pulmonary fibrosis and
 CC psoriasis, viral infections, especially HIV-1 or HIV-2 infection,
 CC cancer, atherosclerosis and autoimmune disorders.

XX Sequence 352 AA;

Query Match 78.5%; Score 124; DB 18; Length 352;
 Best Local Similarity 65.5%; Pred. No. 1.6e-11;
 Matches 19; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 VTEVLAFLHCCLPVLYAFIGOKERNYFL 29
 ||||| |||||:||||:||||:||||| |
 Db 281 vtetgmthccinpiiyafvgekfnyll 309

RESULT 5

W27123
 ID W27123 standard; Protein; 352 AA.

XX W27123;

XX 14-DEC-1997 (first entry)

XX Human chemokine receptor 88C.

XX Chemokine receptor 88C; atherosclerosis; rheumatoid arthritis;
 KW tumour; asthma; viral infection; AIDS; inflammation;
 KW autoimmune disease; therapy; diagnosis; leukocyte trafficking;
 KW G protein coupled receptor; ligand; modulator; antibody; human.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Domain 1..32
 /label= Extracellular_domain
 FT Domain 56..67
 /label= Intracellular_domain
 FT Domain 89..112
 /label= Extracellular_domain
 FT Domain 125..145
 /label= Intracellular_domain
 FT Domain 166..191
 /label= Extracellular_domain
 FT Domain 213..235
 /label= Intracellular_domain
 FT Domain 259..280
 /label= Extracellular_domain
 FT Domain 301..352
 /label= Intracellular_domain

XX WO9722698-A2.

XX 26-JUN-1997.

XX 20-DEC-1996; 96WO-US20759.

XX 07-JUN-1996; 96US-0661393.

XX 20-DEC-1995; 95US-0575967.

XX (ICOS-) ICOS CORP.

XX Gray PW, Raport CJ, Schweickart VL;

XX WPI; 1997-341689/31.

XX N-PSDB; T85161.

XX New nucleic acid encoding chemokine receptors 88-2B and 88C - used
 PT to modulate leukocyte trafficking, e.g. for treatment of
 PT inflammation, tumours, viral infections, autoimmune diseases, etc.
 XX Claim 16; Page 47-48; 65pp; English.

XX This polypeptide sequence comprises novel human chemokine receptor
 CC 88C, a G protein coupled receptor that is involved in leukocyte
 CC trafficking. Its amino sequence was deduced from a cDNA clone
 CC (T85161) isolated from a macrophage library. It shows 62% identity
 CC to CCCKR1. Chemokine receptor 88-2B (see W27124) has also been
 CC identified. 88C and 88-2B receptors and their polypeptide fragments
 CC can be produced in transformed host cells. The receptors, peptides
 CC comprising one or more of the extracellular or intracellular
 CC domains, and anti-receptor antibodies can be used to modulate
 CC receptor activities, particularly ligand and G protein binding, and
 CC are potentially useful in the treatment of
 CC atherosclerosis, rheumatoid arthritis, tumours, asthma, viral
 CC infection, AIDS, inflammatory conditions, pathological immune
 CC response, abnormal haematopoietic processes etc.
 XX
 SQ Sequence 352 AA;

Query Match 78.5%; Score 124; DB 18; Length 352;
 Best Local Similarity 65.5%; Pred. No. 1.6e-11;
 Matches 19; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 VTEVLAFLHCLNPLVYAFIGOKFRNYFL 29
 ||| | |||:||||:||||| |
 Db 281 vtetlgtmthccinpiiyafvgekrnyll 309

RESULT 6
 W27125
 ID W27125 standard; Protein; 352 AA.

XX

AC W27125;

XX

DT 14-DEC-1997 (first entry)

XX

DE Macaque chemokine receptor 88C.

XX

KW Chemokine receptor 88C; atherosclerosis; rheumatoid arthritis;

XX

KW tumour; asthma; viral infection; AIDS; inflammation;

XX

KW autoimmune disease; therapy; diagnosis; leukocyte trafficking;

XX

KW G protein coupled receptor; ligand; modulator; antibody.

XX

OS Macaca sp.

XX

PN W09722698-A2.

XX

PD 26-JUN-1997.

XX

PF 20-DEC-1996; 96WO-US20759.

XX

PR 07-JUN-1996; 96US-0661393.

XX

PR 20-DEC-1995; 95US-0575967.

XX

XX (ICOS-) ICOS CORP.

PA

PI Gray PW, Raport CJ, Schweickart VL;

XX

DR WPI: 1997-341689/31.

XX

DR N-PSDB: T85163.

XX

PT New nucleic acid encoding chemokine receptors 88-2B and 88C - used

XX

PT to modulate leukocyte trafficking, e.g. for treatment of

XX

PT inflammation, tumours, viral infections, autoimmune diseases, etc.

XX

PS Claim 36; Page 57-58; 65pp; English.

CC comprising one or more of the extracellular or intracellular
 CC domains, and anti-receptor antibodies can be used to modulate
 CC receptor activities, particularly ligand and G protein binding, and
 CC are potentially useful in the treatment of
 CC atherosclerosis, rheumatoid arthritis, tumours, asthma, viral
 CC infection, AIDS, inflammatory conditions, pathological immune
 CC response, abnormal haematopoietic processes etc. A hybridoma
 CC that produces an antibody that specifically binds to macaque 88C is
 CC claimed.
 XX
 SQ Sequence 352 AA;

Query Match 78.5%; Score 124; DB 18; Length 352;
 Best Local Similarity 65.5%; Pred. No. 1.6e-11;
 Matches 19; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 VTEVLAFLHCLNPLVYAFIGOKFRNYFL 29
 ||| | |||:||||:||||| |
 Db 281 vtetlgtmthccinpiiyafvgekrnyll 309

RESULT 7
 W07602
 ID W07602 standard; Protein; 352 AA.

XX

AC W07602;

XX

DT 26-FEB-1997 (first entry)

XX

DE Human G-protein chemokine receptor HDGNR10.

XX

KW G-protein chemokine receptor; HDGNR10; signal transduction;

XX

KW haematopoiesis; leukaemia; inflammation; rheumatoid arthritis;

XX

KW diagnosis; therapy.

XX

OS Homo sapiens.

XX

PN W09639437-A1.

XX

PD 12-DEC-1996.

XX

XX 06-JUN-1995; 95WO-US07173.

XX

PR 06-JUN-1995; 95WO-US07173.

XX

XX (HUMA-) HUMAN GENOME SCI INC.

XX

XX Li Y, Ruben SM;

PI

XX WPI: 1997-043072/04.

XX

DR N-PSDB: T44042.

XX

PT Human G-protein chemokine receptor, HDGNR10 - useful to identify

XX

PT (ant)agonists, for treatment of haematopoiesis, leukaemia, chronic

XX

PT and acute inflammation, rheumatoid arthritis, etc.

XX

PS Claim 1; Page 44-46; 61pp; English.

XX

XX Novel human mature G-protein chemokine receptor HDGNR10 (W07602)

CC

CC is a 7-transmembrane protein involved in signal transduction. Its

CC amino acid sequence was deduced from a cDNA clone (T44042) isolated

CC from a human monocyte library. Isolation of the cDNA allows

CC prodn. of recombinant HDGNR10 in host, e.g. E. coli. COS or Sf9,

CC cells. The recombinant receptor can be used to identify agonists

CC or antagonists of the receptor; such cpds. can be used to treat

CC conditions related to the under- and over-expression of G-protein

CC chemokine receptors.

XX

SQ Sequence 352 AA;

Query Match 78.5%; Score 124; DB 18; Length 352;

Best Local Similarity 65.5%; Pred. No. 1.6e-11;
Matches 19; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 VTEVLAFHLHCLNPVLYAFIGQKFRNVEL 29
||| | |||:||||:|||||
Db 281 vtetlgtmthccinpiiyafvgekfnyll 309

RESULT 8
W23835
ID W23835 standard; Protein; 352 AA.
XX W23835;
AC
XX
DT 08-JUN-1998 (first entry)
XX
DE Human CC chemokine receptor 5 (CCR5).
XX
XX CC chemokine receptor 5; CCR5; G-protein coupled receptor;
KW human immunodeficiency virus; HIV; CD4; AIDS; therapy;
KW transgenic animal.
XX
OS Homo sapiens.
FH
FH Key Location/Qualifiers
FH Domain 29..55
FT /label= I
FT /note= "transmembrane domain"
FT 109..120
FT Region
FT /note= "extracellular loop-1 (Claim 19)"
FT Domain 104..126
FT /label= III
FT /note= "transmembrane domain"
FT Domain 143..171
FT /label= IV
FT /note= "transmembrane domain"
FT Region 187..210
FT /note= "extracellular loop-2 (Claim 19)"
FT Domain 194..219
FT /label= V
FT /note= "transmembrane domain"
FT Domain 238..258
FT /label= VI
FT /note= "transmembrane domain"
FT Region 261..276
FT /note= "extracellular loop-3 (Claim 19)"
FT Domain 277..300
FT /label= VII
FT /note= "transmembrane domain"
XX
XX WO9745543-A2.
XX
XX 04-DEC-1997.
XX
XX 28-MAY-1997; 97WO-US09586.
XX
XX 28-MAY-1996; 96US-0018508.
XX
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Alkhatib G, Berger EA, Broder CC, Combadiere C;
PI Feng Y, Kennedy PE, Murphy PM;
XX
XX WPI; 1998-032650/03.
XX N-PSDB; T76920.
XX
XX CC chemokine receptor 5 polypeptide - used to inhibit membrane
PT fusion between HIV and a target cell
XX
XX Claim 68; Fig 1C; 70pp; English.
XX
XX This protein sequence comprises of a novel human macrophage-selective
CC CC chemokine receptor that has been designated CCR5. The sequence

CC was deduced from an isolated cDNA clone (see T76920). An Ala127Ieu
CC variant (see W238340 of CCR5 was also identified. The susceptibility
CC of human macrophages to HIV infection depends on cell surface
CC expression of CD4 and CCR5. CCR5 is a member of the 7-transmembrane
CC superfamily of G-protein coupled cell surface molecules. It plays
CC an essential role in the membrane fusion step of infection by some
CC HIV isolates. The establishment of stable, non-human cell lines
CC and transgenic mammals having cells that coexpress human CD4 and
CC CCR5 provides valuable tools for research of HIV infection.
CC Antibodies that bind to CCR5, CCR5 variants, and CCR5-binding
CC agents capable of blocking membrane fusion between HIV and target
CC cells represent potential anti-HIV therapeutics for macrophage
XX tropic strains of HIV.
XX
SQ Sequence 352 AA;

Query Match 78.5%; Score 124; DB 19; Length 352;
Best Local Similarity 65.5%; Pred. No. 1.6e-11;
Matches 19; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 VTEVLAFHLHCLNPVLYAFIGQKFRNVEL 29
||| | |||:||||:|||||
Db 281 vtetlgtmthccinpiiyafvgekfnyll 309

RESULT 9
W88232
ID W88232 standard; Protein; 352 AA.
XX
XX W88232;
AC
XX
DT 15-MAR-1999 (first entry)
XX
DE HIV-1 co-receptor CCR5.
XX
KW HIV-1; CCR5; CCR5m303; co-receptor; infection; diagnosis; AIDS;
KW gene therapy; human.
XX
OS Homo sapiens.
FH
FH Key Location/Qualifiers
FH Domain 32..56
FT /note= "transmembrane domain 1"
FT Domain 67..87
FT /note= "transmembrane domain 2"
FT Misc-difference 101
FT /note= "corresponds to TGT (CYS) in wild-type CCR5,
FT TGA (Stop) in CCR5m303"
FT Domain 103..124
FT /note= "transmembrane domain 3"
FT Domain 142..167
FT /note= "transmembrane domain 4"
FT Domain 200..223
FT /note= "transmembrane domain 5"
FT Domain 236..260
FT /note= "transmembrane domain 6"
FT Domain 275..301
FT /note= "transmembrane domain 7"
XX
XX WO9854317-A1.
XX
XX 03-DEC-1998.
XX
XX 29-MAY-1998; 98WO-EP03437.
XX
XX 30-MAY-1997; 97US-0048057.
XX
XX (MOND-) FOND MONDIALE RECH & PREVENTION SIDA.
XX Arenzana Siesdedos F, Beretta A, Braun J, Quillent C;
XX WPI; 1999-059835/05.
DR

DR N-PSDB; V84126.

XX New CCR5 variant protein of the HIV-1 co-receptor - useful in

PT developing resistance of CCR5-expressing cells to HIV-1 infection

PT

XX Disclosure; Page 34-35; 55pp; English.

PS

XX This is the amino acid sequence of wild-type human CCR5, which

CC serves as a co-receptor for infection by macrophage-tropic

CC (M-tropic) strains of HIV-1. The invention relates to the

CC identification of a CCR5 variant (see W88231), designated CCR5m303,

CC comprising the first two transmembrane domains of wild-type CCR5,

CC but lacking transmembrane domains 3-7. The presence of the

CC CCR5m303 variant with the wild type CCR5 allele shows a positive

CC correlation with resistance to infection with M-tropic HIV-1

CC strains, and may indicate slower progression of the disease. The

CC detection of CCR5 variants may be used to identify individuals at

CC lower risk of infection relative to the general population who, if

CC infected, may exhibit slower progression to AIDS. Probes and

CC primers (see V84127-36) are provided for use in diagnostic methods

CC for detecting the presence of such variants. A method is provided

CC for inhibiting HIV-1 infection of a cell expressing the CCR5

CC receptor. This involves introducing a nucleic acid encoding a CCR5

CC variant into the cell, thereby reducing the number of functional

CC CCR5 molecules present on the cell surface.

XX

SQ Sequence 352 AA;

Query Match 78.5%; Score 124; DB 20; Length 352;

Best Local Similarity 65.5%; Pred. No. 1.6e-11;

Matches 19; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 VTEVLAFLHCLNPVLYAFIGQKFRNYFL 29

III I III:II::II::II::II::II::II I

Db 281 vtetlgtmthccinpiiyafvgekfnyll 309

RESULT 10

ID Y80128 standard; Protein; 352 AA.

XX

AC Y80128;

XX

DT 19-MAY-2000 (first entry)

XX

DE Human G-protein chemokine receptor HDGNR10 SEQ ID NO:2.

XX

KW Human; G-protein coupled receptor; G-protein chemokine receptor;

KW HDGNR10; diagnosis; haematopoiesis; wound healing; coagulation;

KW angiogenesis; tumour; infection; leukaemia; psoriasis; allergy;

KW T-cell mediated autoimmune disease; atherogenesis; anaphylaxis;

KW inflammation; allergic reaction; silicosis; sarcoidosis;

KW rheumatoid arthritis; hyper-eosinophilia syndrome.

XX

OS Homo sapiens.

XX

PN US6025154-A.

XX

PD 15-FEB-2000.

XX

PF 06-JUN-1995; 95US-0466343.

XX

PR 06-JUN-1995; 95US-0466343.

XX

FA (HUMA-) HUMAN GENOME SCI INC.

XX

PI Li Y, Ruben SM;

XX

XX WPI; 2000-181807/16.

DR N-PSDB; 291481.

XX

PT Isolated nucleic acid encoding human G-protein chemokine receptor

PT

PT useful for diagnostic assays, scientific research and screening for

PT compounds which bind to and activate or inhibit activation of the

XX receptor polypeptides -

PS Claim 1; Fig 1; 22pp; English.

XX

CC The present sequence represents a human G-protein chemokine receptor

CC designated HDGNR10. HDGNR10 polynucleotides are useful in methods of

CC screening for compounds which bind to and either: (1) activate the

CC HDGNR10 polypeptides causing stimulation of haematopoiesis, wound

CC healing, coagulation, and angiogenesis; treatment of solid tumours,

CC chronic infections, leukaemia, T-cell mediated autoimmune diseases,

CC parasitic infections, psoriasis, and to stimulate growth factor

CC activity; or (2) inhibit activation of the HDGNR10 polypeptides which

CC is useful for preventing and/or treating allergy, atherogenesis,

CC anaphylaxis, malignancy, chronic and acute inflammation, histamine and

CC immunoglobulin E-mediated allergic reactions, prostaglandin-independent

CC fever, bone marrow failure, silicosis, sarcoidosis, rheumatoid

CC arthritis shock and hyper-eosinophilia syndrome. The polynucleotides

CC are also useful for diagnostic assays for detecting diseases related to

CC mutations in the nucleic acid sequences encoding the polypeptides and

CC for detecting an altered level of the soluble form of the receptor

CC polypeptides. The polynucleotides are also useful for in vitro purposes

CC related to scientific research, synthesis of DNA and manufacture of

CC DNA vectors.

XX

SQ Sequence 352 AA;

Query Match 78.5%; Score 124; DB 21; Length 352;

Best Local Similarity 65.5%; Pred. No. 1.6e-11;

Matches 19; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 VTEVLAFLHCLNPVLYAFIGQKFRNYFL 29

III I III:II::II::II::II::II::II I

Db 281 vtetlgtmthccinpiiyafvgekfnyll 309

RESULT 11

ID W23834 standard; Protein; 371 AA.

XX

AC W23834;

XX

DT 08-JUN-1998 (first entry)

XX

DE Human CC chemokine receptor 5 (CCR5) A127V variant.

XX

KW CC chemokine receptor 5; CCR5; G-protein coupled receptor;

KW human immunodeficiency virus; HIV; CD4; AIDS; therapy;

KW transgenic animal.

XX

OS Homo sapiens.

XX

XX Key Location/Qualifiers

FT Domain 48..74

FT /label= I

FT /note= "transmembrane domain"

FT Domain 123..145

FT /label= III

FT /note= "transmembrane domain"

FT Domain 162..190

FT /label= IV

FT /note= "transmembrane domain"

FT Domain 213..238

FT /label= V

FT /note= "transmembrane domain"

FT Domain 257..277

FT /label= VI

FT /note= "transmembrane domain"

FT Domain 296..319

FT /label= VII

FT /note= "transmembrane domain"

FT

```

XX PN WO9745543-A2.
XX XX
XX PD 04-DEC-1997.
XX XX
XX PF 28-MAY-1997; 97WO-US09586.
XX XX
XX PR 28-MAY-1996; 96US-0018508.
XX XX
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX XX
XX PI Alkhatib G, Berger EA, Broder CC, Combadiere C;
XX PI Feng Y, Kennedy PE, Murphy PM;
XX DR WPI; 1998-032650/03.
XX DR N-PSDB; T76919.
XX XX
XX CC chemokine receptor 5 polypeptide - used to inhibit membrane
XX CC fusion between HIV and a target cell
XX XX
XX PS Example 1; Fig 1B; 70pp; English.
XX XX
XX CC This protein sequence comprises an Alal27Leu variant of a novel
XX CC human macrophage-selective CC chemokine receptor (see also
XX CC W23835) that has been designated CCR5. The sequence was deduced
XX CC from an isolated cDNA clone (see T76919). The conservative
XX CC variation should not affect the activity of CCR5. The susceptibility
XX CC of human macrophages to HIV infection depends on cell surface
XX CC expression of CD4 and CCR5. CCR5 is a member of the 7-transmembrane
XX CC superfamily of G-protein coupled cell surface molecules. It plays
XX CC an essential role in the membrane fusion step of infection by some
XX CC HIV isolates. The establishment of stable, non-human cell lines
XX CC and transgenic mammals having cells that coexpress human CD4 and
XX CC CCR5 provides valuable tools for research of HIV infection.
XX CC Antibodies that bind to CCR5, CCR5 variants, and CCR5-binding
XX CC agents capable of blocking membrane fusion between HIV and target
XX CC cells represent potential anti-HIV therapeutics for macrophage
XX CC tropic strains of HIV.
XX SQ Sequence 371 AA;

Query Match 78.5%; Score 124; DB 19; Length 371;
Best Local Similarity 65.5%; Pred. No. 1.7e-11;
Matches 19; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy 1 VTEVLAFLHCLNPVLYAFIGQKFRNYFL 29
   ||| | |||:||||:||||:|||||
Db 300 vtetlgmthccinpiiyafvgekfrnyll 328

RESULT 12
Y41280
ID Y41280 standard; Protein; 439 AA.
XX XX
XX AC Y41280;
XX XX
XX DT 11-FEB-2000 (first entry)
XX XX
XX DE Fusion protein containing human chemokine receptor CCR-5.
XX XX
XX KW Prostaglandin; PG; E2EP3 receptor; E2EP2 receptor; CCR-5; human;
XX KW chemokine receptor; ss2 adrenergic receptor; small G-protein rho;
XX KW renal outer medullary potassium ion channel protein; ion-channel protein;
XX KW lambda phage repressor protein; G-protein coupled receptor; bacteria;
XX KW biochemical; vaccine; immunohistochemical; orphan receptor; HIV.
XX XX
XX OS Synthetic.
XX OS Homo sapiens.
XX XX
XX PN WO9953033-A1.
XX XX
XX PD 21-OCT-1999.

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XX PF 16-APR-1999; 99WO-US08214.
XX XX
XX PR 16-APR-1998; 98US-0081989.
XX XX
XX PA (UYVA-) UNIV VANDERBILT.
XX XX
XX PI Breyer RM, Ma L, Kennedy C;
XX XX
XX DR WPI; 1999-620416/53.
XX DR N-PSDB; Z24738.
XX XX
XX PT New nucleic acid constructs for high level expression of eukaryotic
XX PT proteins in bacteria, for producing e.g. chemokine receptor CCR-5 for
XX PT preventing HIV infection
XX XX
XX PS Disclosure; Page 49-53; 8lpp; English.
XX XX
XX CC The invention provides isolated nucleic acid sequences that encode rabbit
XX CC prostaglandin (PG) E2EP3 receptor, human PG E2EP2 receptor, human
XX CC chemokine receptor CCR-5, human ss2 adrenergic receptor, rat renal outer
XX CC medullary potassium ion channel protein or human small G-protein rho,
XX CC together with deduced protein sequences. Also provided is a method for
XX CC the production of eukaryotic proteins by culturing bacteria transformed
XX CC with vectors containing the above nucleic acid sequences or a nucleic
XX CC acid (I) that comprises: (i) first sequence that encodes either a
XX CC sequence comprising at least three positively charged amino acids, or a
XX CC DNA-binding protein, or a lambda phage repressor protein, placed upstream
XX CC of, and in frame with, (ii) a sequence encoding a protein. (I) are used
XX CC for recombinant production of eukaryotic proteins, particularly membrane
XX CC proteins, G-protein coupled receptors or ion-channel proteins, in
XX CC bacteria. These proteins are useful for biochemical or structural
XX CC studies; as therapeutic agents; in diagnostic and screening assays and as
XX CC antigens for use in vaccines, and for raising antibodies that are useful
XX CC as immunohistochemical markers, e.g. for orphan receptors or ion
XX CC channels. Antibodies raised against the chemokine receptor CCR-5 can be
XX CC used (when administered as antiserum or generated in vivo) to prevent
XX CC entry of human immune deficiency virus (HIV) into cells.
XX SQ Sequence 439 AA;

Query Match 78.5%; Score 124; DB 20; Length 439;
Best Local Similarity 65.5%; Pred. No. 2e-11;
Matches 19; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy 1 VTEVLAFLHCLNPVLYAFIGQKFRNYFL 29
   ||| | |||:||||:||||:|||||
Db 359 vtetlgmthccinpiiyafvgekfrnyll 387

RESULT 13
R53932
ID R53932 standard; Protein; 354 AA.
XX XX
XX AC R53932;
XX XX
XX DT 23-FEB-1995 (first entry)
XX XX
XX DE Interleukin 8 (IL-8) receptor.
XX XX
XX KW Interleukin; receptor; antiinflammatory; psoriasis; reperfusion;
XX KW rheumatoid arthritis; allograft; graft rejection.
XX XX
XX OS Homo sapiens.
XX XX
XX PN JP06100595-A.
XX XX
XX PD 12-APR-1994.
XX XX
XX PF 27-MAY-1991; 91JP-0149245.
XX XX
XX PR 27-MAY-1991; 91JP-0149245.

```

XX (UYBO-) UNIV BOSTON.
 XX WPI; 1994-156656/19.
 DR N-PSDB; Q63919.
 XX Recombinant interleukin-8 receptor polypeptide - having
 PT antiinflammatory properties
 XX Claim 1; Figure 1; 13pp; Japanese.
 XX Anti-inflammatory agents containing the interleukin-8 receptor
 CC polypeptide can be used for the treatment of psoriasis, rheumatoid
 CC arthritis and other acute and chronic inflammatory diseases,
 CC including reperfusion and allograft rejection.
 XX Sequence 354 AA;
 SQ

Query Match 76.6%; Score 121; DB 15; Length 354;
 Best Local Similarity 75.0%; Pred. No. 4.7e-11;
 Matches 21; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 AC R28272;
 XX 04-APR-1993 (first entry)
 DT Sequence in a high affinity recombinant rabbit interleukin-8
 DE (IL-8) receptor polypeptide in F3R.
 DE IL-8 receptor polypeptide; G-protein-coupled receptor.
 KW Oryctolagus cuniculus.
 OS WO9218641-A.
 XX 29-OCT-1992.
 PD 10-APR-1992; 92WO-US02977.
 XX 10-APR-1991; 91US-0685101.
 PR 09-JUL-1991; 91US-0726606.
 PR 09-DEC-1991; 91US-0803842.
 XX (REPK) REPLIGEN CORP..
 PA (UYBO-) UNIV BOSTON.
 XX Navarro J, Thomas KM, Witt DP;
 PI WPI; 1992-382123/46.
 DR N-PSDB; Q30011.
 XX Recombinant mammalian interleukin-8 receptor - used for screening
 PT interleukin-8 binding antagonists, used to treat inflammation
 XX Claim 2; Fig 1; 71pp; English.
 XX Rabbit high affinity IL-8 receptor gene was isolated from rabbit
 CC peritoneal neutrophils and used as a source of poly(A)+ RNA, to
 CC produce a rabbit neutrophil cDNA library. 250,000 recombinant
 CC plaques were screened for those which hybridized to an antisense
 CC oligonucleotide (Q30015). This probe was designed based on the
 CC sequence derived from the second transmembrane domain of G-protein-
 CC coupled receptors. After tertiary screening, six plaques were

CC isolated. The insert of one of these plaques, termed F3R was of 2.5
 CC kb in size. This insert was sequenced. The protein deduced from
 CC the F3R clone demonstrates that it belongs to the family of
 CC G-protein-coupled receptors. The deduced protein sequence
 CC indicates seven putative transmembrane segments.
 XX Sequence 355 AA;
 SQ

Query Match 76.6%; Score 121; DB 13; Length 355;
 Best Local Similarity 75.0%; Pred. No. 4.7e-11;
 Matches 21; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 QY 2 TEVLAFHCCLNPNVLYAFIGOKFRNYFL 29
 DB 295 teilgflhscnlpiyafignfrngfl 322
 II:| ||| ||||:||||| ||| ||
 RESULT 15
 R80950
 ID R80950 standard; Protein; 355 AA.
 XX AC R80950;
 XX 24-APR-1996 (first entry)
 DT Recombinant high affinity interleukin-8 receptor subtype A.
 DE IL-8A; IL-8B; receptor; monoclonal antibody; inflammatory disorder;
 KW anaphylaxis; systemic lupus erythematosus; rheumatoid arthritis;
 KW systemic necrotising vasculitis; psoriasis; asthma; allergy; ARDS;
 KW adult respiratory distress syndrome; neutrophil detection.
 XX Oryctolagus cuniculus.
 OS WO9525126-A1.
 XX 21-SEP-1995.
 PD 09-MAR-1995; 95WO-US03032.
 PF 02-MAY-1994; 94US-0237937.
 PR 15-MAR-1994; 94US-0210250.
 XX (REPK) REPLIGEN CORP..
 PA (UYBO-) UNIV BOSTON.
 XX Greenfield EA, Larosa GJ, Navarro J, Thomas KM;
 PI Witt DT;
 XX WPI; 1995-336945/43.
 DR N-PSDB; Q99949.
 XX Monoclonal antibody against recombinant IL-8 receptor polypeptide -
 PT useful for treating inflammatory disorders, for detecting
 PT neutrophil(s) and for isolating IL-8 receptor from liq.mixt.
 XX Claim 2; Fig 1A-B; 74pp; English.
 XX Monoclonal antibodies were raised against recombinant interleukin-8
 CC (IL-8) receptor subtypes A and B from both human and rabbit sources
 CC (R80950-53 encoded by Q99949-52). The A subtype receptor (IL-8rA) is
 CC a high affinity receptor and the B subtype receptor (IL-8rB) is a
 CC low affinity receptor. The monoclonal antibody (mAb) pref. binds to
 CC the IL-8 binding domain thus blocking its activation. The mAbs are
 CC useful for treating inflammatory disorders (see key words) and for
 CC detecting the presence of neutrophils in a biological sample. The
 CC mAbs are also useful in the isolation of IL-8 receptors from a mixture.
 XX Sequence 355 AA;
 SQ

Query Match 76.6%; Score 121; DB 16; Length 355;
 Best Local Similarity 75.0%; Pred. No. 4.7e-11;
 Matches 21; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 QY 2 TEVLAFHCCLNPNVLYAFIGOKFRNYFL 29
 DB 295 teilgflhscnlpiyafignfrngfl 322
 II:| ||| ||||:||||| ||| ||
 RESULT 15
 R80950
 ID R80950 standard; Protein; 355 AA.
 XX AC R80950;
 XX 24-APR-1996 (first entry)
 DT Recombinant high affinity interleukin-8 receptor subtype A.
 DE IL-8A; IL-8B; receptor; monoclonal antibody; inflammatory disorder;
 KW anaphylaxis; systemic lupus erythematosus; rheumatoid arthritis;
 KW systemic necrotising vasculitis; psoriasis; asthma; allergy; ARDS;
 KW adult respiratory distress syndrome; neutrophil detection.
 XX Oryctolagus cuniculus.
 OS WO9525126-A1.
 XX 21-SEP-1995.
 PD 09-MAR-1995; 95WO-US03032.
 PF 02-MAY-1994; 94US-0237937.
 PR 15-MAR-1994; 94US-0210250.
 XX (REPK) REPLIGEN CORP..
 PA (UYBO-) UNIV BOSTON.
 XX Greenfield EA, Larosa GJ, Navarro J, Thomas KM;
 PI Witt DT;
 XX WPI; 1995-336945/43.
 DR N-PSDB; Q99949.
 XX Monoclonal antibody against recombinant IL-8 receptor polypeptide -
 PT useful for treating inflammatory disorders, for detecting
 PT neutrophil(s) and for isolating IL-8 receptor from liq.mixt.
 XX Claim 2; Fig 1A-B; 74pp; English.
 XX Monoclonal antibodies were raised against recombinant interleukin-8
 CC (IL-8) receptor subtypes A and B from both human and rabbit sources
 CC (R80950-53 encoded by Q99949-52). The A subtype receptor (IL-8rA) is
 CC a high affinity receptor and the B subtype receptor (IL-8rB) is a
 CC low affinity receptor. The monoclonal antibody (mAb) pref. binds to
 CC the IL-8 binding domain thus blocking its activation. The mAbs are
 CC useful for treating inflammatory disorders (see key words) and for
 CC detecting the presence of neutrophils in a biological sample. The
 CC mAbs are also useful in the isolation of IL-8 receptors from a mixture.
 XX Sequence 355 AA;
 SQ

Best Local Similarity 75.0%; Pred. No. 4.7e-11;
Matches 21; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 2 TEVLAFHCCLNPNVLYAFIGQKERNYFL 29
||: ||| ||||: ||||| ||| ||
Db 295 tellgflhsclnpliyafignfrngfl 322

Search completed: May 23, 2001, 15:28:33
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OM protein - protein search, using sw model

Run on: May 23, 2001, 15:30:08 ; Search time 95.91 Seconds
(without alignments)
5.809 Million cell updates/sec

Title: US-08-887-977-10_COPY_291_319

Perfect score: 158

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 185757 seqs, 19210857 residues

Total number of hits satisfying chosen parameters: 185757

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Maximum Match 100%

Listing first 45 summaries

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- 4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	124	78.5	352	3	US-08-466-343D-2
2	124	78.5	352	4	US-09-087-232A-13
3	121	76.6	354	1	US-07-759-568-2
4	121	76.6	360	4	US-08-875-573-20
5	120	75.9	355	1	US-08-012-988A-2
6	120	75.9	355	1	US-08-450-393A-5
7	120	75.9	355	4	US-08-446-669-5
8	120	75.9	355	5	PCT-US95-00476-5
9	116	73.4	350	1	US-08-202-056-1
10	116	73.4	350	1	US-08-076-093A-2
11	116	73.4	350	1	US-08-450-393A-7
12	116	73.4	350	1	US-08-410-453A-1
13	116	73.4	350	1	US-08-701-265-2
14	116	73.4	350	1	US-08-410-454A-1
15	116	73.4	350	2	US-08-284-586-2
16	116	73.4	350	2	US-08-410-456A-1
17	116	73.4	350	2	US-08-805-478-2
18	116	73.4	350	2	US-08-802-627A-2
19	116	73.4	350	2	US-08-801-238-2
20	116	73.4	350	2	US-08-801-228-2
21	116	73.4	350	3	US-09-104-296-2
22	116	73.4	350	4	US-08-446-669-7
23	116	73.4	350	5	PCT-US95-00476-7
24	116	73.4	355	1	US-08-153-848-28
25	116	73.4	355	1	US-08-153-848-32
26	116	73.4	355	3	US-09-239-843A-28
27	116	73.4	355	3	US-09-299-843A-32

28	116	73.4	355	5	PCT-US93-11153-28	Sequence 28, Appl
29	116	73.4	355	5	PCT-US93-11153-32	Sequence 32, Appl
30	114	72.2	337	1	US-08-153-848-46	Sequence 46, Appl
31	114	72.2	337	3	US-09-239-843A-46	Sequence 46, Appl
32	114	72.2	337	5	PCT-US93-11153-46	Sequence 46, Appl
33	114	72.2	347	1	US-08-461-244-3	Sequence 3, Appl
34	114	72.2	352	1	US-08-202-056-3	Sequence 3, Appl
35	114	72.2	352	1	US-08-076-093A-4	Sequence 4, Appl
36	114	72.2	352	1	US-08-450-393A-6	Sequence 6, Appl
37	114	72.2	352	1	US-08-701-265-4	Sequence 4, Appl
38	114	72.2	352	2	US-08-284-586-4	Sequence 4, Appl
39	114	72.2	352	2	US-08-805-478-4	Sequence 4, Appl
40	114	72.2	352	2	US-08-802-627A-4	Sequence 4, Appl
41	114	72.2	352	2	US-08-801-238-4	Sequence 4, Appl
42	114	72.2	352	2	US-08-801-228-4	Sequence 4, Appl
43	114	72.2	352	3	US-09-104-296-4	Sequence 4, Appl
44	114	72.2	352	4	US-08-446-669-6	Sequence 6, Appl
45	114	72.2	352	5	PCT-US95-00476-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1
US-08-466-343D-2
; Sequence 2, Application US/08466343D
; Patent No. 6025154
; GENERAL INFORMATION:
; APPLICANT: LI, YI
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING HUMAN G-PROTEIN
; TITLE OF INVENTION: CHEMOKINE RECEPTOR HDGNR10 (AS AMENDED)
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVE., NW, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,343D
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.1150000/EKS/KLM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-466-343D-2

Query Match 78.5%; Score 124; DB 3; Length 352;
Best Local Similarity 65.5%; Pred. No. 2.4e-09;
Matches 19; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

OY 1 VTEVLAFLHCLNPLVYAFIGQKERNYFL 29
||| | |||:||||:|||||
Db 281 VTETLGLTHCCINPIIYAFVGEKERNYLL 309

```
RESULT 2
US-09-087-232A-13
; Sequence 13, Application US/09087232A
; Patent No. 6153431
; GENERAL INFORMATION:
; APPLICANT: Quillent et al.
; TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS CO-RECEPTOR
; TITLE OF INVENTION: VARIANTS ASSOCIATED WITH RESISTANCE TO VIRUS INFECTION.
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Baker & Botts, L.L.P. attn. Lisa Kole
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/087,232A
; FILING DATE: 28 MAY 1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/048,057
; FILING DATE: 30 MAY 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: KOLE, LISA B.
; REGISTRATION NUMBER: 35,225
; REFERENCE/DOCKET NUMBER: AP 31115
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 408-2628
; TELEFAX: (212) 765-2519
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-087-232A-13

Query Match 78.5%; Score 124; DB 4; Length 352;
Best Local Similarity 65.5%; Pred. No. 2.4e-09;
Matches 19; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Oy 1 VTEVLAFLHCLNPVLYAFYFGKFRNYFL 29
||| | ||| ||| ||| ||| ||| |
Db 281 VTETLGNTHCCINPIIYAFYGERFRNYLL 309

RESULT 3
US-07-759-568-2
; Sequence 2, Application US/07759568
; Patent No. 5374506
; GENERAL INFORMATION:
; APPLICANT: Murphy, Philip M.
; TITLE OF INVENTION: Cloning of cDNA Encoding a Functional
; TITLE OF INVENTION: Human Interleukin-8 Receptor
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cushman, Darby & Cushman
; STREET: 1615 L Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036-5601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/759,568
; FILING DATE: 19910913
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Scott, Watson T.
; REGISTRATION NUMBER: 26581
; REFERENCE/DOCKET NUMBER: WTS/5683/91535/WBH
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3000
; TELEFAX: 202-822-0944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 354 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-759-568-2

Query Match 76.6%; Score 121; DB 1; Length 354;
Best Local Similarity 75.0%; Pred. No. 5.9e-09;
Matches 21; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Oy 2 TEVLAFLHCLNPVLYAFYFGKFRNYFL 29
||| | ||| ||| ||| ||| ||| |
Db 294 TEILGLHSLNPVLYAFYFGKFRNGFL 321

RESULT 4
US-08-875-573-20
; Sequence 20, Application US/08875573
; Patent No. 6150132
; GENERAL INFORMATION:
; APPLICANT: Wells, Timothy N.C.
; APPLICANT: Power, Christine A.
; TITLE OF INVENTION: A-CHEMOKINE RECEPTOR ABLE TO BIND TO
; TITLE OF INVENTION: MCP-1, MIP-1 ALPHA AND/OR RANTES. ITS USES
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHUYE P.C.
; STREET: 1100 No. 6150132th Glebe Rd. 8th floor
; CITY: Arlington
; STATE: VA
; COUNTRY: USA
; ZIP: 22201-4741
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,573
; FILING DATE: 31-OCT-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB96/00143
; FILING DATE: 24-JAN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9501683.8
; FILING DATE: 27-JAN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilson, Mary J.
; REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 1430-172
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4000
; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
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;
; LENGTH: 360 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-875-573-20

Query Match 76.6%; Score 121; DB 4; Length 360;
Best Local Similarity 67.9%; Pred. No. 6e-09;
Matches 19; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 2 TEVLAFHCLNPNVLYAFIGQKFRNYL 29
|||:|||||:|:|:|:|
Db 289 TETLAFVHCCLNPIIYFLGKFRKYL 316

RESULT 5
US-08-012-988A-2
; Sequence 2, Application US/08012988A
; Patent No. 5652133
; GENERAL INFORMATION:
; APPLICANT: Murphy, Philip M.
; TITLE OF INVENTION: Cloning and Expression of Human
; TITLE OF INVENTION: Macrophage Inflammatory Protein-1 alpha (MIP-1
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94610
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/012,988A
; FILING DATE: 19930128
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Kenneth A.
; REGISTRATION NUMBER: 31,677
; REFERENCE/DOCKET NUMBER: 15280-118
; TELEPHONE: 415-543-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-012-988A-2

Query Match 75.9%; Score 120; DB 1; Length 355;
Best Local Similarity 66.7%; Pred. No. 8.1e-09;
Matches 18; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY 1 VTEVLAFHCLNPNVLYAFIGQKFRNY 27
||||:|||||:|:|:|:|
Db 285 VTEVIATHCCLNPNVLYAFVGERFRKY 311

RESULT 6
US-08-450-393A-5
; Sequence 5, Application US/08450393A
; Patent No. 5707815
; GENERAL INFORMATION:
; APPLICANT: Charo, Israel

;
; APPLICANT: Coughlin, Shaun
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
; STREET: 5 Palo Alto Square
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,393A
; FILING DATE: May 25, 1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Cserf, Luann
; REGISTRATION NUMBER: 31,822
; REFERENCE/DOCKET NUMBER: UCAL-237/02US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5165
; TELEFAX: 415-8857-0663
; TELEX: 380816COOLEYFA
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-450-393A-5

Query Match 75.9%; Score 120; DB 1; Length 355;
Best Local Similarity 66.7%; Pred. No. 8.1e-09;
Matches 18; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY 1 VTEVLAFHCLNPNVLYAFIGQKFRNY 27
||||:|||||:|:|:|:|
Db 285 VTEVIATHCCLNPNVLYAFVGERFRKY 311

RESULT 7
US-08-446-669-5
; Sequence 5, Application US/08446669
; Patent No. 6132987
; GENERAL INFORMATION:
; APPLICANT: Charo, Israel
; APPLICANT: Coughlin, Shaun
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
; STREET: 5 Palo Alto Square
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,669
; FILING DATE: May 25, 1995

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Neeley, Richard
REGISTRATION NUMBER: 30,092
REFERENCE/DOCKET NUMBER: UCAL-237/0105
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-843-5000
TELEFAX: 415-857-0663
TELEX: 380816COOLEYPA
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-446-669-5

Query Match 75.9%; Score 120; DB 4; Length 355;
Best Local Similarity 66.7%; Pred. No. 8.1e-09;
Matches 18; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

Qy 1 VTEVLAFLHCCCLNPVLYAFIGQKFRNY 27
Db 285 VTEVIATHTCCVNPVYAFVGERFRKY 311

RESULT 8
PCT-US95-00476-5
Sequence 5, Application PC/TUS9500476
GENERAL INFORMATION:
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Robbins, Berliner & Carson
STREET: 201 N. Figueroa Street, 5th Floor
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90012-2628
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/00476
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Berliner, Robert
REGISTRATION NUMBER: 20,121
REFERENCE/DOCKET NUMBER: 5555-291
TELECOMMUNICATION INFORMATION:
TELEPHONE: 310-977-1001
TELEFAX: 310-977-1003
TELEX:
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
PCT-US95-00476-5

Query Match 75.9%; Score 120; DB 5; Length 355;

Best Local Similarity 66.7%; Pred. No. 8.1e-09;
Matches 18; Conservative 7; Mismatches 2; Indels 0; Gaps 0;
Qy 1 VTEVLAFLHCCCLNPVLYAFIGQKFRNY 27
Db 285 VTEVIATHTCCVNPVYAFVGERFRKY 311
RESULT 9
US-08-202-056-1
Sequence 1, Application US/08202056
Patent No. 5440021
GENERAL INFORMATION:
APPLICANT: Chuntharapai, Anan
APPLICANT: Hebert, Caroline
APPLICANT: Kim, Kyung Jin
APPLICANT: Lee, James
TITLE OF INVENTION: Antibodies to Human IL-8 Type B Receptor
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/202,056
FILING DATE: 25-FEB-1994
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/677211
FILING DATE: 29-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: 706P3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 350 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-202-056-1

Query Match 73.4%; Score 116; DB 1; Length 350;
Best Local Similarity 71.4%; Pred. No. 2.7e-08;
Matches 20; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 2 TEVLAFLHCCCLNPVLYAFIGQKFRNYEL 29
Db 290 TEILGLHCLNPVLYAFIGQKFRNYEL 317

RESULT 10
US-08-076-093A-2
Sequence 2, Application US/08076093A
Patent No. 5543503
GENERAL INFORMATION:
APPLICANT: Chuntharapai, Anan
APPLICANT: Lee, James
APPLICANT: Hebert, Caroline
APPLICANT: Jin Kim, K.
TITLE OF INVENTION: Antibodies to Human PF4A Receptors

NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/076.093A
FILING DATE: 11-Jun-1993
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/810782
FILING DATE: 19-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/677211
FILING DATE: 29-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: 706P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 350 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-076-093A-2

Query Match 73.4%; Score 116; DB 1; Length 350;
Best Local Similarity 71.4%; Pred. No. 2.7e-08;
Matches 20; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 2 TEVLAFHCLNPVLYAFIGOKERNYFL 29
||:| ||| |||||:||||| ||: ||
Db 290 TEILGFLHCLNPIIYAFIGNFRHGFL 317

RESULT 11
US-08-450-393A-7
Sequence 7, Application US/08450393A
Patent No. 5707815
GENERAL INFORMATION:
APPLICANT: Charo, Israel
APPLICANT: Coughlin, Shaun
TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
TITLE OF INVENTION: PROTEIN RECEPTORS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
STREET: 5 Palo Alto Square
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94306-2155
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450.393A
FILING DATE: May 25, 1995

CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Cseri, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: UCAL-237/02US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-843-5165
TELEFAX: 415-8857-0663
TELEX: 380816CooleyPA
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 350 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-450-393A-7

Query Match 73.4%; Score 116; DB 1; Length 350;
Best Local Similarity 71.4%; Pred. No. 2.7e-08;
Matches 20; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 2 TEVLAFHCLNPVLYAFIGOKERNYFL 29
||:| ||| |||||:||||| ||: ||
Db 290 TEILGFLHCLNPIIYAFIGNFRHGFL 317

RESULT 12
US-08-410-453A-1
Sequence 1, Application US/08410453A
Patent No. 5767063
GENERAL INFORMATION:
APPLICANT: Lee, James,
APPLICANT: Holmes, William E.,
APPLICANT: Woods, William I.,
TITLE OF INVENTION: Human PF4A Receptors and Their Use
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/410.453A
FILING DATE: 24-Mar-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/234494
FILING DATE: 28-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/677211
FILING DATE: 29-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P0706C1D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5530
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 350 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear

US-08-410-453A-1

Query Match 73.4%; Score 116; DB 1; Length 350;
Best Local Similarity 71.4%; Pred. No. 2.7e-08;
Matches 20; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 2 TEVLAFLHCLNPNVLYAFIGQKFRNYFL 29
||:| ||| ||||:||||| ||: ||
Db 290 TEILGFLHCLNPIIYAFIQNFRHGFL 317

RESULT 13

US-08-701-265-2

; Sequence 2, Application US/08701265
; Patent No. 5776457

; GENERAL INFORMATION:

; APPLICANT: Chuntharapai, Anan

; APPLICANT: Lee, James

; APPLICANT: Hebert, Caroline

; APPLICANT: Jin Kim, K.

; TITLE OF INVENTION: Antibodies to Human PF4A Receptors

; NUMBER OF SEQUENCES: 6

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.

; STREET: 460 Point San Bruno Blvd

; CITY: South San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94080

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: WinPatIn (Genentech)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/701,265

; FILING DATE: 22-AUG-1996

; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/076093

; FILING DATE: 11-Jun-1993

; APPLICATION NUMBER: 07/810782

; FILING DATE: 19-DEC-1991

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/677211

; FILING DATE: 29-MAR-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Love, Richard B.

; REGISTRATION NUMBER: 34,659

; REFERENCE/DOCKET NUMBER: 706P2

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415/225-5530

; TELEFAX: 415/952-9881

; TELEX: 910/371-7168

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 350 amino acids

; TYPE: Amino Acid

; TOPOLOGY: Linear

US-08-701-265-2

Query Match 73.4%; Score 116; DB 1; Length 350;
Best Local Similarity 71.4%; Pred. No. 2.7e-08;
Matches 20; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 2 TEVLAFLHCLNPNVLYAFIGQKFRNYFL 29
||:| ||| ||||:||||| ||: ||
Db 290 TEILGFLHCLNPIIYAFIQNFRHGFL 317

RESULT 14

US-08-410-454A-1

; Sequence 1, Application US/08410454A

; Patent No. 5783415

; GENERAL INFORMATION:

; APPLICANT: Lee, James,

; APPLICANT: Holmes, William E.,

; APPLICANT: Woods, William I.

; TITLE OF INVENTION: Human PF4A Receptors and Their Use

; NUMBER OF SEQUENCES: 2

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.

; STREET: 460 Point San Bruno Blvd

; CITY: South San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94080

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: WinPatIn (Genentech)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/410,454A

; FILING DATE: 24-Mar-1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/234494

; FILING DATE: 28-APR-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/677211

; FILING DATE: 29-MAR-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Love, Richard B.

; REGISTRATION NUMBER: 34,659

; REFERENCE/DOCKET NUMBER: P0706C1D3

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415/225-5530

; TELEFAX: 415/952-9881

; TELEX: 910/371-7168

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 350 amino acids

; TYPE: Amino Acid

; TOPOLOGY: Linear

US-08-410-454A-1

Query Match 73.4%; Score 116; DB 1; Length 350;
Best Local Similarity 71.4%; Pred. No. 2.7e-08;
Matches 20; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 2 TEVLAFLHCLNPNVLYAFIGQKFRNYFL 29
||:| ||| ||||:||||| ||: ||
Db 290 TEILGFLHCLNPIIYAFIQNFRHGFL 317

RESULT 15

US-08-284-586-2

; Sequence 2, Application US/08284586

; Patent No. 5840856

; GENERAL INFORMATION:

; APPLICANT: Chuntharapai, Anan

; APPLICANT: Lee, James

; APPLICANT: Hebert, Caroline

; APPLICANT: Jin Kim, K.

; TITLE OF INVENTION: Antibodies to Human PF4A Receptors

; NUMBER OF SEQUENCES: 6

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.

; STREET: 460 Point San Bruno Blvd

; CITY: South San Francisco

; STATE: California

; COUNTRY: USA

```

;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/284,586
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/076,093A
; FILING DATE: 11-Jun-1993
; APPLICATION NUMBER: 07/810782
; FILING DATE: 19-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/677211
; FILING DATE: 29-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: 706P2
; TELEPHONE: 415/225-5530
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 2:
; LENGTH: 350 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-284-586-2

```

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Query Match      73.4%; Score 116; DB 2; Length 350;
Best Local Similarity 71.4%; Pred. NO. 2.7e-08;
Matches 20; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

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```

QY  2 TEVLAFHCLNPNVLYAFICQKERNYFL 29
Db  290 TEILGELHCLNPIIYAFICQNERHGFL 317

```

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Search completed: May 23, 2001, 15:30:09
Job time: 416 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 23, 2001, 15:32:03 ; Search time 110.15 Seconds
(without alignments)
18.093 Million cell updates/sec

Title: US-08-887-977-10_COPY_291_319

Perfect score: 158

Sequence: 1 VTEVLAFLHCLNPVLYAFIGQKFRNYFL 29

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 198801 seqs, 68722935 residues

Total number of hits satisfying chosen parameters: 198801

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_67:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	158	100.0	369	JC5068	G protein-coupled
2	124	78.5	352	A43113	chemokine (C-C) re
3	121	76.6	354	A23669	interleukin-8 rece
4	121	76.6	355	JQ1231	interleukin-8 rece
5	121	76.6	360	A57160	chemokine (C-C) re
6	120	75.9	355	G02436	chemokine (C-C) re
7	120	75.9	355	A45177	chemokine (C-C) re
8	116	73.4	350	A39445	interleukin-8 rece
9	116	73.4	355	JC4304	orphan G protein-c
10	115	72.8	359	A48921	interleukin-8 rece
11	115	72.8	359	I49341	MIP-1 alpha recept
12	115	72.8	360	JC4587	chemokine (C-C) re
13	114	72.2	352	A45747	neuropeptide Y/pep
14	114	72.2	353	S28787	neuropeptide Y/pep
15	114	72.2	354	I58186	probable G protein
16	114	72.2	355	JC5067	G protein-coupled
17	114	72.2	360	JC2443	chemokine (C-C) re
18	113	71.5	358	A37552	interleukin-8 rece
19	113	71.5	374	I38450	chemokine (C-C) re
20	112	70.9	356	I49340	MIP-1 alpha recept
21	111	70.3	356	S42096	interleukin-8 rece
22	110	69.6	352	G00048	fusin (LESTRA) - c
23	109.5	69.3	323	Q08ED3	HHRF3 protein - hu
24	109	69.0	383	S55594	G protein-coupled
25	107	67.7	354	T09353	G protein-coupled
26	107	67.7	355	I49339	macrophage inflam
27	107	67.7	360	A53611	interleukin-8 rece
28	101	63.9	367	JE0349	interferon-inducib
29	100	63.3	350	JN0621	G protein-coupled

30	97	61.4	333	2	I65989	G protein-coupled
31	94	59.5	378	2	A45680	G protein-coupled
32	94	59.5	378	2	B55735	lymphocyte-specifi
33	92	58.2	359	2	S15403	angiotensin II rec
34	91	57.6	362	2	A39714	G protein-coupled
35	91	57.6	362	2	A30341	G protein-coupled
36	90	57.0	359	2	JC1104	angiotensin II rec
37	90	57.0	359	2	S44425	angiotensin II rec
38	90	57.0	359	2	JC1194	angiotensin II rec
39	90	57.0	359	2	A48857	angiotensin II rec
40	90	57.0	359	2	A42656	angiotensin II rec
41	90	57.0	359	2	JQ1516	angiotensin II rec
42	90	57.0	359	2	JH0621	angiotensin II rec
43	90	57.0	359	2	JC2134	angiotensin II rec
44	89	56.3	350	2	A42009	N-formyl peptide r
45	89	56.3	378	2	A55735	G protein-coupled

ALIGNMENTS

RESULT 1

JC5068

G protein-coupled receptor CKR-L3 - human

C:Species: Homo sapiens (man)

C:Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 21-Jul-2000

C:Accession: JC5068

R:Zaballos, A.; Varona, R.; Gutierrez, J.; Lind, P.; Marquez, G.

Biochem. Biophys. Res. Commun. 227, 846-853, 1996

A:Title: Molecular cloning and RNA expression of two new human chemokine receptor-lik

A:Reference number: JC5067; MUID:97040707

A:Accession: JC5068

A:Molecule type: DNA

A:Residues: 1-369 <ZAB>

A:Cross-references: EMBL:279784; NID:gl668737; PIDN:CAB02144.1; PID:gl668738

C:Comment: This protein belongs to the family of alpha chemokine receptors.

C:Genetics:

A:Gene: GDB:CMKBR6; STRL22: GPR29; CCR6: CKR-L3; GPR-CY4

A:Cross-references: GDB:5370639; OMIM:601835

A:Map position: 6q27-6q27

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor; transmembrane protein

F:42-68/Domain: transmembrane #status predicted <TM1>

F:79-99/Domain: transmembrane #status predicted <TM2>

F:115-136/Domain: transmembrane #status predicted <TM3>

F:160-180/Domain: transmembrane #status predicted <TM4>

F:212-233/Domain: transmembrane #status predicted <TM5>

F:250-271/Domain: transmembrane #status predicted <TM6>

F:292-315/Domain: transmembrane #status predicted <TM7>

Query Match 100.0%; Score 158; DB 2; Length 369;

Best Local Similarity 100.0%; Pred. No. 2.1e-15;

Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VTEVLAFLHCLNPVLYAFIGQKFRNYFL 29

Db 295 VTEVLAFLHCLNPVLYAFIGQKFRNYFL 323

RESULT 2

A43113

chemokine (C-C) receptor 5 - human

N:Alternate names: C-C CKR-5; CCR5

C:Species: Homo sapiens (man)

C:Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 20-Jun-2000

C:Accession: A43113; S71808; A58834; A58832; G02653; A58833

R:Samson, M.; Labbe, O.; Mollereau, C.; Vassart, G.; Parmentier, M.

Biochemistry 35, 3362-3367, 1996

A:Title: Molecular cloning and functional expression of a new human CC-chemokine rece

A:Reference number: A43113; MUID:96241590

A:Accession: A43113

A:Molecule type: mRNA

A:Residues: 1-352 <SAM1>
A:Cross-references: GB:X91492; NID:g1262810; PIDN:CAA62796.1; PID:g1262811
R:Samson, M.; Libert, F.; Doranz, B.J.; Rucker, J.; Liesnard, C.; Farber, C.M.; Saragost
M.; Imai, T.; Rana, S.; Yi, Y.; Smyth, R.J.; Collman, R.G.; Doms, R.W.; Vassart, G.; Pa
Nature 382, 722-725, 1996
A:Title: Resistance to HIV-1 infection in caucasian individuals bearing mutant alleles of
A:Reference number: S71808; MUID:96345670
A:Accession: S71808
A:Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 182-206; 207-230 <SAM2>
A:Accession: A58834
A:Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-184, 'IKDSHLAGPAAACHGHLILGNPKNSASVSK' <SAM3>
A:Cross-references: PIDN:X99393; NID:g1524062; PIDN:CAA67767.1; PID:g1524063
A:Note: this frameshift mutation results in a non-functional receptor but confers a degra
nd may have had a selective advantage by conferring resistance to Yersinia plague infect
J:Combadere, C.; Ahuja, S.K.; Tiffany, H.L.; Murphy, P.M.
R. Leukoc. Biol. 60, 147-152, 1996
A:Title: Cloning and functional expression of CC CKR5, a human monocyte CC chemokine rec
A:Reference number: A58832; MUID:96295970
A:Accession: A58832
A:Molecule type: mRNA
A:Residues: 1-352 <COM1>
A:Cross-references: GB:U57840; NID:g1502408; PIDN:AAB17071.1; PID:g1502409
A:Experimental source: clone 8, endotoxin-stimulated peripheral blood monocytes
R:Combadere, C.
submitted to the EMBL Data Library, May 1996
A:Reference number: H01541
A:Accession: G02653
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-89, 'L', '91-352 <COM2>
A:Cross-references: EMBL:U57840
R:Raport, C.J.; Gosling, J.; Schweickart, V.L.; Gray, P.W.; Charo, I.F.
J. Biol. Chem. 271, 17161-17166, 1996
A:Title: Molecular cloning and functional characterization of a novel human CC chemokine
A:Reference number: A58833; MUID:96291862
A:Accession: A58833
A:Molecule type: mRNA
A:Residues: 1-352 <RAP>
A:Cross-references: GB:U54994; NID:g1457945; PIDN:AAU50598.1; PID:g1457946
C:Comment: This is a receptor for chemokines MIP-1alpha (see PIR:A30574), MIP-1beta (see
C:Comment: Macrophage- and dual-tropic strains of HIV-1 bind to a complex of chemokine
C:Genetics:
A:Gene: GDB:CMKBR5; CCR5; CCR-5; CC-CCR-5; CCR5; ChemR13
A:Cross-references: GDB:1230510; OMIM:601373
A:Map position: 3p21-3p21
C:Function:
A:Description: G protein-coupled receptor for chemokines MIP-1alpha, MIP-1beta and RANTR
A:Note: probably acts to control granulocyte proliferation and differentiation.
A:Superfamily: vertebrate rhodopsin
C:Keywords: AIDS; G protein-coupled receptor; glycoprotein; phosphoprotein; transmembran
F:32-56/Domain: transmembrane #status predicted <TM1>
F:67-87/Domain: transmembrane #status predicted <TM2>
F:103-124/Domain: transmembrane #status predicted <TM3>
F:142-166/Domain: transmembrane #status predicted <TM4>
F:193-218/Domain: transmembrane #status predicted <TM5>
F:236-257/Domain: transmembrane #status predicted <TM6>
F:285-300/Domain: transmembrane #status predicted <TM7>
F:260-269, 101-178/Disulfide bonds: #status predicted
F:268/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:336, 337, 342/Binding site: phosphate (Ser) (covalent) #status predicted
F:340, 343/Binding site: phosphate (Thr) (covalent) #status predicted

Query Match 78.5%; Score 124; DB 2; Length 352;
Best Local Similarity 65.5%; Pred. No. 1.7e-10;
Matches 19; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 VTEVLAFHLCCLNPVLYAFIQGKFRNYFL 29
||| | |||:||||:||||| |

Db 281 VTETLGMTHCCINPIIYAFVGEKFRNYLL 309

RESULT 3

A23669 interleukin-8 receptor, high affinity - rabbit

N:Alternate names: fMLP receptor
C:Species: Oryctolagus cuniculus (domestic rabbit)

C:Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 05-Nov-1999

C:Accession: A23669

R:Thomas, K.M.; Pyun, H.Y.; Navarro, J.

J. Biol. Chem. 265, 20661-20664, 1990

A:Title: Molecular cloning of the fMet-Leu-Phe receptor from neutrophils.

A:Reference number: A23669; MUID:91056034

A:Accession: A23669

A:Molecule type: mRNA

A:Residues: 1-354 <THO>

A:Cross-references: GB:M58021; GB:J05705; NID:g165442; PIDN:AAA31377.1; PID:g165443

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor; glycoprotein; membrane protein; neutrophil

Query Match 76.6%; Score 121; DB 2; Length 354;

Best Local Similarity 75.0%; Pred. No. 4.7e-10;

Matches 21; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 TEVLAFHLCCLNPVLYAFIQGKFRNYFL 29

||| | |||:||||:||||| |

Db 294 TEILGFLHSCCLNPVLYAFIQGFRNGFL 321

RESULT 4

JQ1231 interleukin-8 receptor - rabbit

C:Species: Oryctolagus cuniculus (domestic rabbit)

C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 05-Nov-1999

C:Accession: JQ1231; A46483

R:Beckmann, M.P.; Munger, W.E.; Kozlosky, C.; VandenBos, T.; Price, V.; Lyman, S.; Ge

Biochem. Biophys. Res. Commun. 179, 784-789, 1991

A:Title: Molecular characterization of the interleukin-8 receptor.

A:Reference number: JQ1231; MUID:91378994

A:Accession: JQ1231

A:Molecule type: DNA

A:Residues: 1-355 <BEC>

A:Cross-references: GB:M74240; NID:g165438; PIDN:AAA31375.1; PID:g165439

R:Lee, J.; Kuang, W.J.; Rice, G.C.; Wood, W.I.

J. Immunol. 148, 1261-1264, 1992

A:Title: Characterization of complementary DNA clones encoding the rabbit IL-8 recept

A:Reference number: A46483; MUID:92148149

A:Accession: A46483

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-355 <LEE>

A:Cross-references: GB:M82873; NID:g165440; PIDN:AAA31376.1; PID:g165441

A:Experimental source: neutrophils

A:Note: sequence extracted from NCBI backbone (NCBI:81526, NCBIP:81530)

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 76.6%; Score 121; DB 2; Length 355;

Best Local Similarity 75.0%; Pred. No. 4.7e-10;

Matches 21; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 TEVLAFHLCCLNPVLYAFIQGKFRNYFL 29

||| | |||:||||:||||| |

Db 295 TEILGFLHSCCLNPVLYAFIQGFRNGFL 322

RESULT 5

A57160

N:Alternate names: C-C receptor 4 - human

C:Keywords: C-C receptor 4 - human

key words: protein coupled receptor; glycoprotein; phosphoprotein; transmembrane protein


```
RESULT 8
A39445
Interleukin-8 receptor type A - human
N:Alternate names: interleukin-8 receptor, high-affinity
C:Species: Homo sapiens (man)
F:66-88/Domain: transmembrane #status predicted <TM1>
F:104-125/Domain: transmembrane #status predicted <TM3>
F:146-165/Domain: transmembrane #status predicted <TM4>
F:197-217/Domain: transmembrane #status predicted <TM5>
F:230-254/Domain: transmembrane #status predicted <TM6>
F:275-296/Domain: transmembrane #status predicted <TM7>
A:Map position: 3pter-p21
A:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; lymphokine; transmembrane protein
F:35-57/Domain: transmembrane #status predicted <TM1>
F:66-88/Domain: transmembrane #status predicted <TM2>
F:104-125/Domain: transmembrane #status predicted <TM3>
F:146-165/Domain: transmembrane #status predicted <TM4>
F:197-217/Domain: transmembrane #status predicted <TM5>
F:230-254/Domain: transmembrane #status predicted <TM6>
F:275-296/Domain: transmembrane #status predicted <TM7>
A:Title: The high-affinity interleukin 8 receptor gene (IL8RA) maps to the 2q33-q36 region
A:Reference number: 137449; MUID:93252387
A:Accession: 137449
A:Molecule type: DNA
A:Residues: 1-350 <RES>
A:Cross-references: EMBL:X65858; NID:g312046; PIDN:CAA646688.1; PID:g312047
R:Ahuja, S.K.; Shetty, A.; Tiffany, H.L.; Murphy, P.M.
J. Biol. Chem. 269, 26381-26389, 1994
A:Title: Comparison of the genomic organization and promoter function for human interleukin 8 receptor gene
A:Reference number: 137898; MUID:95014476
A:Accession: 138710
A:Molecule type: DNA
A:Residues: 1-350 <RE2>
A:Cross-references: EMBL:U11870; NID:g511804; PIDN:AAA64378.1; PID:g511805
A:Accession: 138711
A:Molecule type: mRNA
A:Residues: 1-16 <RE3>
A:Cross-references: EMBL:U11871; NID:g511806; PIDN:AAA64379.1; PID:g733002
R:Holmes, W.E.; Lee, J.; Kuang, W.J.; Rice, G.C.; Wood, W.I.
Science 253, 1278-1280, 1991
A:Title: Structure and functional expression of a human interleukin-8 receptor.
A:Reference number: A39445; MUID:91368199
A:Accession: A39445
A:Molecule type: mRNA
A:Residues: 1-275, 'T', 277-350 <HOL>
A:Cross-references: GB:M68932; NID:g186369; PIDN:AAA59159.1; PID:g186370
C:Genetics:
A:Gene: GDB:IL8RA
A:Cross-references: GDB:135039; OMIM:146929
A:Map position: 2q35-2q35
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; glycoprotein; membrane protein

Query Match 73.4%; Score 116; DB 2; Length 350;
Best Local Similarity 71.4%; Pred. No. 2.5e-09;
Matches 20; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 2 TEVLAFLHCLNPVLYAFIGQKFRNYFL 29
||| ||| |||||:||||| ||| |||
DB 290 TEILGLHCLNPVLYAFIGQKFRNYFL 317

RESULT 9
JC4304
orphan G protein-coupled receptor - human
N:Alternate names: V28 protein
C:Species: Homo sapiens (man)
F:66-88/Domain: transmembrane #status predicted <TM1>
F:104-125/Domain: transmembrane #status predicted <TM3>
F:146-165/Domain: transmembrane #status predicted <TM4>
F:197-217/Domain: transmembrane #status predicted <TM5>
F:230-254/Domain: transmembrane #status predicted <TM6>
F:275-296/Domain: transmembrane #status predicted <TM7>
A:Map position: 3pter-p21
A:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; lymphokine; transmembrane protein
F:35-57/Domain: transmembrane #status predicted <TM1>
F:66-88/Domain: transmembrane #status predicted <TM2>
F:104-125/Domain: transmembrane #status predicted <TM3>
F:146-165/Domain: transmembrane #status predicted <TM4>
F:197-217/Domain: transmembrane #status predicted <TM5>
F:230-254/Domain: transmembrane #status predicted <TM6>
F:275-296/Domain: transmembrane #status predicted <TM7>
A:Title: The orphan G-protein-coupled receptor-encoding gene V28 is closely related to G protein-coupled receptor V28
A:Reference number: JC4304; MUID:96011651
A:Accession: JC4304
A:Molecule type: mRNA
A:Residues: 1-355 <RAP>
A:Cross-references: GB:U20350; NID:g665580; PIDN:AAA91783.1; PID:g665581
A:Experimental source: peripheral blood mononuclear cell
C:Comment: This protein is a cell-surface receptor which recognizes extracellular signal
C:Genetics:
A:Gene: V28
```

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Query Match 73.4%; Score 116; DB 2; Length 355;
Best Local Similarity 70.4%; Pred. No. 2.5e-09;
Matches 19; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 VTEVLAFLHCLNPVLYAFIGQKFRNY 27
||| ||| |||||:||||| ||| |||
DB 277 VTEVAFSHCLNPVLYAFIGQKFRNY 303

RESULT 10
A48921
Interleukin-8 receptor type B - mouse
N:Alternate names: G-protein coupled receptor Gpcrl6
C:Species: Mus musculus (house mouse)
F:66-88/Domain: transmembrane #status predicted <TM1>
F:104-125/Domain: transmembrane #status predicted <TM3>
F:146-165/Domain: transmembrane #status predicted <TM4>
F:197-217/Domain: transmembrane #status predicted <TM5>
F:230-254/Domain: transmembrane #status predicted <TM6>
F:275-296/Domain: transmembrane #status predicted <TM7>
A:Map position: 3pter-p21
A:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; lymphokine; transmembrane protein
F:35-57/Domain: transmembrane #status predicted <TM1>
F:66-88/Domain: transmembrane #status predicted <TM2>
F:104-125/Domain: transmembrane #status predicted <TM3>
F:146-165/Domain: transmembrane #status predicted <TM4>
F:197-217/Domain: transmembrane #status predicted <TM5>
F:230-254/Domain: transmembrane #status predicted <TM6>
F:275-296/Domain: transmembrane #status predicted <TM7>
A:Title: The murine homologue of the human interleukin-8 receptor type B maps near the
A:Reference number: A48921; MUID:94117014
A:Accession: A48921
A:Molecule type: DNA
A:Residues: 1-359 <CER>
A:Cross-references: GB:L12637; NID:g435093; PIDN:AAA39305.1; PID:g435094
R:Suzuki, H.; Prado, G.N.; Wilkinson, N.; Navarro, J.
J. Biol. Chem. 269, 18263-18266, 1994
A:Title: The N terminus of interleukin-8 (IL-8) receptor confers high affinity binding
A:Reference number: A53677; MUID:94308043
A:Accession: A53677
A:Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-359 <SUZ>
A:Cross-references: GB:L126549
A:Note: sequence extracted from NCBI backbone (NCBI:P149812)
R:Lee, J.; Cacalano, G.; Camerato, T.; Toy, K.; Moore, M.W.; Wood, W.I.
J. Immunol. 155, 2158-2164, 1995
A:Title: Chemokine binding and activities mediated by the mouse IL-8 receptor.
A:Reference number: I49348; MUID:95363183
A:Accession: I49348
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-359 <RES>
A:Cross-references: EMBL:U31207; NID:g950174; PIDN:AAC52239.1; PID:g950175
R:Bozic, C.R.; Gerard, N.P.; von Uexkull-Guldenband, C.; Kolakowski, L.F.
J. Biol. Chem. 269, 29355-29358, 1994
A:Title: The murine interleukin 8 type B receptor homologue and its ligands. Expressi
A:Reference number: I55421; MUID:95050766
A:Accession: I55421
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-359 <RE2>
A:Cross-references: GB:L13239; NID:g293665; PIDN:AAA62109.1; PID:g293666
R:Wilkie, T.M.; Chen, Y.; Gilbert, D.J.; Moore, K.J.; Yu, L.; Simon, M.I.; Copeland,
Genomics 18, 175-184, 1993
A:Title: Identification, chromosomal location, and genome organization of mammalian G
A:Reference number: A48909; MUID:94116980
A:Accession: A48909
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 145-258 <WTL>
A:Cross-references: GB:L20337; NID:g438800; PIDN:AAA16853.1; PID:g438801
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Search completed: May 23, 2001, 15:32:03
Job time: 510 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 23, 2001, 15:36:21 ; Search time 62.39 seconds
(without alignments)
15.923 Million cell updates/sec

Title: US-08-887-977-10_COPY_291_319

Perfect score: 158

Sequence: 1 VTEVLAFLHCLNPVLYAFIGKFRNYFL 29

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	158	100.0	374	1	CKR6_HUMAN
2	151	95.6	367	1	CKR6_MOUSE
3	124	78.5	352	1	CKR5_CERAE
4	124	78.5	352	1	CKR5_CERTO
5	124	78.5	352	1	CKR5_GORGO
6	124	78.5	352	1	CKR5_HUMAN
7	124	78.5	352	1	CKR5_HYLLE
8	124	78.5	352	1	CKR5_MACMU
9	124	78.5	352	1	CKR5_PANTR
10	124	78.5	352	1	CKR5_PAPHA
11	124	78.5	352	1	CKR5_PONPY
12	124	78.5	352	1	CKR5_PYGHI
13	124	78.5	352	1	CKR5_PYGNE
14	124	78.5	352	1	CKR5_TRAFR
15	124	78.5	352	1	CKR5_TRAPH
16	123	77.8	354	1	CKR5_RAT
17	121	76.6	355	1	IL8A_RABIT
18	121	76.6	360	1	CKR1_HUMAN
19	120	75.9	355	1	CKR1_HUMAN
20	120	75.9	355	1	CKR3_HUMAN
21	119	75.3	355	1	CKR3_CERAE
22	118	74.7	353	1	CKR8_MOUSE
23	116	73.4	350	1	IL8A_GORGO
24	116	73.4	350	1	IL8A_HUMAN
25	116	73.4	350	1	IL8A_PANTR
26	116	73.4	355	1	C3X1_HUMAN
27	115	72.8	349	1	CKR4_RAT
28	115	72.8	355	1	CKR3_MACMU
29	115	72.8	359	1	CKR4_MOUSE
30	115	72.8	359	1	CKR3_MOUSE
31	115	72.8	359	1	IL8B_MOUSE
32	115	72.8	359	1	IL8B_RAT
33	115	72.8	360	1	CKR4_MOUSE

34 115 72.8 373 1 CKR2_MOUSE
35 114 72.2 349 1 IL8A_RAT
36 114 72.2 352 1 CKR4_CERTO
37 114 72.2 352 1 CKR4_HUMAN
38 114 72.2 352 1 CKR4_MACMU
39 114 72.2 352 1 CKR4_PAPAN
40 114 72.2 353 1 CKR4_BOVIN
41 114 72.2 353 1 CKR4_FELCA
42 114 72.2 354 1 C3X1_MOUSE
43 114 72.2 354 1 C3X1_RAT
44 114 72.2 354 1 CKR5_MOUSE
45 114 72.2 355 1 CKR8_HUMAN

P51683 mus musculus
P70612 rattus norv
O62747 cercopithec
P30991 homo sapien
P79394 macaca mula
P56491 papio anubi
P25930 bos taurus
P56498 felis silve
O920d9 mus musculus
P35411 rattus norv
P51682 mus musculus
P51685 homo sapien

ALIGNMENTS

RESULT 1
CKR6_HUMAN STANDARD; PRT; 374 AA.
AC P51684; Q92846; P78553;
DT 01-OCT-1996 (Rel. 34, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE C-C CHEMOKINE RECEPTOR TYPE 6 (C-C CKR-6) (CCR-6) (LARC
DE RECEPTOR) (GPR-CY4) (GPCY4) (CHEMOKINE RECEPTOR-LIKE 3) (CKR-L3)
DE (DRY6).
GN CCR6 OR CMKBR6 OR STRL22 OR GPR29 OR CKRL3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID:9606;
RN [1]
RP SEQUENCE FROM N.A., AND FUNCTION.
RX MEDLINE=97313465; PubMed=9169459;
RA Baba M., Imai T., Nishimura M., Kakizaki M., Takagi S., Hieshima K.,
RA Nomiya H., Yoshie O.;
RT "Identification of CCR6, the specific receptor for a novel
RT lymphocyte-directed CC chemokine LARC."
RL J. Biol. Chem. 272:14893-14898(1997).
[2]
RP SEQUENCE FROM N.A.
RA Lautens L.L., Modi W., Bonner T.I.;
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
[3]
RP SEQUENCE FROM N.A.
RX MEDLINE=97040707; PubMed=8886020;
RA Zaballios A., Varona R., Gutierrez J., Lind P., Marquez G.;
RT "Molecular cloning and RNA expression of two new human chemokine
RT receptor-like genes."
RL Biochem. Biophys. Res. Commun. 227:846-853(1996).
[4]
RP SEQUENCE FROM N.A.
RA McCoy R., Perlmutter D.H.;
RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
[5]
RP SEQUENCE FROM N.A.
RX MEDLINE=97224503; PubMed=9070937;
RA Liao F., Lee H.-H., Farber J.M.;
RT "Cloning of STRL22, a new human gene encoding a G-protein-coupled
RT receptor related to chemokine receptors and located on chromosome
RT 6q27".
RL Genomics 40:175-180(1997).
CC -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-3-
CC ALPHA/LARC AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE
CC INTRACELLULAR CALCIUM IONS LEVELS.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- TISSUE SPECIFICITY: SPLEEN, LYMPH NODES, APPENDIX, AND FETAL
CC LIVER. EXPRESSED IN LYMPHOCYTES, T CELLS AND B CELLS BUT NOT IN
CC NATURAL KILLER CELLS, MONOCYTES, OR GRANULOCYTES.
CC -!- INDUCTION: INTERLEUKIN-2.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -!- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-6 IS THE INITIATOR.


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RESULT 3
CKR5_CERAE
ID CKR5_CERAE STANDARD; PRT; 352 AA.
AC PS6493;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE C-C CHEMOKINE RECEPTOR TYPE 5 (C-C CKR-5) (CCR-5) (CCR5).
GN CKR5 OR CMKR5.
OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9534;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=98001387; PubMed=9343222;
RA Kuhlmann S.E., Platt E.J., Kozak S.L., Kabat D.;
RT "Polymorphisms in the CKR5 genes of African green monkeys and mice
RT implicate specific amino acids in infections by simian and human
RT immunodeficiency viruses."
RL J. Virol. 71:8642-8656(1997).
RN [2]
RP SEQUENCE FROM N.A.
RA Murayama Y., Matsunaga S., Inoue-Murayama M.;
RT "CDNA sequence of African green monkey CCR-5 chemokine receptor
RT gene."
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
CC MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
CC INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE
CC IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
CC DIFFERENTIATION.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC
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CC
CC EMBL; U83324; AAC51795.1; -
CC EMBL; U83325; AAC51796.1; -
CC EMBL; AB015944; BAA31328.1; -
CC GCRDb; GCR_2465; -
CC GCRDb; GCR_2466; -
CC InterPro; IPR000276; -
CC InterPro; IPR000355; -
CC InterPro; IPR002240; -
CC Pfam; PF00001; 7tm.1; 1.
CC PRINTS; PR00237; GPCRHHODPSN.
CC PRINTS; PR00657; CCHHEMOKINER.
CC PRINTS; PRO1110; CHEMOKINER5.
CC PROSITE; PS00237; G_PROTEIN_RECEP_FL_1; 1.
CC PROSITE; PS0262; G_PROTEIN_RECEP_FL_2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein; Polymorphism.
FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 31 58
FT DOMAIN 59 68
FT TRANSMEM 69 89
FT TRANSMEM 90 102
FT TRANSMEM 103 124
FT TRANSMEM 125 141
FT TRANSMEM 142 166
FT TRANSMEM 167 198
FT TRANSMEM 199 218
FT TRANSMEM 219 235
FT TRANSMEM 236 260

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FT DOMAIN 261 277
FT TRANSMEM 278 301 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 302 352 7 (POTENTIAL).
FT DISULFID 101 178 CYTOPLASMIC (POTENTIAL).
FT VARIANT 14 178 BY SIMILARITY.
FT VARIANT 352 352 N -> Y.
FT SEQUENCE 352 AA; 40561 MW; 7F52E690C72EC29A CRC64;
SQ
Query Match. 78.5%; Score 124; DB 1; Length 352;
Best Local Similarity 65.5%; Pred. No. 5.3e-10;
Matches 19; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
QY 1 VTEVLAFLLHCCCLNPVLYAFIGOKFRNYFL 29
DB 281 VTETLGMTHCCINPIIYAFVGEKFRNYLL 309
RESULT 4
CKR5_CERTO
ID CKR5_CERTO STANDARD; PRT; 352 AA.
AC O62743; O62744; O62745; O62746;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE C-C CHEMOKINE RECEPTOR TYPE 5 (C-C CKR-5) (CCR-5) (CCR5).
GN CKR5 OR CMKR5.
OS Cercopithecus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9531;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ISOLATE 079, 085, 087 AND 089;
RX MEDLINE=96321155; PubMed=9656999;
RA Chen Z., Gettie A., Ho D.D., Marx P.A.;
RT "Primary SIVsm isolates use the CKR5 coreceptor from sooty mangabey
RT naturally infected in west Africa: a comparison of coreceptor usage
RT of primary SIVsm, HIV-2, and SIVmac."
RL Virology 246:113-124(1998).
CC -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
CC MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
CC INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE
CC IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
CC DIFFERENTIATION.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CC EMBL; AF051902; AAC39830.1; -
CC EMBL; AF051903; AAC39831.1; -
CC EMBL; AF051904; AAC39832.1; -
CC EMBL; AF051905; AAC39833.1; -
CC InterPro; IPR000276; -
CC InterPro; IPR000355; -
CC InterPro; IPR002240; -
CC Pfam; PF00001; 7tm.1; 1.
CC PRINTS; PR00237; GPCRHHODPSN.
CC PRINTS; PR00657; CCHHEMOKINER.
CC PRINTS; PRO1110; CHEMOKINER5.
CC PROSITE; PS00237; G_PROTEIN_RECEP_FL_1; 1.
CC PROSITE; PS0262; G_PROTEIN_RECEP_FL_2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 31 58

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FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 69 89 2 (POTENTIAL).
FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 124 3 (POTENTIAL).
FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 142 166 4 (POTENTIAL).
FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 199 218 5 (POTENTIAL).
FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 236 260 6 (POTENTIAL).
FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 278 301 7 (POTENTIAL).
FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
FT DISULFID 101 178 BY SIMILARITY.
FT VARIANT 2 2 D -> E (IN ISOLATE 087).
FT VARIANT 3 3 Y -> D (IN ISOLATE 079).
FT VARIANT 25 25 V -> G (IN ISOLATE 087).
FT VARIANT 100 100 M -> K (IN ISOLATE 079).
FT VARIANT 107 107 L -> V (IN ISOLATE 089).
FT VARIANT 134 134 V -> G (IN ISOLATE 079).
FT VARIANT 146 146 V -> L (IN ISOLATES 085 AND 089).
FT VARIANT 340 340 T -> I (IN ISOLATE 079).
SQ SEQUENCE 352 AA; 40489 MW; 20A196E2D47B49CA CRC64;

Query Match 78.5%; Score 124; DB 1; Length 352;
Best Local Similarity 65.5%; Pred. No. 5.3e-10;
Matches 19; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 VTEVLAFLHCCLNPLVYAFIGQKFRNYEL 29
DB 281 VTETLGTHCCINPIIYAFVGEKFRNYLL 309

RESULT 5
CCR5_GORGO STANDARD; PRT; 352 AA.
AC P56439;
AT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE C-C CHEMOKINE RECEPTOR TYPE 5 (C-C CCR-5) (CCR-5) (CCR5).
GN CCR5 OR CMKBR5.
OS Gorilla gorilla gorilla (Lowland gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
OX NCBI_TaxID=9595;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97268687; PubMed=9108095;
RA Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,
RA Sharon M., Samson M., Lu Z.H., Clements J.E., Murphy-Corb M.,
RA Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;
RT "Differential utilization of CCR5 by macrophage and T cell tropic
simian immunodeficiency virus strains.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).
CC -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
CC MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
CC INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE
CC IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
CC DIFFERENTIATION.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CC -----
DR EMBL; AF005659; AAB62553.1; -.
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DR GCRDb; GCR_1372; -.
DR InterPro; IPR000276; -.
DR InterPro; IPR000355; -.
DR InterPro; IPR002240; -.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHDOPSN.
DR PRINTS; PR00657; CCHEMOKINER.
DR PRINTS; PR01110; CHEMOKINER.
DR PROSITE; PS00237; G-PROTEIN_RECEP_FL_1; 1.
DR PROSITE; PS0262; G-PROTEIN_RECEP_FL_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 31 58 1 (POTENTIAL).
FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 69 89 2 (POTENTIAL).
FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 124 3 (POTENTIAL).
FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 142 166 4 (POTENTIAL).
FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 199 218 5 (POTENTIAL).
FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 236 260 6 (POTENTIAL).
FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 278 301 7 (POTENTIAL).
FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
FT DISULFID 101 178 BY SIMILARITY.
SQ SEQUENCE 352 AA; 40515 MW; D0E6FCB9FE5EAC84 CRC64;

Query Match 78.5%; Score 124; DB 1; Length 352;
Best Local Similarity 65.5%; Pred. No. 5.3e-10;
Matches 19; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 VTEVLAFLHCCLNPLVYAFIGQKFRNYEL 29
DB 281 VTETLGTHCCINPIIYAFVGEKFRNYLL 309

RESULT 6
CCR5_HUMAN STANDARD; PRT; 352 AA.
ID CCR5_HUMAN STANDARD; PRT; 352 AA.
AC P51681; O14692; O14693; O14695; O14697; O14698; O14699;
AC O14700; O14701; O14702; O14703; O14704; O14705; O14706; O14707;
OC O14708;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE C-C CHEMOKINE RECEPTOR TYPE 5 (C-C CCR-5) (CCR-5) (CCR5)
DE (HIV-1 FUSION CO-RECEPTOR) (CHEMR13).
GN CCR5 OR CMKBR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96241590; PubMed=8639485;
RA Samson M., Labbe O., Mollereau C., Vassart G., Parmentier M.;
RT "Molecular cloning and functional expression of a new human
CC-chemokine receptor gene.";
RL Biochemistry 35:3362-3367(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96291862; PubMed=8663314;
RA Raport C.J., Gosling J., Schweichart V.L., Gray P.W., Charo I.F.;
RT "Molecular cloning and functional characterization of a novel human
CC chemokine receptor (CCR5) for RANTES, MIP-1beta, and MIP-1alpha.";
RL J. Biol. Chem. 271:17161-17166(1996).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=96295970; PubMed=8699119;
RA Combadiere C., Ahuja S.K., Tiffany H.L., Murphy P.M.;
```

RT "Cloning and functional expression of CC CKR5, a human monocyte CC
RT chemokine receptor selective for MIP-1(alpha), MIP-1(beta), and
RT RANTES";
RL J. Leukoc. Biol. 60:147-152(1996).
RN [4]

SEQUENCE FROM N.A.

RA McCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D.,
RA Nham M., Parnell L., Dedhia N., Ansari A., Mardis E., Schutz K.,
RA Goj L., la Bastide M., Kaplan N., Greco T., Touchman J.,
RA Muzny D., Chen C.N., Evans C., Fitzgerald M., See L.H., Tang M.,
RA Porcel B.M., Dragan Y., Giacalone J., Pae A., Powell E.,
RA Solinsky K.A., Desilva U., Diaz-Perez S., Zhou X., Yu Y.,
RA Watanabe M., Doggett N., Garcia D., Sagripanti J.L.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
RN [5]

SEQUENCE FROM N.A.

RP MEDLINE-98001387; PubMed-9343222;

RA Kuhnmann S.E., Platt E.J., Kozak S.L., Kabat D.;

RT "Polymorphisms in the CCR5 genes of African green monkeys and mice
RT implicate specific amino acids in infections by simian and human
RT immunodeficiency viruses";
RL J. Virol. 71:8642-8656(1997).
RN [6]

SEQUENCE FROM N.A., AND POLYMORPHISMS.

RP MEDLINE-98022612; PubMed-9359654;

RA Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B.,

RA Ho D.D.;

RT "HIV type 1 subtypes, coreceptor usage, and CCR5 polymorphism";
RL AIDS Res. Hum. Retroviruses 13:1357-1366(1997).
RN [7]

SEQUENCE FROM N.A.

RP MEDLINE-98049523; PubMed-9388201;

RA Mummidi S., Ahuja S.S., McDaniel B.L., Ahuja S.K.;

RT "The human CC chemokine receptor 5 (CCR5) gene. Multiple transcripts
RT with 5'-end heterogeneity, dual promoter usage, and evidence for
RT polymorphisms within the regulatory regions and noncoding exons";
RL J. Biol. Chem. 272:30662-30671(1997).
RN [8]

CHARACTERIZATION OF ITS HIV-1 RECEPTOR FUNCTION.

RP MEDLINE-96260017; PubMed-8649511;

RA Deng H., Liu R., Elmleier W., Choe S., Unutmaz D., Burkhardt M.,

RA di Marzio P., Marmon S., Sutton R.E., Hill C.M., Davis C.B.,

RA Peiper S.C., Schall T.J., Littman D.R., Landau N.R.;

RT "Identification of a major co-receptor for primary isolates of
RT HIV-1";
RL Nature 381:661-666(1996).
RN [9]

CHARACTERIZATION OF ITS HIV-1 RECEPTOR FUNCTION.

RP MEDLINE-96260018; PubMed-8649512;

RA Draglic T., Litwin V., Allaway G.P., Martin S.R., Huang Y.,

RA Nagashima K.A., Cayan C., Maddon P.J., Koup R.A., Moore J.P.,

RA Paxton W.A.;

RT "HIV-1 entry into CD4+ cells is mediated by the chemokine receptor
RT CC-CKR-5";
RL Nature 381:667-673(1996).

CC -1- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
CC MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
CC INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE
CC IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
CC DIFFERENTIATION. ACTS AS CO-RECEPTOR WITH CD4 FOR PRIMARY NON-
CC SYNCTIUM-INDUCING STRAINS (NSI) (MACROPHAGE-TROPIC) OF HIV-1
CC VIRUS. IT PROMOTES ENV-MEDIATED FUSION OF THE VIRUS.

CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

CC -1- TISSUE SPECIFICITY: FOUND IN PROMYELOCYTIC CELLS.

CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

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CC or send an email to license@isb-sib.ch).

CC EMBL; X91492; CAA62796.1; -
DR EMBL; U54994; AAC50598.1; -
DR EMBL; U57840; AAB17071.1; -
DR EMBL; U95626; AAB57793.1; -
DR EMBL; U83326; AAC51797.1; -
DR EMBL; AF011500; AAB65700.1; -
DR EMBL; AF011501; AAB65701.1; -
DR EMBL; AF011502; AAB65702.1; -
DR EMBL; AF011503; AAB65703.1; -
DR EMBL; AF011505; AAB65705.1; -
DR EMBL; AF011506; AAB65706.1; -
DR EMBL; AF011507; AAB65707.1; -
DR EMBL; AF011508; AAB65708.1; -
DR EMBL; AF011509; AAB65709.1; -
DR EMBL; AF011510; AAB65710.1; -
DR EMBL; AF011511; AAB65711.1; -
DR EMBL; AF011512; AAB65712.1; -
DR EMBL; AF011513; AAB65713.1; -
DR EMBL; AF011514; AAB65714.1; -
DR EMBL; AF011515; AAB65715.1; -
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DR EMBL; AF011518; AAB65718.1; -
DR EMBL; AF011519; AAB65719.1; -
DR EMBL; AF011520; AAB65720.1; -
DR EMBL; AF011521; AAB65721.1; -
DR EMBL; AF011522; AAB65722.1; -
DR EMBL; AF011523; AAB65723.1; -
DR EMBL; AF011524; AAB65724.1; -
DR EMBL; AF011525; AAB65725.1; -
DR EMBL; AF011526; AAB65726.1; -
DR EMBL; AF011527; AAB65727.1; -
DR EMBL; AF011528; AAB65728.1; -
DR EMBL; AF011529; AAB65729.1; -
DR EMBL; AF011530; AAB65730.1; -
DR EMBL; AF011531; AAB65731.1; -
DR EMBL; AF011532; AAB65732.1; -
DR EMBL; AF011533; AAB65733.1; -
DR EMBL; AF011535; AAB65735.1; -
DR EMBL; AF031237; AAB94735.1; -
DR GCRDb; GCR_1923; -
DR GCRDb; GCR_1927; -
DR GCRDb; GCR_2116; -
DR GCRDb; GCR_2454; -
DR GCRDb; GCR_2497; -
DR MIM; 601373; -
DR InterPro; IPR000276; -
DR InterPro; IPR000355; -
DR InterPro; IPR002240; -
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPS.N.
DR PRINTS; PR00657; CCHEMOKINER.
DR PRINTS; PR01110; CHEMOKINERS.
DR PROSITE; PS00237; G-PROTEIN_RECEP_FL_1; 1.
DR PROSITE; PS00262; G-PROTEIN_RECEP_FL_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Polymorphism.
FT DOMAIN 1 30
FT TRANSMEM 31 58
FT DOMAIN 59 68
FT TRANSMEM 69 89
FT DOMAIN 90 102
FT TRANSMEM 103 124
FT DOMAIN 125 141
FT TRANSMEM 142 166
FT DOMAIN 167 198
FT TRANSMEM 199 218
FT DOMAIN 219 235
FT TRANSMEM 236 260
FT DOMAIN 261 277
FT TRANSMEM 278 301
FT DOMAIN 302 352
FT DISULFID 101 178
BY SIMILARITY.


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FT CARBOHYD 268 268 N-LINKED (GLCNAC. .) (POTENTIAL).
FT VARIANT 10 10 /FTID=VAR_003481.
FT VARIANT 31 31 R -> H (IN INCR5-72A).
FT VARIANT 34 34 P -> L (IN TZCR5-179).
FT VARIANT 34 34 /FTID=VAR_003482.
FT VARIANT 62 62 K -> R (IN UGCR5-145B).
FT VARIANT 62 62 /FTID=VAR_003483.
FT VARIANT 68 68 Y -> H (IN ZWCR5-7).
FT VARIANT 68 68 /FTID=VAR_003484.
FT VARIANT 95 95 D -> N (IN MWCR5-107).
FT VARIANT 95 95 /FTID=VAR_003485.
FT VARIANT 97 97 G -> E (IN INCR5-467).
FT VARIANT 97 97 /FTID=VAR_003486.
FT VARIANT 122 122 L -> P (IN ZWCR5-7).
FT VARIANT 122 122 /FTID=VAR_003487.
FT VARIANT 158 158 F -> S (IN UGCR5-145A).
FT VARIANT 158 158 /FTID=VAR_003488.
FT VARIANT 176 176 Y -> C (IN KEGR5-116).
FT VARIANT 176 176 /FTID=VAR_003489.
FT VARIANT 177 177 T -> A (IN INCR5-45C).
FT VARIANT 177 177 /FTID=VAR_003490.

Query Match 78.5%; Score 124; DB 1; Length 352;
Best Local Similarity 65.5%; Pred. No. 5.3e-10;
Matches 19; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 VTEVLAFLHCLNPVLYAFVIGKFRNYFL 29
DB 281 VTETLGMTHCCINPIIYAFVGEKFRNYLL 309

RESULT 7
ID CKR5_HYLLE STANDARD; PRT; 352 AA.
AC 097883;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE C-C CHEMOKINE RECEPTOR TYPE 5 (C-C CKR-5) (CCR-5) (CCR5).
GN CKR5 OR CMKBR5.
OS Hylobates leucogenys (White-cheeked gibbon).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
OX NCBI_TaxID=61853;
RN [1]
RP ZHANG Y.-W., ZHANG Y.-P.;
RA "Sequence evolution of chemokine receptor CCR5 gene in primates.";
RT Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
RL FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
CC MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
CC INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE
CC IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
CC DIFFERENTIATION.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CC -----
DR EMBL; AF075451; AADI9863.1; -
DR InterPro; IPR000248; -
DR InterPro; IPR000276; -
DR InterPro; IPR000355; -
DR InterPro; IPR002236; -
DR InterPro; IPR002237; -
DR InterPro; IPR002240; -
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DR PFAM; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PRINTS; PR00241; ANGIOTENSINR.
DR PRINTS; PR00657; CCHEMOKINER.
DR PRINTS; PR01106; CHEMOKINER1.
DR PRINTS; PR01107; CHEMOKINER2.
DR PRINTS; PR01110; CHEMOKINER5.
DR PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G-PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 31 58 1 (POTENTIAL).
FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 69 89 2 (POTENTIAL).
FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 124 3 (POTENTIAL).
FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 142 166 4 (POTENTIAL).
FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 199 218 5 (POTENTIAL).
FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 236 260 6 (POTENTIAL).
FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 278 301 7 (POTENTIAL).
FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
FT DISULFID 101 178 BY SIMILARITY.
SQ SEQUENCE 352 AA; 40445 MW; 4F8E4F344CEB7C91 CRC64;

Query Match 78.5%; Score 124; DB 1; Length 352;
Best Local Similarity 65.5%; Pred. No. 5.3e-10;
Matches 19; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 VTEVLAFLHCLNPVLYAFVIGKFRNYFL 29
DB 281 VTETLGMTHCCINPIIYAFVGEKFRNYLL 309

RESULT 8
ID CKR5_MACMU STANDARD; PRT; 352 AA.
AC P79436; O02746;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE C-C CHEMOKINE RECEPTOR TYPE 5 (C-C CKR-5) (CCR-5) (CCR5).
GN CKR5 OR CMKBR5.
OS Macaca mulatta (Rhesus macaque).
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey), and
OS Macaca nemestrina (Pig-tailed macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9544, 9541, 9545;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=M.mulatta;
RX MEDLINE=97184592; PubMed=9032394;
RA Marcon L., Choe H., Martin K.A., Farzan M., Ponath P.D., Wu L.,
RA Newman W., Gerard N., Gerard C., Sodroski J.;
RT "Utilization of C-C chemokine receptor 5 by the envelope
RT glycoproteins of a pathogenic simian immunodeficiency virus,
RT SiVnac239."
RL J. Virol. 71:2522-2527(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=M.mulatta; STRAIN=INDIAN MACAQUE;
RX MEDLINE=97213934; PubMed=9060623;
RA Chen Z., Zhou P., Ho D.D., Landau N.R., Marx P.A.;
RT "Genetically divergent strains of simian immunodeficiency virus use
RT CCR5 as a coreceptor for entry."
RL J. Virol. 71:2705-2714(1997).
RN [3]
```

RP SEQUENCE FROM N.A.
RC SPECIES=M.mulatta;
RA Hauer D.A., Margulies B.J., Clements J.E.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
RN [4]

RP SEQUENCE FROM N.A.
RC SPECIES=M.mulatta, M.fascicularis, and M.nemestrina;
RX MEDLINE=97268687; PubMed=9108095;
RA Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,
RA Sharron M., Samson M., Lu Z.H., Clements J.E., Murphy-Corb M.,
RA Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;
RT "Differential utilization of CCR5 by macrophage and T cell tropic
simian immunodeficiency virus strains.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).
CC -1- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE
IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
DIFFERENTIATION.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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DR EMBL; U77672; AAC51109.1; -
DR EMBL; U73739; AAC51158.1; -
DR EMBL; U96762; AAC34132.1; -
DR EMBL; AF005660; AAB62554.1; -
DR EMBL; AF005661; AAB62555.1; -
DR EMBL; AF005662; AAB62556.1; -
DR GCRDB; GCR_1296; -
DR GCRDB; GCR_1369; -
DR GCRDB; GCR_1370; -
DR GCRDB; GCR_1371; -
DR GCRDB; GCR_1639; -
DR GCRDB; GCR_1641; -
DR InterPro; IPR000276; -
DR InterPro; IPR000355; -
DR InterPro; IPR002240; -
DR Pfam; PF00001; 7tm1.1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PRINTS; PR00657; CCHEMOKINER.
DR PRINTS; PR01110; CHEMOKINERS.
DR PROSITE; PS00237; G_PROTEIN_RECF_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECF_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 31 58 1 (POTENTIAL).
FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 69 89 2 (POTENTIAL).
FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 124 3 (POTENTIAL).
FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 142 166 4 (POTENTIAL).
FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 199 218 5 (POTENTIAL).
FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 236 260 6 (POTENTIAL).
FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 278 301 7 (POTENTIAL).
FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
FT DISULFID 101 178 BY SIMILARITY.
FT CARBOHYD 268 268 N-LINKED (GLCNAC...) (POTENTIAL).
FT CONFLICT 241 241 M -> I (IN REF. 3).
FT CONFLICT 292 292 I -> M (IN REF. 3).
SQ SEQUENCE 352 AA; 40507 MW; 58B96C85909FACB2 CRC64;

Query Match 78.5%; Score 124; DB 1; Length 352;
Best Local Similarity 65.5%; Pred. No. 5.3e-10;
Matches 19; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 VTEVLAFHCCCLNPNVLYAFIGQKFRNYEL 29
DB 281 VTETLGMTHCCINPIIYAFVGEKFRNYLL 309

RESULT 9
CKR5_PANTR STANDARD; PRT; 352 AA.
ID CKR5_PANTR
AC P56440; O02778;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE C-C CHEMOKINE RECEPTOR TYPE 5 (C-C CKR-5) (CC-CKR-5) (CCR5).
GN CKR5 OR CMKBR5.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97268687; PubMed=9108095;
RA Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,
RA Sharron M., Samson M., Lu Z.H., Clements J.E., Murphy-Corb M.,
RA Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;
RT "Differential utilization of CCR5 by macrophage and T cell tropic
simian immunodeficiency virus strains.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).
RN [2]
RP SEQUENCE FROM N.A.
RA Zimmerman P.A., Buckler-White A., Alkhatib G.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=98022612; PubMed=9359654;
RA Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B.,
RA HO D.D.;
RT "HIV type 1 subtypes, coreceptor usage, and CCR5 polymorphism.";
RL AIDS Res. Hum. Retroviruses 13:1357-1366(1997).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=97426118; PubMed=9282822;
RA Zacharova V., Zachar V., Goustin A.S.;
RT "Sequence of chemokine receptor gene CCR5 in chimpanzees, a natural
HIV type 1 host.";
RL AIDS Res. Hum. Retroviruses 13:1159-1161(1997).
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=98090115; PubMed=9430250;
RA Pretet J.-L., Zerbib A., Girard M., Guillet J.-G., Butor C.;
RT "Chimpanzee CXCR4 and CCR5 act as coreceptors for HIV type 1.";
RL AIDS Res. Hum. Retroviruses 13:1583-1587(1997).
CC -1- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE
IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
DIFFERENTIATION.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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DR EMBL; AF005663; AAB62557.1; -

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DR EMBL; U94329; AAB58446.1; -
DR EMBL; AF011542; AAB65742.1; -
DR EMBL; U97666; AAC51670.1; -
DR EMBL; AF011540; AAB65740.1; -
DR EMBL; U89797; AAC03717.1; -
DR GCRDb; GCR_1284; -
DR GCRDb; GCR_1367; -
DR GCRDb; GCR_2432; -
DR InterPro; IPR000276; -
DR InterPro; IPR000355; -
DR InterPro; IPR002240; -
DR Pfam; PF00001; 7tm.1.1;
DR PRINTS; PR00237; GPCRHHODPSN.
DR PRINTS; PR00657; CCHEMOKINER5.
DR PRINTS; PR01110; CHEMOKINER5.
DR PROSITE; PS00237; G_PROTEIN_RECF_F1_1;
DR PROSITE; PS0262; G_PROTEIN_RECF_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 31 58 1 (POTENTIAL).
FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 69 89 2 (POTENTIAL).
FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 124 3 (POTENTIAL).
FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 142 166 4 (POTENTIAL).
FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 199 218 5 (POTENTIAL).
FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 236 260 6 (POTENTIAL).
FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 278 301 7 (POTENTIAL).
FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
FT DISULFID 101 178 BY SIMILARITY.
FT CARBOHYD 268 268 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 123 123 T -> S (IN REF. 1).
SQ SEQUENCE 352 AA; 40539 MW; 4A33E69BB80FE34C CRC64;

Query Match 78.5%; Score 124; DB 1; Length 352;
Best Local Similarity 65.5%; Pred. No. 5.3e-10;
Matches 19; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy 1 VTEVIAFLHCCNLNPLYAFVIGKFRNYFL 29
    ||| | |||:||||:||||:|||||
Db 281 VTETLGTHCCINPIIYAFVIGKFRNYLL 309

RESULT 10
ID CKR5_PAPHA STANDARD; PRT; 352 AA.
AC P56441;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE C-C CHEMOKINE RECEPTOR TYPE 5 (C-C CKR-5) (CCR-5) (CCR5).
GN CKR5 OR CMKBR5.
OS Papio hamadryas (Hamadryas baboon), and Papio anubis (Olive baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Papio.
OX NCBI_TaxID=9557; 9555;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=P.hamadryas;
RX MEDLINE=97268687; PubMed=9108095;
RA Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,
RA Sharton M., Samson M., Lu Z.H., Clements J.E., Murphy-Corb M.,
RA Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;
RT "Differential utilization of CCR5 by macrophage and T cell tropic
RL simian immunodeficiency virus strains";
RN Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).
[2]

SEQUENCE FROM N.A.
SPECIES=P.hamadryas;
MEDLINE=99210133; PubMed=10195758;
Saksena N.K., Wang B., Novembre F.J., Bolton W., Smit T.K., Lal R.B.;
"Species-specific changes in the CCR5 gene from African and Asian
nonhuman primates.";
AIDS Res. Hum. Retroviruses 15:479-483(1999).
[3]
SEQUENCE FROM N.A.
SPECIES=P.anubis;
Benton P.A., Timanus D.K., Shearer M.H., Lee D.R., Kennedy R.C.;
Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
-!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE
IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
DIFFERENTIATION.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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EMBL; AF005658; AAB62552.1; -
EMBL; AF105287; AAD20556.1; -
EMBL; AF105288; AAD20557.1; -
EMBL; AF105289; AAD20558.1; -
EMBL; AF105290; AAD20559.1; -
EMBL; AF023452; AAC63830.1; -
GCRDb; GCR_1373; -
GCRDb; GCR_2539; -
InterPro; IPR000276; -
InterPro; IPR000355; -
InterPro; IPR002240; -
Pfam; PF00001; 7tm.1.1;
PRINTS; PR00237; GPCRHHODPSN.
PRINTS; PR00657; CCHEMOKINER.
PRINTS; PR01110; CHEMOKINER5.
PROSITE; PS00237; G_PROTEIN_RECF_F1_1; 1.
PROSITE; PS0262; G_PROTEIN_RECF_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 31 58 1 (POTENTIAL).
FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 69 89 2 (POTENTIAL).
FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 124 3 (POTENTIAL).
FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 142 166 4 (POTENTIAL).
FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 199 218 5 (POTENTIAL).
FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 236 260 6 (POTENTIAL).
FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 278 301 7 (POTENTIAL).
FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
FT DISULFID 101 178 BY SIMILARITY.
FT CARBOHYD 268 268 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 123 123 T -> S (IN REF. 1).
SQ SEQUENCE 352 AA; 40489 MW; 5E1504A9BA1FE8B2 CRC64;

Query Match 78.5%; Score 124; DB 1; Length 352;
Best Local Similarity 65.5%; Pred. No. 5.3e-10;
Matches 19; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy 1 VTEVIAFLHCCNLNPLYAFVIGKFRNYFL 29
    ||| | |||:||||:||||:|||||
Db 281 VTETLGTHCCINPIIYAFVIGKFRNYLL 309

SEQUENCE FROM N.A.
SPECIES=P.hamadryas;
MEDLINE=97268687; PubMed=9108095;
Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,
Sharton M., Samson M., Lu Z.H., Clements J.E., Murphy-Corb M.,
Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;
"Differential utilization of CCR5 by macrophage and T cell tropic
simian immunodeficiency virus strains";
Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).
[2]

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Best Local Similarity 65.5%; Pred. No. 5.3e-10;
Matches 19; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

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RESULT 11
CKR5_PONPY
ID CKR5_PONPY STANDARD; PRT; 352 AA.
AC O97881;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE 30-MAY-2000 (Rel. 39, Last annotation update)
DE C-C CHEMOKINE RECEPTOR TYPE 5 (C-C CKR-5) (CCR-5) (CCR5).
GN CKR5 OR CMKR5.
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang Y.-W., Zhang Y.-P.;
RT "Sequence evolution of chemokine receptor CCR5 gene in primates.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
CC MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
CC INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE
CC IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
CC DIFFERENTIATION.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CC
CC EMBL; AF075446; AAD19858.1;
CC InterPro: IPR000248;
CC InterPro: IPR000276;
CC InterPro: IPR000355;
CC InterPro: IPR002236;
CC InterPro: IPR002237;
CC InterPro: IPR002240;
CC Pfam: PF00001; 7tm_1; 1.
CC PRINTS; PR00237; GPCRHHODPSN.
CC PRINTS; PR00241; ANGIOTENSINR.
CC PRINTS; PR00657; CCHEMOKINER.
CC PRINTS; PR01106; CHEMOKINER1.
CC PRINTS; PR01107; CHEMOKINER2.
CC PRINTS; PR01110; CHEMOKINER5.
CC PROSITE; PS00237; G_PROTEIN_RECF_F1_1; 1.
CC PROSITE; PS0262; G_PROTEIN_RECF_F1_2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein.
CC DOMAIN 1 30
CC TRANSMEM 31 58
CC DOMAIN 59 68
CC TRANSMEM 69 89
CC DOMAIN 90 102
CC TRANSMEM 103 124
CC DOMAIN 125 141
CC TRANSMEM 142 166
CC DOMAIN 167 198
CC TRANSMEM 199 218
CC DOMAIN 219 235
CC TRANSMEM 236 260
CC DOMAIN 261 277
CC TRANSMEM 278 302
CC DOMAIN 302 352
CC BY SIMILARITY.
CC DISULFID 101 178
CC SEQUENCE 352 AA; 40527 MW; F4E2F47135AF658A CRO64;

RESULT 12
CKR5_PYGBI
ID CKR5_PYGBI STANDARD; PRT; 352 AA.
AC O97880;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE C-C CHEMOKINE RECEPTOR TYPE 5 (C-C CKR-5) (CCR-5) (CCR5).
GN CKR5 OR CMKR5.
OS Pygathrix bieti (Black snub-nosed monkey) (Rhinopithecus bieti).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;
OC Pygathrix.
OX NCBI_TaxID=61621;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang Y.-W., Zhang Y.-P.;
RT "Sequence evolution of chemokine receptor CCR5 gene in primates.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
CC MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
CC INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE
CC IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
CC DIFFERENTIATION.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CC
CC EMBL; AF075445; AAD19857.1;
CC InterPro: IPR000248;
CC InterPro: IPR000276;
CC InterPro: IPR000355;
CC InterPro: IPR002236;
CC InterPro: IPR002240;
CC Pfam: PF00001; 7tm_1; 1.
CC PRINTS; PR00237; GPCRHHODPSN.
CC PRINTS; PR00241; ANGIOTENSINR.
CC PRINTS; PR00657; CCHEMOKINER.
CC PRINTS; PR01106; CHEMOKINER1.
CC PRINTS; PR01110; CHEMOKINER5.
CC PROSITE; PS00237; G_PROTEIN_RECF_F1_1; 1.
CC PROSITE; PS0262; G_PROTEIN_RECF_F1_2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein.
CC DOMAIN 1 30
CC TRANSMEM 31 58
CC DOMAIN 59 68
CC TRANSMEM 69 89
CC DOMAIN 90 102
CC TRANSMEM 103 124
CC DOMAIN 125 141
CC TRANSMEM 142 166
CC DOMAIN 167 198
CC TRANSMEM 199 218
CC DOMAIN 219 235
CC TRANSMEM 236 260
CC DOMAIN 261 277
CC TRANSMEM 278 301
CC DOMAIN 302 352
CC BY SIMILARITY.
CC DISULFID 101 178
CC SEQUENCE 352 AA; 40527 MW; F4E2F47135AF658A CRO64;

Query Match 78.5%; Score 124; DB 1; Length 352;

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FT DISULFID 101 178 BY SIMILARITY
SQ SEQUENCE 352 AA; 40585 MW; 4366F142730F938F CRC64;

Query Match 78.5%; Score 124; DB 1; Length 352;
Best Local Similarity 65.5%; Pred. No. 5.3e-10;
Matches 19; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Oy 1 VTEVLAFLHCCINPVLVAFYAFIGKERNYFL 29
    ||| | |||:||||:||||:|||||
Db 281 VTETLGMTHCCINPIIVAFVGEKFRNYLL 309

RESULT 13
CKR5_PYGNE
ID CKR5_PYGNE STANDARD; PRT; 352 AA.
AC O97882;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE C-C CHEMOKINE RECEPTOR TYPE 5 (C-C CKR-5) (CCR-5) (CCR5).
GN CCR5 OR CMKBR5.
OS Pygathrix nemaeus (Dove langur).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;
OC Pygathrix.
OX NCBI_TaxID=54133;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang Y.-W., Zhang Y.-P.;
RT "Sequence evolution of chemokine receptor CCR5 gene in primates.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
CC MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
CC INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE
CC IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
CC DIFFERENTIATION.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CC -----
CC EMBL; AF075448; AAD19860.1;
CC InterPro; IPR000248;
CC InterPro; IPR000276;
CC InterPro; IPR000355;
CC InterPro; IPR002236;
CC InterPro; IPR002237;
CC InterPro; IPR002240;
CC Pfam; PF00001; 7tm.1; 1.
CC PRINTS; PR00237; GPCRHHODOPSIN.
CC PRINTS; PR00241; ANGIOTENSINR.
CC PRINTS; PR00657; CCHEMOKINER.
CC PRINTS; PR01106; CHEMOKINER1.
CC PRINTS; PR01107; CHEMOKINER2.
CC PRINTS; PR01110; CHEMOKINER5.
CC PROSITE; PS00237; G_PROTEIN_RECEPTOR_F1_1; 1.
CC PROSITE; PS00262; G_PROTEIN_RECEPTOR_F1_2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein.
KW DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 31 58
FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 69 89
FT TRANSMEM 90 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 124
FT TRANSMEM 125 141 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 142 166 4 (POTENTIAL).
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FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 199 218 5 (POTENTIAL).
FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 236 260 6 (POTENTIAL).
FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 278 301 7 (POTENTIAL).
FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
FT DISULFID 101 178 BY SIMILARITY.
SQ SEQUENCE 352 AA; 40532 MW; FE4F9D98D3B3E861 CRC64;

Query Match 78.5%; Score 124; DB 1; Length 352;
Best Local Similarity 65.5%; Pred. No. 5.3e-10;
Matches 19; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Oy 1 VTEVLAFLHCCINPVLVAFYAFIGKERNYFL 29
    ||| | |||:||||:||||:|||||
Db 281 VTETLGMTHCCINPIIVAFVGEKFRNYLL 309

RESULT 14
CKR5_TRAFR
ID CKR5_TRAFR STANDARD; PRT; 352 AA.
AC O97878;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE C-C CHEMOKINE RECEPTOR TYPE 5 (C-C CKR-5) (CC-CKR-5) (CCR5).
GN CCR5 OR CMKBR5.
OS Trachypithecus francoisi (Francois' langur) (Indochinese langur).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;
OC Trachypithecus.
OX NCBI_TaxID=54180;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang Y.-W., Zhang Y.-P.;
RT "Sequence evolution of chemokine receptor CCR5 gene in primates.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
CC MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
CC INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE
CC IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
CC DIFFERENTIATION.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CC -----
CC EMBL; AF075442; AAD19854.1;
CC InterPro; IPR000248;
CC InterPro; IPR000276;
CC InterPro; IPR000355;
CC InterPro; IPR002236;
CC InterPro; IPR002237;
CC InterPro; IPR002240;
CC Pfam; PF00001; 7tm.1; 1.
CC PRINTS; PR00237; GPCRHHODOPSIN.
CC PRINTS; PR00241; ANGIOTENSINR.
CC PRINTS; PR00657; CCHEMOKINER.
CC PRINTS; PR01106; CHEMOKINER1.
CC PRINTS; PR01107; CHEMOKINER2.
CC PRINTS; PR01110; CHEMOKINER5.
CC PROSITE; PS00237; G_PROTEIN_RECEPTOR_F1_1; 1.
CC PROSITE; PS00262; G_PROTEIN_RECEPTOR_F1_2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein.
KW DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
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FT TRANSMEM 31 58 1 (POTENTIAL).
FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 69 89 2 (POTENTIAL).
FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 124 3 (POTENTIAL).
FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 142 166 4 (POTENTIAL).
FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 199 218 5 (POTENTIAL).
FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 236 260 6 (POTENTIAL).
FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 278 301 7 (POTENTIAL).
FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
FT DISULFID 101 178 BY SIMILARITY.
SQ SEQUENCE 352 AA; 40496 MW; 4366PF148C255938F CRC64;

Query Match 78.5%; Score 124; DB 1; Length 352;
Best Local Similarity 65.5%; Pred. No. 5.3e-10;
Matches 19; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 VTEVLAFLHCLNPLVLYAFVIGQKERNYFL 29
   ||| | |||:||||:|||||
DB 281 VTETLGMTHCCINPIIYAFVGEKERNYLL 309

RESULT 15
CNR5_TRAPH STANDARD; PRT; 352 AA.
AC O97879;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE C-C-CHEMOKINE RECEPTOR TYPE 5 (C-C CNR-5) (CCR-5) (CCR5).
GN CNR5 OR CMKBR5.
OS Trachypithecus phayrei (Phayre's leaf monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
OC Trachypithecus.
OX CNR5_TaxID=61618;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang Y.-W., Zhang Y.-P.;
RT "Sequence evolution of chemokine receptor CNR5 gene in primates.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
CC MIP-1 FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
CC MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
CC INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE
CC IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
CC DIFFERENTIATION.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CC EMBL; AF075443; AADI9855.1; -
CC InterPro; IPR000248; -
CC InterPro; IPR000276; -
CC InterPro; IPR000355; -
CC InterPro; IPR002236; -
CC InterPro; IPR002237; -
CC InterPro; IPR002240; -
CC Pfam; PF00001; 7tm.1; 1.
CC PRINTS; PR00237; GPCRRHODOPSN.
CC PRINTS; PR00241; ANGIOTENSINR.
CC PRINTS; PR00657; CCHEMOKINER.
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DR PRINTS; PR01106; CHEMOKINER1.
DR PRINTS; PR01107; CHEMOKINER2.
DR PRINTS; PR01110; CHEMOKINER5.
DR PROSITE; PS00237; G-PROTEIN_RECEP_FL_1; 1.
DR PROSITE; PS0262; G-PROTEIN_RECEP_FL_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 31 58 1 (POTENTIAL).
FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 69 89 2 (POTENTIAL).
FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 124 3 (POTENTIAL).
FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 142 166 4 (POTENTIAL).
FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 199 218 5 (POTENTIAL).
FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 236 260 6 (POTENTIAL).
FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 278 301 7 (POTENTIAL).
FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
FT DISULFID 101 178 BY SIMILARITY.
SQ SEQUENCE 352 AA; 40509 MW; 4366PF148D3A5938F CRC64;

Query Match 78.5%; Score 124; DB 1; Length 352;
Best Local Similarity 65.5%; Pred. No. 5.3e-10;
Matches 19; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 VTEVLAFLHCLNPLVLYAFVIGQKERNYFL 29
   ||| | |||:||||:|||||
DB 281 VTETLGMTHCCINPIIYAFVGEKERNYLL 309
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Search completed: May 23, 2001, 15:36:21
Job time: 652 sec

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	141	89.2		367	11	Q9rlv0	mus musculus
2	124	78.5		333	4	Q14694	homo sapien
3	124	78.5		334	6	Q9TUQ7	erythrocebu
4	124	78.5		339	4	Q9UN28	homo sapien
5	124	78.5		339	4	Q9UN27	homo sapien
6	124	78.5		339	4	Q9UN26	homo sapien
7	124	78.5		339	4	Q9UN25	homo sapien
8	124	78.5		339	4	Q9UN24	homo sapien
9	124	78.5		339	4	Q9UN23	homo sapien
10	124	78.5		339	4	Q9UBT9	homo sapien
11	124	78.5		339	4	Q9UBJ7	homo sapien
12	124	78.5		339	6	Q9TUX1	hylobates c
13	124	78.5		339	6	Q9TUX0	hylobates c
14	124	78.5		339	6	Q9TUX9	hylobates c
15	124	78.5		339	6	Q9TUW8	gorilla gor
16	124	78.5		339	6	Q9TUW7	pan troglod
17	124	78.5		339	6	Q9TUW6	pan troglod
18	124	78.5		339	6	Q9TUW5	pan troglod
19	124	78.5		339	6	Q9TUW4	pan troglod


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O14694
ID O14694 PRELIMINARY; PRT; 333 AA.
AC O14694;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE CCR5 RECEPTOR (FRAGMENT).
GN CCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B.,
RA Ho D.D.;
RL AIDS Res. Hum. Retroviruses 0:0-0(1997).
DR EMBL: AF011504; AAB65704.1; -
DR INTERPRO: IPR000190; -
DR INTERPRO: IPR000276; -
DR INTERPRO: IPR000355; -
DR INTERPRO: IPR001277; -
DR INTERPRO: IPR002236; -
DR INTERPRO: IPR002237; -
DR INTERPRO: IPR002238; -
DR INTERPRO: IPR002240; -
DR PFAM: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCRHHODOPSN.
DR PRINTS: PR00635; ANGIOTENSINR.
DR PRINTS: PR00645; LCR1ORPHANR.
DR PRINTS: PR00657; CCHEMOKINER.
DR PRINTS: PR01106; CHEMOKINER1.
DR PRINTS: PR01107; CHEMOKINER2.
DR PRINTS: PR01110; CHEMOKINER5.
DR PROSITE: PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
FT NON_TER 333
SQ SEQUENCE 333 AA; 38174 MW; AEFBA07A67893AEB CRC64;

Query Match 78.5%; Score 124; DB 4; Length 333;
Best Local Similarity 65.5%; Pred. No. 3.5e-11;
Matches 19; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 VTEVLAFLHCCLNPLVYAFIQKFRNYFL 29
   ||| | |||:||||:|||||
Db 262 VTETLGMTHCCINPIIYAFVGEKFRNYLL 290

RESULT 3
ID Q9TU07 PRELIMINARY; PRT; 334 AA.
AC Q9TU07;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE C-C CHEMOKINE RECEPTOR 5 (FRAGMENT).
GN CCR5.
OS Erythrocybus patas (Red guenon) (Hussar).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Erythrocybus.
OX NCBI_TaxID=9538;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF162049; AAD47804.1; -
DR INTERPRO: IPR000248; -
DR INTERPRO: IPR000276; -

QY 1 VTEVLAFLHCCLNPLVYAFIQKFRNYFL 29
   ||| | |||:||||:|||||
Db 262 VTETLGMTHCCINPIIYAFVGEKFRNYLL 290

RESULT 3
ID Q9TU07 PRELIMINARY; PRT; 334 AA.
AC Q9TU07;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE C-C CHEMOKINE RECEPTOR 5 (FRAGMENT).
GN CCR5.
OS Erythrocybus patas (Red guenon) (Hussar).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Erythrocybus.
OX NCBI_TaxID=9538;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF162049; AAD47804.1; -
DR INTERPRO: IPR000248; -
DR INTERPRO: IPR000276; -

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DR INTERPRO: IPR000355; -
DR INTERPRO: IPR001277; -
DR INTERPRO: IPR002236; -
DR INTERPRO: IPR002237; -
DR INTERPRO: IPR002240; -
DR PFAM: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCRHHODOPSN.
DR PRINTS: PR00241; ANGIOTENSINR.
DR PRINTS: PR00645; LCR1ORPHANR.
DR PRINTS: PR00657; CCHEMOKINER.
DR PRINTS: PR01106; CHEMOKINER1.
DR PRINTS: PR01107; CHEMOKINER2.
DR PRINTS: PR01110; CHEMOKINER5.
DR PROSITE: PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
KW Receptor.
FT NON_TER 334
SQ SEQUENCE 334 AA; 38460 MW; B19D0CEC667B69F0 CRC64;

Query Match 78.5%; Score 124; DB 6; Length 334;
Best Local Similarity 65.5%; Pred. No. 3.5e-11;
Matches 19; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 VTEVLAFLHCCLNPLVYAFIQKFRNYFL 29
   ||| | |||:||||:|||||
Db 269 VTETLGMTHCCINPIIYAFVGEKFRNYLL 297

RESULT 4
ID Q9UN28 PRELIMINARY; PRT; 339 AA.
AC Q9UN28;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE C-C CHEMOKINE RECEPTOR 5 (FRAGMENT).
GN CCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF161913; AAD47670.1; -
DR INTERPRO: IPR000190; -
DR INTERPRO: IPR000248; -
DR INTERPRO: IPR000276; -
DR INTERPRO: IPR000355; -
DR INTERPRO: IPR001277; -
DR INTERPRO: IPR002236; -
DR INTERPRO: IPR002237; -
DR INTERPRO: IPR002240; -
DR PFAM: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCRHHODOPSN.
DR PRINTS: PR00241; ANGIOTENSINR.
DR PRINTS: PR00635; ANGIOTENSINR.
DR PRINTS: PR00645; LCR1ORPHANR.
DR PRINTS: PR00657; CCHEMOKINER.
DR PRINTS: PR01106; CHEMOKINER1.
DR PRINTS: PR01107; CHEMOKINER2.
DR PRINTS: PR01110; CHEMOKINER5.
DR PROSITE: PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
KW Receptor.
FT NON_TER 339
SQ SEQUENCE 339 AA; 39183 MW; 56C819F92D6DB1A6 CRC64;

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Query Match 78.5%; Score 124; DB 4; Length 339;
 Best Local Similarity 65.5%; Pred. No. 3.6e-11;
 Matches 19; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 VTEVLAFLHCLNPVLYAFVIGKFRNYFL 29
 ||| | |||:||||:||||:||||| |
 Db 274 VTETLGMTHCCINPIIYAFVGEKFRNYLL 302

RESULT 5

QUN27 PRELIMINARY; PRT; 339 AA.
 AC QUN27;
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)
 DE C-C CHEMOKINE RECEPTOR 5 (FRAGMENT).
 GN CCR5.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kunstan K., Chen Z., Korber B., Orondek J., Stanton J., Agy M.,
 RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
 RT "Sequences of the CCR5 genes from diverse simian and prosimian
 species";
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF161914; AAD47671.1; -
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PRINTS; PR00241; ANGIOTENSINR.
 DR PRINTS; PR00635; ANGIOTENSINR.
 DR PRINTS; PR00645; LCRIORPHANR.
 DR PRINTS; PR00657; CCHEMOKINER.
 DR PRINTS; PR01106; CHEMOKINER1.
 DR PRINTS; PR01107; CHEMOKINER2.
 DR PRINTS; PR01110; CHEMOKINER5.
 DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
 KW Receptor.
 FT NON_TER 1
 FT NON_TER 339
 SQ SEQUENCE 339 AA; 39086 MW; 88AD8B44E2CB4EC2 CRC64;

Query Match 78.5%; Score 124; DB 4; Length 339;
 Best Local Similarity 65.5%; Pred. No. 3.6e-11;
 Matches 19; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 VTEVLAFLHCLNPVLYAFVIGKFRNYFL 29
 ||| | |||:||||:||||:||||| |
 Db 274 VTETLGMTHCCINPIIYAFVGEKFRNYLL 302

RESULT 6

QUN26 PRELIMINARY; PRT; 339 AA.
 AC QUN26;
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)
 DE C-C CHEMOKINE RECEPTOR 5 (FRAGMENT).
 GN CCR5.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kunstan K., Chen Z., Korber B., Orondek J., Stanton J., Agy M.,
 RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
 RT "Sequences of the CCR5 genes from diverse simian and prosimian
 species";
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF161914; AAD47671.1; -
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PRINTS; PR00241; ANGIOTENSINR.
 DR PRINTS; PR00635; ANGIOTENSINR.
 DR PRINTS; PR00645; LCRIORPHANR.
 DR PRINTS; PR00657; CCHEMOKINER.
 DR PRINTS; PR01106; CHEMOKINER1.
 DR PRINTS; PR01107; CHEMOKINER2.
 DR PRINTS; PR01110; CHEMOKINER5.
 DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
 KW Receptor.
 FT NON_TER 1
 FT NON_TER 339
 SQ SEQUENCE 339 AA; 39086 MW; 88AD8B44E2CB4EC2 CRC64;

Query Match 78.5%; Score 124; DB 4; Length 339;
 Best Local Similarity 65.5%; Pred. No. 3.6e-11;
 Matches 19; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 VTEVLAFLHCLNPVLYAFVIGKFRNYFL 29
 ||| | |||:||||:||||:||||| |
 Db 274 VTETLGMTHCCINPIIYAFVGEKFRNYLL 302

RESULT 7

QUN25 PRELIMINARY; PRT; 339 AA.
 AC QUN25;
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)
 DE C-C CHEMOKINE RECEPTOR 5 (FRAGMENT).
 GN CCR5.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
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 RP SEQUENCE FROM N.A.
 RA Kunstan K., Chen Z., Korber B., Orondek J., Stanton J., Agy M.,
 RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
 RT "Sequences of the CCR5 genes from diverse simian and prosimian
 species";
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF161914; AAD47671.1; -
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PRINTS; PR00241; ANGIOTENSINR.
 DR PRINTS; PR00635; ANGIOTENSINR.
 DR PRINTS; PR00645; LCRIORPHANR.
 DR PRINTS; PR00657; CCHEMOKINER.
 DR PRINTS; PR01106; CHEMOKINER1.
 DR PRINTS; PR01107; CHEMOKINER2.
 DR PRINTS; PR01110; CHEMOKINER5.
 DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
 KW Receptor.
 FT NON_TER 1
 FT NON_TER 339
 SQ SEQUENCE 339 AA; 39086 MW; 88AD8B44E2CB4EC2 CRC64;

Query Match 78.5%; Score 124; DB 4; Length 339;
 Best Local Similarity 65.5%; Pred. No. 3.6e-11;
 Matches 19; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 VTEVLAFLHCLNPVLYAFVIGKFRNYFL 29
 ||| | |||:||||:||||:||||| |
 Db 274 VTETLGMTHCCINPIIYAFVGEKFRNYLL 302

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kunstan K., Chen Z., Korber B., Orondek J., Stanton J., Agy M.,
 RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
 RT "Sequences of the CCR5 genes from diverse simian and prosimian
 species";
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF161914; AAD47673.1; -
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PRINTS; PR00241; ANGIOTENSINR.
 DR PRINTS; PR00635; ANGIOTENSINR.
 DR PRINTS; PR00645; LCRIORPHANR.
 DR PRINTS; PR00657; CCHEMOKINER.
 DR PRINTS; PR01106; CHEMOKINER1.
 DR PRINTS; PR01107; CHEMOKINER2.
 DR PRINTS; PR01110; CHEMOKINER5.
 DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
 KW Receptor.
 FT NON_TER 1
 FT NON_TER 339
 SQ SEQUENCE 339 AA; 39162 MW; A56369FE0529F4AB CRC64;

Query Match 78.5%; Score 124; DB 4; Length 339;
 Best Local Similarity 65.5%; Pred. No. 3.6e-11;
 Matches 19; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 VTEVLAFLHCLNPVLYAFVIGKFRNYFL 29
 ||| | |||:||||:||||:||||| |
 Db 274 VTETLGMTHCCINPIIYAFVGEKFRNYLL 302

RESULT 7

QUN25 PRELIMINARY; PRT; 339 AA.
 AC QUN25;
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)
 DE C-C CHEMOKINE RECEPTOR 5 (FRAGMENT).
 GN CCR5.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kunstan K., Chen Z., Korber B., Orondek J., Stanton J., Agy M.,
 RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
 RT "Sequences of the CCR5 genes from diverse simian and prosimian
 species";
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF161914; AAD47673.1; -
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PRINTS; PR00241; ANGIOTENSINR.
 DR PRINTS; PR00635; ANGIOTENSINR.
 DR PRINTS; PR00645; LCRIORPHANR.
 DR PRINTS; PR00657; CCHEMOKINER.
 DR PRINTS; PR01106; CHEMOKINER1.
 DR PRINTS; PR01107; CHEMOKINER2.
 DR PRINTS; PR01110; CHEMOKINER5.
 DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
 KW Receptor.
 FT NON_TER 1
 FT NON_TER 339
 SQ SEQUENCE 339 AA; 39162 MW; A56369FE0529F4AB CRC64;

Query Match 78.5%; Score 124; DB 4; Length 339;
 Best Local Similarity 65.5%; Pred. No. 3.6e-11;
 Matches 19; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 VTEVLAFLHCLNPVLYAFVIGKFRNYFL 29
 ||| | |||:||||:||||:||||| |
 Db 274 VTETLGMTHCCINPIIYAFVGEKFRNYLL 302

RESULT 7

QUN25 PRELIMINARY; PRT; 339 AA.
 AC QUN25;
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)
 DE C-C CHEMOKINE RECEPTOR 5 (FRAGMENT).
 GN CCR5.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kunstan K., Chen Z., Korber B., Orondek J., Stanton J., Agy M.,
 RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
 RT "Sequences of the CCR5 genes from diverse simian and prosimian
 species";
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF161914; AAD47673.1; -
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PRINTS; PR00241; ANGIOTENSINR.
 DR PRINTS; PR00635; ANGIOTENSINR.
 DR PRINTS; PR00645; LCRIORPHANR.
 DR PRINTS; PR00657; CCHEMOKINER.
 DR PRINTS; PR01106; CHEMOKINER1.
 DR PRINTS; PR01107; CHEMOKINER2.
 DR PRINTS; PR01110; CHEMOKINER5.
 DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
 KW Receptor.
 FT NON_TER 1
 FT NON_TER 339
 SQ SEQUENCE 339 AA; 39162 MW; A56369FE0529F4AB CRC64;

Query Match 78.5%; Score 124; DB 4; Length 339;
 Best Local Similarity 65.5%; Pred. No. 3.6e-11;
 Matches 19; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 VTEVLAFLHCLNPVLYAFVIGKFRNYFL 29
 ||| | |||:||||:||||:||||| |
 Db 274 VTETLGMTHCCINPIIYAFVGEKFRNYLL 302

RESULT 7

QUN25 PRELIMINARY; PRT; 339 AA.
 AC QUN25;
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)
 DE C-C CHEMOKINE RECEPTOR 5 (FRAGMENT).
 GN CCR5.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kunstan K., Chen Z., Korber B., Orondek J., Stanton J., Agy M.,
 RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
 RT "Sequences of the CCR5 genes from diverse simian and prosimian
 species";
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.

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DR INTERPRO: IPR002240; -.
DR PFAM: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCRHHODPSN.
DR PRINTS: PR00241; ANGIOTENSINR.
DR PRINTS: PR00635; ANGIOTENSINR.
DR PRINTS: PR00645; LCRIORPHANR.
DR PRINTS: PR00657; CCHEMOKINER.
DR PRINTS: PR01106; CHEMOKINER1.
DR PRINTS: PR01107; CHEMOKINER2.
DR PRINTS: PR01110; CHEMOKINER5.
DR PROSITE: PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
KW Receptor.
FT NON_TER 1 339
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39146 MW; 10FE05FES371D4B3 CRC64;

Query Match 78.5%; Score 124; DB 4; Length 339;
Best Local Similarity 65.5%; Pred. No. 3.6e-11;
Matches 19; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 VTEVLAFLHCLNPLVLYAFVIGQKFRNYFL 29
   ||| | |||:||||:|||||
Db 274 VTETLGMTHCCINPIYAFVGEKFRNYLL 302

RESULT 8
Q9UN24 PRELIMINARY; PRT; 339 AA.
AC Q9UN24;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE C-C CHEMOKINE RECEPTOR 5 (FRAGMENT).
GN CCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Orondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF161919; AAD47676.1; -.
DR INTERPRO: IPR000190; -.
DR Q9UN24;
DR INTERPRO: IPR000248; -.
DR INTERPRO: IPR000276; -.
DR INTERPRO: IPR000355; -.
DR INTERPRO: IPR001277; -.
DR INTERPRO: IPR002236; -.
DR INTERPRO: IPR002237; -.
DR INTERPRO: IPR002240; -.
DR PFAM: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCRHHODPSN.
DR PRINTS: PR00241; ANGIOTENSINR.
DR PRINTS: PR00635; ANGIOTENSINR.
DR PRINTS: PR00645; LCRIORPHANR.
DR PRINTS: PR00657; CCHEMOKINER.
DR PRINTS: PR01106; CHEMOKINER1.
DR PRINTS: PR01107; CHEMOKINER2.
DR PRINTS: PR01110; CHEMOKINER5.
DR PROSITE: PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
KW Receptor.
FT NON_TER 1 339
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39115 MW; 3C6369F922C91AA7 CRC64;

Query Match 78.5%; Score 124; DB 4; Length 339;
Best Local Similarity 65.5%; Pred. No. 3.6e-11;
Matches 19; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 VTEVLAFLHCLNPLVLYAFVIGQKFRNYFL 29
   ||| | |||:||||:|||||
Db 274 VTETLGMTHCCINPIYAFVGEKFRNYLL 302

RESULT 10
Q9UBT9 PRELIMINARY; PRT; 339 AA.
AC Q9UBT9;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE C-C CHEMOKINE RECEPTOR 5 (FRAGMENT).
GN CCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR ENBL; AF161915; AAD47672.1; -
DR ENBL; AF161909; AAD47666.1; -
DR ENBL; AF161910; AAD47667.1; -
DR ENBL; AF161911; AAD47668.1; -
DR ENBL; AF161912; AAD47669.1; -
DR INTERPRO; IPR000190; -
DR INTERPRO; IPR000248; -
DR INTERPRO; IPR000276; -
DR INTERPRO; IPR000355; -
DR INTERPRO; IPR001277; -
DR INTERPRO; IPR002236; -
DR INTERPRO; IPR002237; -
DR INTERPRO; IPR002240; -
DR PFAM; PF00001; 7tm_1; 1.
DR PRINTS; PRO0237; GPCRHHODOPS.
DR PRINTS; PRO0241; ANGIOTENSINR.
DR PRINTS; PRO0635; ANGIOTENSINR.
DR PRINTS; PRO0645; LCRIORPHANR.
DR PRINTS; PRO0657; CCHEMOKINER.
DR PRINTS; PRO1106; CHEMOKINER1.
DR PRINTS; PRO1107; CHEMOKINER2.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 39114 MW; 3C6369F92C29F4A7 CRC64;

Query Match 78.5%; Score 124; DB 4; Length 339;
Best Local Similarity 65.5%; Pred. No. 3.6e-11;
Matches 19; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 VTEVLAFLHCCLNPLVYAFIGQKFRNYFL 29
   ||| | |||:||||:||||:|||||
Db 274 VTETLGWTHCCINPIIYAFVGEKERNYLL 302

RESULT 11
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AC Q9UBJ7;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE C-C CHEMOKINE RECEPTOR 5 (FRAGMENT).
GN CCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR ENBL; AF161921; AAD47678.1; -
DR ENBL; AF161917; AAD47674.1; -
DR INTERPRO; IPR000190; -
DR INTERPRO; IPR000248; -
DR INTERPRO; IPR000276; -
DR INTERPRO; IPR000355; -
DR INTERPRO; IPR001277; -
DR INTERPRO; IPR002236; -
DR INTERPRO; IPR002237; -
DR INTERPRO; IPR002240; -
DR PFAM; PF00001; 7tm_1; 1.
DR PRINTS; PRO0237; GPCRHHODOPS.
DR PRINTS; PRO0241; ANGIOTENSINR.
DR PRINTS; PRO0635; ANGIOTENSINR.
DR PRINTS; PRO0645; LCRIORPHANR.
DR PRINTS; PRO0657; CCHEMOKINER.
DR PRINTS; PRO1106; CHEMOKINER1.
DR PRINTS; PRO1107; CHEMOKINER2.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 39114 MW; 3C6369F92C29F4A7 CRC64;

Query Match 78.5%; Score 124; DB 4; Length 339;
Best Local Similarity 65.5%; Pred. No. 3.6e-11;
Matches 19; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 VTEVLAFLHCCLNPLVYAFIGQKFRNYFL 29
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Db 274 VTETLGWTHCCINPIIYAFVGEKERNYLL 302

RESULT 12
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AC Q9TUX1;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE C-C CHEMOKINE RECEPTOR 5 (FRAGMENT).
GN CCR5.
OS Hylobates concolor (crested gibbon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
OX NCBI_TaxID=29089;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR ENBL; AF161887; AAD47644.1; -
DR INTERPRO; IPR000190; -
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DR INTERPRO; IPR000276; -
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DR INTERPRO; IPR001277; -
DR INTERPRO; IPR002236; -
DR INTERPRO; IPR002237; -
DR INTERPRO; IPR002240; -
DR PFAM; PF00001; 7tm_1; 1.
DR PRINTS; PRO0237; GPCRHHODOPS.
DR PRINTS; PRO0241; ANGIOTENSINR.
DR PRINTS; PRO0635; ANGIOTENSINR.
DR PRINTS; PRO0645; LCRIORPHANR.
DR PRINTS; PRO0657; CCHEMOKINER.
DR PRINTS; PRO1106; CHEMOKINER1.
DR PRINTS; PRO1107; CHEMOKINER2.
DR PRINTS; PRO1110; CHEMOKINER5.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 39075 MW; 09257FBFB834C4AE CRC64;
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DR INTERPRO; IPR002236; -
DR INTERPRO; IPR002237; -
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DR PRINTS; PRO0237; GPCRHHODOPS.
DR PRINTS; PRO0241; ANGIOTENSINR.
DR PRINTS; PRO0635; ANGIOTENSINR.
DR PRINTS; PRO0645; LCRIORPHANR.
DR PRINTS; PRO0657; CCHEMOKINER.
DR PRINTS; PRO1106; CHEMOKINER1.
DR PRINTS; PRO1107; CHEMOKINER2.
DR PRINTS; PRO1110; CHEMOKINER5.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 39128 MW; 9C3369FFFFF1F2F27A CRC64;

Query Match 78.5%; Score 124; DB 4; Length 339;
Best Local Similarity 65.5%; Pred. No. 3.6e-11;
Matches 19; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 VTEVLAFLHCCLNPLVYAFIGQKFRNYFL 29
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Db 274 VTETLGWTHCCINPIIYAFVGEKERNYLL 302

RESULT 12
Q9TUX1 PRELIMINARY; PRT; 339 AA.
AC Q9TUX1;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE C-C CHEMOKINE RECEPTOR 5 (FRAGMENT).
GN CCR5.
OS Hylobates concolor (crested gibbon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
OX NCBI_TaxID=29089;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR ENBL; AF161887; AAD47644.1; -
DR INTERPRO; IPR000190; -
DR INTERPRO; IPR000248; -
DR INTERPRO; IPR000276; -
DR INTERPRO; IPR000355; -
DR INTERPRO; IPR001277; -
DR INTERPRO; IPR002236; -
DR INTERPRO; IPR002237; -
DR INTERPRO; IPR002240; -
DR PFAM; PF00001; 7tm_1; 1.
DR PRINTS; PRO0237; GPCRHHODOPS.
DR PRINTS; PRO0241; ANGIOTENSINR.
DR PRINTS; PRO0635; ANGIOTENSINR.
DR PRINTS; PRO0645; LCRIORPHANR.
DR PRINTS; PRO0657; CCHEMOKINER.
DR PRINTS; PRO1106; CHEMOKINER1.
DR PRINTS; PRO1107; CHEMOKINER2.
DR PRINTS; PRO1110; CHEMOKINER5.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 39075 MW; 09257FBFB834C4AE CRC64;
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OS *Hylobates concolor* (crested gibbon).

DR PFAM; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PRINTS; PR00241; ANGIOTENSINR.
 DR PRINTS; PR00635; ANGIOTENSINR.
 DR PRINTS; PR00645; LCR1ORPHANR.
 DR PRINTS; PR00657; CCEMOKINER.
 DR PRINTS; PR01106; CHEMOKINER1.
 DR PRINTS; PR01107; CHEMOKINER2.
 DR PRINTS; PR01110; CHEMOKINER5.
 DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
 KW Receptor.
 FT NON_TER 1 1
 FT NON_TER 339 339
 SQ SEQUENCE 339 AA; 39079 MW; A4A79753DA2F7AAF CRC64;

Query Match 78.5%; Score 124; DB 6; Length 339;
 Best Local Similarity 65.5%; Pred. No. 3.6e-11;
 Matches 19; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy 1 VTEVLAFHCLNPVLYAFIGOKERNYEL 29
 ||| | |||:|:|:|:|:|:|:|
 Db 274 VTEGLWTHCCINPIIYAFVGEKFRNVL 302

Search completed: May 23, 2001, 15:35:18
 Job time: 624 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 23, 2001, 15:28:33 ; Search time 184.73 Seconds
(without alignments)
13.925 Million cell updates/sec

Title: US-08-887-977-10_COPY_320_364

Perfect score: 237

Sequence: 1 KILKDLWCVRKRYKSGFSC.....ENISQTSATDNDNASFT 45

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 390729 seqs, 57163235 residues

Total number of hits satisfying chosen parameters: 390729

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A.Geneseq_0401.*

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- 2: /SID56/gcgdata/geneseq/geneseq/AA1981.DAT.*
- 3: /SID56/gcgdata/geneseq/geneseq/AA1982.DAT.*
- 4: /SID56/gcgdata/geneseq/geneseq/AA1983.DAT.*
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- 8: /SID56/gcgdata/geneseq/geneseq/AA1987.DAT.*
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- 22: /SID56/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query %	Length	ID	Description
1	237	100.0	365	19	W48086	Human dendritic ce
2	237	100.0	365	21	Y97077	Primate (human) ch
3	56	23.6	280	21	G25793	Arabidopsis thalia
4	56	23.6	282	21	G25792	Arabidopsis thalia
5	56	23.6	292	21	G25791	Arabidopsis thalia
6	56	23.6	720	20	Y05452	Human heregulin-11
7	56	23.6	720	20	Y97618	Human heregulin-11
8	55	23.2	166	21	B27319	B. napus NIM1 homo
9	55	23.2	461	21	Y77450	Leptospira kirschn
10	52	21.9	166	21	B27320	B. napus NIM1 homo
11	52	21.9	476	19	W37241	Heterodera glycine

12	52	21.9	484	19	W43910	Heterodera glycine
13	52	21.9	800	11	R07713	Human low density
14	51.5	21.7	768	20	W98108	Caenorhabditis ele
15	51	21.5	81	20	Y28848	Maize basal endosp
16	51	21.5	246	20	Y37499	Protein which is s
17	51	21.5	512	21	G28030	Arabidopsis thalia
18	51	21.5	545	21	G28029	Arabidopsis thalia
19	51	21.5	606	21	G28028	Arabidopsis thalia
20	51	21.5	860	15	R47157	Sequence of human
21	51	21.5	910	21	G48217	Arabidopsis thalia
22	51	21.5	957	21	G48216	Arabidopsis thalia
23	51	21.5	991	21	G48215	Arabidopsis thalia
24	50	21.1	141	21	G36206	Arabidopsis thalia
25	50	21.1	169	21	G36205	Arabidopsis thalia
26	50	21.1	183	21	G36204	Arabidopsis thalia
27	50	21.1	500	21	B19742	Rat acyl CoA:chole
28	50	21.1	500	21	Y54139	Acyl-CoA:cholester
29	50	21.1	713	20	W97617	Mouse neuregulin r
30	49.5	20.9	89	21	G27687	Arabidopsis thalia
31	49.5	20.9	96	21	G27686	Arabidopsis thalia
32	49.5	20.9	291	21	G13753	Arabidopsis thalia
33	49.5	20.9	291	21	G51750	Arabidopsis thalia
34	49.5	20.9	353	21	G13752	Arabidopsis thalia
35	49.5	20.9	353	21	G51749	Arabidopsis thalia
36	49.5	20.9	456	21	G13751	Arabidopsis thalia
37	49.5	20.9	456	21	G51748	Arabidopsis thalia
38	49	20.7	149	21	G29834	Arabidopsis thalia
39	49	20.7	189	20	Y42390	Alternative readin
40	49	20.7	497	21	Y94523	Mouse diacylglycer
41	49	20.7	498	21	Y44562	Mouse diacylglycer
42	48.5	20.5	250	21	G35200	Zea mays protein f
43	48.5	20.5	272	18	W00925	HASNPV polypeptide
44	48	20.3	106	18	W14541	Streptococcus pneu
45	48	20.3	152	21	B33196	Pinus radiata tran

ALIGNMENTS

RESULT 1

ID	W48086	Standard; Protein; 365 AA.
XX	W48086;	
AC	W48086;	
XX	11-JUN-1998	(first entry)
DT	Human dendritic cell chemokine receptor.	
DE	Human; thymus expressed chemokine; TECK; MIP-3alpha; MIP-3beta; receptor; dendritic cell; macrophage; inflammation; asthma.	
KW	Human; thymus expressed chemokine; TECK; MIP-3alpha; MIP-3beta; receptor; dendritic cell; macrophage; inflammation; asthma.	
OS	Homo sapiens.	
XX		
XX		
PH	Key	Location/Qualifiers
FT	Misc-difference 193	/note= "encoded by CAN"
FT		
XX	W09801557-A2.	
PN		
XX		
PD	15-JAN-1998.	
XX		
PF	02-JUL-1997;	97WO-US10819.
XX		
PR	04-JUN-1997;	97US-0048593.
PR	05-JUL-1996;	96US-0675814.
PR	11-OCT-1996;	96US-0028329.
XX	(SCHE) SCHERING CORP.	
PA	Gish KC, Schall TJ, Vicari A, Wang W, Zlotnik A;	
PI		
XX	WPI; 1998-101054/09.	
DR		

CC population of cells expressing a MIP-3-alpha receptor. The methods are
 CC useful for treating a mammalian subject with a skin disease or condition
 CC e.g. cancer, metastasis, psoriasis, atopic or contact dermatitis,
 CC systemic lupus erythematosus and lichen ruber planus, or for treating
 CC skin transplants or grafts.
 XX
 XX Sequence 365 AA;
 SQ

Query Match 100.0%; Score 237; DB 21; Length 365;
 Best Local Similarity 100.0%; Pred. No. 4.3e-26;
 Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps

OY 1 KILKDLWCVRKYKSGFGSCAGRYSENISRQTSQTSADNDNASSFT 45
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 Db 320 kilkdwcrrkyksgfgscagrysenisrqtsetadndnassft 364

RESULT 3
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 ID G25793 standard; Protein; 280 AA.
 XX
 XX G25793;
 XX
 XX
 DT 17-OCT-2000 (first entry)
 XX
 XX Arabidopsis thaliana protein fragment SEQ ID NO: 30000.
 KW Protein identification; signal transduction pathway; metabolic pathway;
 KW hybridisation assay; genetic mapping; gene expression control; promoter;
 KW termination sequence.
 XX
 XX Arabidopsis thaliana.
 OS
 XX
 XX EP1033405-A2.
 PN
 XX
 PD 06-SEP-2000.
 XX
 XX 25-FEB-2000; 2000EP-0301439.
 XX
 XX 25-FEB-1999; 99US-0121825.
 PR 05-MAR-1999; 99US-0123180.
 PR 09-MAR-1999; 99US-0123548.
 PR 23-MAR-1999; 99US-0125788.
 PR 25-MAR-1999; 99US-0126264.
 PR 29-MAR-1999; 99US-0126785.
 PR 01-APR-1999; 99US-0127462.
 PR 06-APR-1999; 99US-0128234.
 PR 08-APR-1999; 99US-0128714.
 PR 16-APR-1999; 99US-0129845.
 PR 19-APR-1999; 99US-0130077.
 PR 21-APR-1999; 99US-0130449.
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PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
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PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 14-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
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PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
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PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
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PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
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PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
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PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143342.
PR 14-JUL-1999; 99US-0143624.
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PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
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PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
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PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
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PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
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PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
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PR 08-OCT-1999; 99US-0158232.
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PR 13-OCT-1999; 99US-0159293.
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PR 26-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.

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PR 29-OCT-1999; 99US-0162142.
Query Match 23.6%; Score 56; DB 21; Length 280;
Best Local Similarity 26.1%; Pred. No. 4.7;
Matches 12; Conservative 15; Mismatches 15; Indels 4; Gaps 3;
QY 3 LKDLW-CVRRKYSKSGRS-CAGRISENIISROTSTADNDNASSFT 45
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Db 70 iknlwnscikkklmkkgidpithkplsevgketnr-sdnnnstsfs 114

RESULT 4
G25792
ID G25792 standard; Protein; 282 AA.
XX AC
XX G25792;
XX DT 17-OCT-2000 (first entry)
XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 29999.
XX KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX OS Arabidopsis thaliana.
XX PN EP1033405-A2.
XX PD 06-SEP-2000.
XX PF 25-FEB-2000; 2000EP-0301439.
XX PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
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PR 06-APR-1999; 99US-0128234.
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PR 16-APR-1999; 99US-0129845.
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PR 28-MAY-1999; 99US-0136782.
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PR 04-JUN-1999; 99US-0137508.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
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PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
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PR 16-JUN-1999; 99US-0139453.
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PR 18-JUN-1999; 99US-0139454.
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PR 21-JUL-1999; 99US-0144814.
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PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
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PR 27-JUL-1999; 99US-0145913.
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PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
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XX AC Y05452;
 XX DT 06-JUL-1999 (first entry)
 XX DE Human heregulin-like factor sequence.
 XX KW Human heregulin-like factor; HLF; cell growth regulator; diagnosis;
 XX KW neural system disorder; cancer.
 XX OS Homo sapiens.
 XX PN W09857989-A1.
 XX PD 23-DEC-1998.
 XX PF 16-JUN-1998; 98WO-US12403.
 XX PR 17-JUN-1997; 97US-0049942.
 XX PA (HUMA-) HUMAN GENOME SCI INC.
 XX PA (GEOU) UNIV GEORGETOWN.
 XX PI Hijazi MM, King CR, Ruben SM, Young P;
 XX PS WPI; 1999-095327/08.
 XX PT New isolated heregulin-like factor - used to develop products for
 XX PT the diagnosis and treatment of disorders involving regulation of
 XX PT cell growth, particularly cancers
 XX PS Disclosure; Page 97-99; 118pp; English.
 XX CC This sequence is the human heregulin-like factor (HLF) of the
 XX CC invention. The HLF is involved in the regulation of cell growth.
 XX CC Detection of different levels of expression of the HLF gene can be used
 XX CC for the diagnosis of disorders, e.g. in the neural system. In
 XX CC particular, detection of different levels of HLF gene expression in cells
 XX CC or body fluid of an individual can be used for diagnosing cancer. The
 XX CC products can also be used in the treatment of disorders involving
 XX CC abnormal levels of HLF activity.
 XX SQ Sequence 720 AA;
 Query Match 23.6%; Score 56; DB 20; Length 720;
 Best Local Similarity 41.2%; Pred. No. 15;
 Matches 14; Conservative 2; Mismatches 14; Indels 4; Gaps 1;
 QY 6 LWCVR-----KYKSGFSCAGRYSENISROTSET 35
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 Db 542 lwcverpldlykssgiktdqntsmqlpsret 575
 RESULT 7
 W97618
 ID W97618 standard; Protein; 720 AA.
 XX AC W97618;
 XX DT 10-MAY-1999 (first entry)
 XX DE Human heregulin related ligand NRG3.
 XX KW Neuroregulin related ligand; NRG3; hNRG3B1; human; ErbB4 receptor;
 XX KW signal transduction; nervous system disorder; neurodegeneration;
 XX KW neuropathy; therapy; diagnosis.
 XX OS Homo sapiens.
 XX FH Key Location/Qualifiers
 XX FT Domain 1..360
 FT /note= "extracellular domain, specifically claimed"

FT Region 66..91 in Claim 5(a)"
 FT /note= "hydrophobic region"
 FT Region 101..284
 FT /note= "mucin-like Ser/Thr-rich region, contains
 FT sites for O-linked glycosylation"
 FT Domain 285..354
 FT /note= "EGF-like domain"
 FT Domain 356..394
 FT /note= "transmembrane domain"
 XX W09902681-A1.
 XX PN 21-JAN-1999.
 XX PD 30-JUN-1998; 98WO-US13411.
 XX PF 24-JUL-1997; 97US-0899437.
 XX PR 09-JUL-1997; 97US-0052019.
 XX PA (GETH) GENENTECH INC.
 XX PI Godowski PJ, Mark MR, Zhang D;
 XX PS WPI; 1999-120882/10.
 XX DR N-PSDB; X06988.
 XX PT New isolated neuroregulin related ligand-3 - used to develop products
 XX PT for treating nervous system disorders, e.g. stroke, ischaemia,
 XX PT infection, malignancy, Alzheimer's disease or Down's syndrome
 XX PS Claim 5(b); Page 66-69; 101pp; English.
 XX CC This is the amino acid sequence of human neuroregulin related ligand
 XX CC NRG3, a novel member of the epidermal growth factor (EGF)-like
 XX CC family of protein ligands that binds to the ErbB4 receptor, but not
 XX CC to the ErbB2 or ErbB3 receptor, and which activates ErbB4 receptor
 XX CC tyrosine phosphorylation. The sequence was deduced from the
 XX CC nucleotide sequence of a cDNA clone (see X06988) from a foetal brain
 XX CC library. The EGF-like domain of NRG3 is distinct from those of NRG1
 XX CC or NRG2, and NRG3 displays receptor binding characteristics that are
 XX CC distinct from those of other neuroregulins. An alternatively spliced
 XX CC form of human NRG3 is provided in W97619. The invention provides
 XX CC human and murine NRG3 polypeptides (see also W97617), expression
 XX CC vectors, host cells and methods for the recombinant production of
 XX CC NRG3s. The NRG3 polypeptides and polynucleotides and can be used to
 XX CC enhance the survival, proliferation or differentiation of cells
 XX CC having the ErbB4 receptor in vivo and in vitro. They can be used to
 XX CC prevent or treat damage to a nerve or damage to other NRG3-expressing
 XX CC or NRG3-responsive cells, e.g. brain, heart, or kidney cells. In
 XX CC particular, they can be used to treat diseases which involve neural
 XX CC cell growth such as demyelination, or damage or loss of glial cells
 XX CC (e.g. multiple sclerosis). They can be used to treat patients whose
 XX CC nervous system has been damaged by e.g. trauma, surgery, stroke,
 XX CC ischaemia, infection, metabolic disease, nutritional deficiency,
 XX CC malignancy, or toxic agents. NRG3 can also be used to treat
 XX CC motor neuron disorders such as amyotrophic lateral sclerosis (Lou
 XX CC Gehrig's disease), Bell's palsy, conditions involving spinal
 XX CC muscular atrophy or paralysis, neurodegenerative disorders such as
 XX CC Alzheimer's disease, Parkinson's disease, epilepsy, multiple
 XX CC sclerosis, Huntington's chorea, Down's syndrome, nerve deafness,
 XX CC and Meniere's disease. They can also be used to treat neuropathies
 XX CC associated with systemic disease including post-polio syndrome,
 XX CC hereditary neuropathies including Charcot-Marie-Tooth disease,
 XX CC Refsum's disease, abetalipoproteinemia, Tangier disease, Krabbe's
 XX CC disease, metachromatic leukodystrophy, Fabry's disease and
 XX CC Dejerine-Sottas syndrome, to treat disease of skeletal muscle of
 XX CC smooth muscle, such as muscular dystrophy or diseases caused by
 XX CC skeletal or smooth muscle wasting. The products can also be used
 XX CC for detection, diagnosis, for the production of transgenic or
 XX CC knockout animals or for drug screening.
 XX SQ Sequence 720 AA;

QY 9 VRRKYSSGFSCAGRYSENISRQTSETAD '37
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RESUL 10
B27320
ID B27320 standard: Protein: 166 AA.

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Best Local Similarity 37.5%; Pred. No. 34;
Matches 12; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

Qy 12 KYKSGGFCAGRYSENISRQTSFADNDNASS 43
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Db 322 kkkstgvcsgssgssgssgssgssgss 353

RESULT 12
W43910
ID W43910 standard; Protein; 484 AA.
XX
AC W43910;

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XX 17-JUN-1998 (first entry)
 DT Heterodera glycines svp encoded cellulase.
 XX
 DE
 XX
 KW Cellulase activity; nematode; crop protection; parasitic;
 KW subventral oesophageal protein.
 XX
 OS Heterodera glycines.
 XX
 PN EP818538-A1.
 XX
 PD 14-JAN-1998.
 XX
 XX 08-JUL-1996; 96EP-0201890.
 PF
 XX 08-JUL-1996; 96EP-0201890.
 PR
 XX (RIJK-) RIJSLANDBOUWUNIVERSITEIT WAGENINGEN.
 PA
 XX Bakker J, De Boer JM, Gommers FJ, Goverse A, Helder J;
 PI Roosten J, Schots A, Schouten A, Smart G, Stiekema WJ;
 PI Stokkermans JPW;
 XX
 XX WPI: 1998-065307/07.
 DR N-PSDB; T86645.
 DR
 XX Nematodal cellulase peptide(s) - useful as industrial cellulolytic
 PT enzymes or for plant protection
 PT
 XX Claim 1; Pages 18-20; 28pp; English.
 PS
 XX The sequence is that of a peptide having cellulase activity.
 CC The peptide comprises at least a fragment of nematode subventral
 CC oesophageal proteins (svp's). can be used as a cellulolytic enzyme
 CC in the food and beverage industry, in the paper or clothing
 CC industry, or in waste treatment. The peptide or antibodies
 CC directed against it can be used to protect plants against
 CC parasitic nematodes.
 CC
 XX Sequence 484 AA;
 SQ

Query Match 21.9%; Score 52; DB 19; Length 484;
 Best Local Similarity 37.5%; Pred. No. 35;
 Matches 12; Conservative 8; Mismatches 12; Indels 0; Gaps 0;
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 Db 293 kkkstgvcsgsgsgsgsgsgsgsgsgsgsgss 324

RESULT 13
 R07713
 ID R07713 standard; protein; 800 AA.
 XX
 AC R07713;
 XX
 DT 20-FEB-1991 (first entry)
 XX
 DE Human low density lipoprotein receptor.
 DE
 XX LDL; Familial Hypercholesterolaemia.
 KW
 XX Homo sapiens.
 OS
 XX
 XX Key Location/Qualifiers
 FH Peptide 1..21
 FT /label=signal peptide
 FT Domain 729..750
 FT /label-transmembrane region
 FT Modified-site 97..99
 FT /label-N-glycosylation site

FT Modified-site 156..158
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 FT Modified-site 272..274
 FT /label=N-glycosylation site
 FT Modified-site 515..517
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 FT Modified-site 272..274
 FT /label=N-glycosylation site
 XX
 XX US4966837-A.
 PN
 XX 30-OCT-1990.
 PD
 XX 30-OCT-1986; 86US-0925702.
 PF
 XX 30-OCT-1986; 86US-0925702.
 PR
 XX (TEXA) UNIVERSITY OF TEXAS SYSTEM.
 PA
 XX Brown MS, Golstein JL, Russell DW;
 PI
 XX WPI: 1990-347914/46.
 DR P-PSDB; R07713.
 DR
 XX Diagnosis of LDL receptor gene mutation by fragmentation of DNA,
 PT separating fragments and patterns, identifying fragments corresp.
 PT to the gene, and comparing with normal gene pattern.
 PT
 XX Disclosure; Fig 3; 36pp; English.
 PS
 XX The sequence was deduced from cDNA carried on pLDR-2, a plasmid
 CC constructed by ligating p101 (contg. the 3' end) and p203 (contg.
 CC the 5'end). These plasmids were isolated from a cDNA library
 CC pred. from human fetal adrenal poly(A)+ RNA. The sequence can be
 CC used to make probes for the diagnosis of Familial Hyper-
 CC cholesterolaemia.
 CC
 XX Sequence 800 AA;
 SQ

Query Match 21.9%; Score 52; DB 11; Length 800;
 Best Local Similarity 35.1%; Pred. No. 64;
 Matches 13; Conservative 5; Mismatches 17; Indels 2; Gaps 1;
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 Db 63 clsvtfksgdfscggrvncrcipfwrcdgydcnsgs 99

RESULT 14
 W98108
 ID W98108 standard; Protein; 768 AA.
 XX
 AC W98108;
 XX
 DT 21-JUN-1999 (first entry)
 XX
 DE Caenorhabditis elegans elongation factor-2 kinase (eEF-2 kinase).
 DE
 XX Elongation factor-2 kinase; eEF-2 kinase; nematode; protein kinase;
 KW inhibitor; breast cancer; therapy.
 KW
 XX Caenorhabditis elegans.
 OS
 XX
 XX Key Location/Qualifiers
 FH Region 66..79
 FT /note= "predicted amphipathic alpha-helix
 FT structure"
 FT
 XX W09909199-A2.
 PN
 XX

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OM protein - protein search, using sw model

Run on: May 23, 2001, 15:30:09 ; Search time 95.91 Seconds
(without alignments)
9.014 Million cell updates/sec

Title: US-08-887-977-10_COPY_320_364

Perfect score: 237

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Searched: 185757 seqs, 19210857 residues

Total number of hits satisfying chosen parameters: 185757

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents_AA.*

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- 4: /cgn2_6/ptodata/2/iaa/6B_COMB.pap.*
- 5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pap.*
- 6: /cgn2_6/ptodata/2/iaa/backfiles1.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	56	23.6	720	4	US-08-899-437-6
2	55	23.2	461	4	US-09-122-210-2
3	50	21.1	713	4	US-08-899-437-2
4	48.5	20.5	272	4	US-09-029-213B-27
5	48.5	20.5	3177	2	US-08-477-451-4
6	48	20.3	2182	2	US-08-487-826B-16
7	48	20.3	3169	2	US-08-477-451-6
8	47.5	20.0	491	1	US-08-206-176-4
9	47	19.8	345	3	US-08-718-738-2
10	47	19.8	345	5	PCT-US95-03323A-2
11	47	19.8	356	1	US-08-228-162-2
12	47	19.8	860	1	US-08-092-817-4
13	47	19.8	1074	2	US-08-470-058-2
14	47	19.8	1074	3	US-09-037-188-2
15	47	19.8	1410	2	US-08-470-058-4
16	47	19.8	1410	3	US-09-037-188-4
17	46.5	19.6	413	3	US-08-390-333A-7
18	46.5	19.6	426	3	US-08-390-333A-1
19	46	19.4	379	1	US-07-723-002C-4
20	46	19.4	2205	1	US-08-093-453B-2
21	45	19.0	323	3	US-09-041-889-28
22	45	19.0	377	3	US-09-041-889-29
23	45	19.0	541	2	US-08-540-804-16
24	45	19.0	541	2	US-08-218-265-16
25	45	19.0	541	3	US-08-521-872-16
26	44.5	18.8	501	1	US-08-331-394-4
27	44.5	18.8	501	1	US-08-250-858-4

28	44.5	18.8	501	1	US-08-446-915-4	Sequence 4, Appli
29	44.5	18.8	501	2	US-08-744-139-4	Sequence 4, Appli
30	44.5	18.8	501	5	PCT-US95-06639-4	Sequence 4, Appli
31	44.5	18.8	1702	5	PCT-US95-10661A-5	Sequence 5, Appli
32	44.5	18.8	1848	5	PCT-US95-10661A-6	Sequence 6, Appli
33	44	18.6	117	1	US-08-274-661B-39	Sequence 39, Appli
34	44	18.6	119	1	US-08-340-539A-17	Sequence 17, Appli
35	44	18.6	410	1	US-08-471-033-40	Sequence 40, Appli
36	44	18.6	410	1	US-08-471-033-43	Sequence 43, Appli
37	44	18.6	410	2	US-08-471-044-40	Sequence 40, Appli
38	44	18.6	410	2	US-08-471-044-43	Sequence 43, Appli
39	44	18.6	410	2	US-08-463-483A-40	Sequence 40, Appli
40	44	18.6	410	2	US-08-463-483A-43	Sequence 43, Appli
41	44	18.6	410	2	US-08-471-046A-40	Sequence 40, Appli
42	44	18.6	410	2	US-08-471-046A-43	Sequence 43, Appli
43	44	18.6	410	2	US-08-470-566B-40	Sequence 40, Appli
44	44	18.6	410	2	US-08-470-566B-43	Sequence 43, Appli
45	44	18.6	410	2	US-08-469-334-40	Sequence 40, Appli

ALIGNMENTS

RESULT 1
US-08-899-437-6
; Sequence 6, Application US/08899437
; Patent No. 6121415
; GENERAL INFORMATION:
; APPLICANT: Godowski, Paul J., Mark, Melanie Rose, Zhang, Dong Xiao
; TITLE OF INVENTION: ErbB Receptor-Specific Neuregulin Related
; TITLE OF INVENTION: Ligands and Uses Therefor
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/899,437
; FILING DATE: 24-Jul-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Conley, Deirdre L.
; REGISTRATION NUMBER: 36,487
; REFERENCE/DOCKET NUMBER: P1084R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-2066
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 720 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; FEATURE:
; NAME/KEY: INRG3B1 amino acid sequence
; LOCATION: 1-720
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
US-08-899-437-6

Query Match 23.6%; Score 56; DB 4; Length 720;
Best Local Similarity 41.2%; Pred. No. 9.7;
Matches 14; Conservative 2; Mismatches 14; Indels 4; Gaps 1;
QY 6 LMCVRR----KYKSSGFSCAGRYSENISRQTSSET 35

RESULT 5
US-08-477-451-4
; Sequence 4, Application US/08477451
; Patent No. 5928865
; GENERAL INFORMATION:
; APPLICANT: Covacci, Antonello
; TITLE OF INVENTION: Helicobacter Pylori CagI Region
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation

QY 3 LKDLWCVRKYSKSGF--SCAGRYSENISRQTSSET 35


```

; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
PCT-US95-03323A-2

Query Match 19.8%; Score 47; DB 5; Length 345;
Best Local Similarity 31.4%; Pred. No. 71;
Matches 11; Conservative 5; Mismatches 17; Indels 2; Gaps 1;

QY 7 WCVRRKYGSGFSC--AGRYSENISR--QTSETADNDNAS 39
   | | | | | | | | | | | | | | | | | | | |
Db 44 WYPEKYGSGFRCIHGEKVDPIVTEQAKESGLD 78

RESULT 11
US-08-228-162-2
; Sequence 2, Application US/08228162
; Patent No. 5521071
; GENERAL INFORMATION:
; APPLICANT: Attie, Alan D
; APPLICANT: Sturley, Stephen L
; APPLICANT: Gretch, Daniel G
; TITLE OF INVENTION: Soluble LDL Receptor and Gene
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nicholas J. Seay, Quarles & Brady
; STREET: P.O. Box 2113
; CITY: Madison
; STATE: WI
; COUNTRY: USA
; ZIP: 53701-2113
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/228,162
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Seay, Nicholas J
; REGISTRATION NUMBER: 27,386
; REFERENCE/DOCKET NUMBER: 9629692026
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608)251-5000
; TELEFAX: (608)251-9166
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 356 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-228-162-2

Query Match 19.8%; Score 47; DB 1; Length 356;
Best Local Similarity 35.1%; Pred. No. 74;
Matches 13; Conservative 4; Mismatches 18; Indels 2; Gaps 1;

QY 8 CVRRKYGSGFSCAGRYSENISR--QTSETADNDNAS 42
   | | | | | | | | | | | | | | | | | | | |
Db 63 CLSVTCCKGDFSCGGRVNRCPQFWRCDGQVDCDNGS 99

RESULT 12
US-08-092-817-4
; Sequence 4, Application US/08092817
; Patent No. 5496926
; GENERAL INFORMATION:
; APPLICANT: Heartlein, Michael W.
; APPLICANT: Lemontt, Jeffrey F.
; TITLE OF INVENTION: Chimeric Proteins For Use in Transport
; TITLE OF INVENTION: of a Selected Substance Into Cells
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

```

```

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,058
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: TKT93-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1074 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-470-058-2

Query Match 19.8%; Score 47; DB 2; Length 1074;
Best Local Similarity 35.1%; Pred. No. 2.7e+02;
Matches 13; Conservative 4; Mismatches 18; Indels 2; Gaps 1;

QY 8 CVRRKYKSGFSCAGRYSENISR--QTSETADNDNAS 42
I: || ||| || : : : |||
Db 63 CLSVTCKSGDFSCGGRVNRNCIPQFWRCDGQVDCDNGS 99

RESULT 14
US-09-037-188-2
; Sequence 2, Application US/09037188
; Patent No. 602921
; GENERAL INFORMATION:
; APPLICANT: Heartlein, Michael W.
; APPLICANT: Lemontt, Jeffrey F.
; APPLICANT: Concino, Michael F.
; TITLE OF INVENTION: CHIMERIC PROTEINS FOR USE
; IN TRANSPORT OF A SELECTED SUBSTANCE INTO CELLS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/037,188
; FILING DATE: 02-MAR-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Ph.D., J.D., Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 07236/009002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1074 amino acids
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; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-09-037-188-2

Query Match 19.8%; Score 47; DB 3; Length 1074;
Best Local Similarity 35.1%; Pred. No. 2.7e+02;
Matches 13; Conservative 4; Mismatches 18; Indels 2; Gaps 1;

QY 8 CVRRKYKSGFSCAGRYSENISR--QTSETADNDNAS 42
I: || ||| || : : : |||
Db 63 CLSVTCKSGDFSCGGRVNRNCIPQFWRCDGQVDCDNGS 99

RESULT 15
US-08-470-058-4
; Sequence 4, Application US/08470058
; Patent No. 5817789
; GENERAL INFORMATION:
; APPLICANT: Heartlein, Michael W.
; APPLICANT: Lemontt, Jeffrey F.
; TITLE OF INVENTION: Chimeric Proteins For Use in Transport
; OF A Selected Substance Into Cells
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,058
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: TKT93-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1410 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-470-058-4

Query Match 19.8%; Score 47; DB 2; Length 1410;
Best Local Similarity 35.1%; Pred. No. 3.7e+02;
Matches 13; Conservative 4; Mismatches 18; Indels 2; Gaps 1;

QY 8 CVRRKYKSGFSCAGRYSENISR--QTSETADNDNAS 42
I: || ||| || : : : |||
Db 63 CLSVTCKSGDFSCGGRVNRNCIPQFWRCDGQVDCDNGS 99

Search completed: May 23, 2001, 15:30:10
Job time: 417 sec
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 23, 2001, 15:32:03 ; Search time 110.15 Seconds
(without alignments)
28.076 Million cell updates/sec

Title: US-08-887-977-10_COPY_320_364

Perfect score: 237

Sequence: 1 KILKDLWCVRKRYKSGFSC.....ENISQTSADNDNASFT 45

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 198801 seqs, 68722935 residues

Total number of hits satisfying chosen parameters: 198801

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_67:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	237	100.0	369	JC5068	G protein-coupled
2	64	27.0	1025	T10259	RNA-directed DNA p
3	63	26.6	245	T41291	conserved hypothet
4	59	24.9	515	T45644	hypothetical prote
5	57.5	24.3	959	S61155	hypothetical prote
6	56	23.6	1237	GNFF42	retrovirus-related
7	56	23.6	1500	A42210	alpha-1-macroglobu
8	54.5	23.0	1459	T24088	hypothetical prote
9	54	22.8	409	A47527	transcription fact
10	54	22.8	1671	S71628	sensory transducti
11	53.5	22.6	978	T16948	hypothetical prote
12	53	22.4	412	XNCHDC	aspartate transami
13	52.5	22.2	933	T33621	hypothetical prote
14	52.5	22.2	957	T10633	hypothetical prote
15	52	21.9	160	A82733	conserved hypothet
16	52	21.9	355	T29251	hypothetical prote
17	52	21.9	369	S70847	outer membrane por
18	52	21.9	791	T41573	hypothetical prote
19	51.5	21.7	127	D82479	hypothetical prote
20	51.5	21.7	383	T37171	hypothetical prote
21	51.5	21.7	2222	A36028	DNA-directed DNA p
22	51	21.5	152	T41310	hypothetical prote
23	51	21.5	173	C71484	hypothetical prote
24	51	21.5	1188	T05324	hypothetical prote
25	50.5	21.3	614	T47749	hypothetical prote
26	50.5	21.3	1135	T30561	Scythe protein - A
27	50.5	21.3	1392	T01908	hypothetical prote
28	50.5	21.3	1515	T04204	hypothetical prote
29	50	21.1	142	T41313	hypothetical prote

30 50 21.1 152 2 I41311
31 50 21.1 152 2 I41312
32 50 21.1 210 2 T21120
33 50 21.1 713 2 T44447
34 49.5 20.9 479 2 T01922
35 49.5 20.9 730 2 T46074
36 49.5 20.9 1040 2 T08190
37 49 20.7 129 1 L2OVE
38 49 20.7 178 2 S74871
39 49 20.7 257 2 T31609
40 49 20.7 262 2 T02115
41 49 20.7 711 2 T30107
42 49 20.7 746 2 S62365
43 49 20.7 786 2 T18469
44 49 20.7 1414 2 T33236
45 48.5 20.5 351 1 JSBYP1

hypothetical prote
hypothetical prote
hypothetical prote
neuregulin-3 limpo
hypothetical prote
hypothetical prote
lysozyme (EC 3.2.1
transposase slr124
hypothetical prote
hypothetical prote
SNF1-related prote
hypothetical prote
hypothetical prote
centromere-binding

ALIGNMENTS

RESULT 1

JC5068

G protein-coupled receptor CKR-L3 - human

C:Species: Homo sapiens (man)

C:Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 21-Jul-2000

C:Accession: JC5068

R:Zaballos, A.; Varona, R.; Gutierrez, J.; Lind, P.; Marquez, G.

Biochem. Biophys. Res. Commun. 227, 846-853, 1996

A:Title: Molecular cloning and RNA expression of two new human chemokine receptor-lik

A:Reference number: JC5067; MUID:97040707

A:Accession: JC5068

A:Molecule type: DNA

A:Residues: 1-369 <ZAB>

A:Cross-references: EMBL:Z79784; NID:gl668737; PIDN:CAB02144.1; PID:gl668738

C:Comment: This protein belongs to the family of alpha chemokine receptors.

C:Genetics:

A:Gene: GDB:CMKBR6; STRL22; GPR29; CCR6; CKR-L3; GPR-CY4

A:Cross-references: GDB:5370639; OMIM:601835

A:Map position: 6q27-6q27

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor; transmembrane protein

F:42-68/Domain: transmembrane #status predicted <TM1>

F:79-99/Domain: transmembrane #status predicted <TM2>

F:115-136/Domain: transmembrane #status predicted <TM3>

F:160-180/Domain: transmembrane #status predicted <TM4>

F:212-233/Domain: transmembrane #status predicted <TM5>

F:250-271/Domain: transmembrane #status predicted <TM6>

F:292-315/Domain: transmembrane #status predicted <TM7>

Query Match 100.0%; Score 237; DB 2; Length 369;

Best Local Similarity 100.0%; Pred. No. 1.le-23;

Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KILKDLWCVRKRYKSGSCAGRYSENISRQTSQTSADNDNASFT 45

Db 324 KILKDLWCVRKRYKSGSCAGRYSENISRQTSQTSADNDNASFT 368

RESULT 2

T10259

CNA-directed DNA polymerase (EC 2.7.7.49) - pteromalid wasp (Nasonia vitripennis) ret

C:Species: Nasonia vitripennis

C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000

C:Accession: T10259; I44490

R:Burke, W.D.; Malik, H.S.; Lathe III, W.C.; Eickbush, T.H.

Nature 392, 141-142, 1998

A:Title: Are retrotransposons long-term hitchhikers?

A:Reference number: 217001; MUID:98175715

A:Accession: T10259

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-1025 <BUR>
A:Cross-references: EMBL:L00950; NID:g3559783; PIDN:AAC34927.1; PID:g2317818
R:Burke, W.D.; Eickbush, D.G.; Xiong, Y.; Jakubczak, J.; Eickbush, T.H.
Mol. Biol. Evol. 10, 163-185, 1993
A:Title: Sequence relationship of retrotransposable elements R1 and R2 within and between
A:Reference number: A44490; MUID:93196484
A:Contents: retrotransposable element R2
A:Accession: T44490
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 314-956, 'Q', 'A', '971', 'AA' <BU2>
A:Note: sequence extracted from NCBI backbone (NCBIP:127243)
C:Genetics:
A:Mobile element: retrotransposon R2
C:Keywords: nucleotidyltransferase

Query Match 27.08; Score 64; DB 2; Length 1025;
Best Local Similarity 43.9%; Pred. No. 2.3;
Matches 18; Conservative 6; Mismatches 11; Indels 6; Gaps 2;

Qy 8 CVRR-KYKSGFSCAGRYSENISROTSETADNDNAS 42
Db 125 CLRQKKYKTRVARRAENRARETELRLTETADDPAS 165

RESULT 3
T41291
conserved hypothetical protein SPCC31H12.03c - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C:Accession: T41291
R:Wood, V.; Rajandream, M.A.; Barrell, B.G.; Rieger, M.
submitted to the EMBL Data Library, September 1998
A:Reference number: 221985
A:Accession: T41291
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-245 <WOO>
A:Cross-references: EMBL:AL031824; PIDN:CAA21220.1; GSPDB:GN00068; SPDB:SPCC31H12.03c
A:Experimental source: strain 972h-; cosmid c31H12
C:Genetics:
A:Gene: SPDB:SPCC31H12.03c
A:Map position: 3

Query Match 26.68; Score 63; DB 2; Length 245;
Best Local Similarity 40.08; Pred. No. 0.71;
Matches 14; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

Qy 9 VRRKYKSGFSCAGRYSENISROTSETADNDNAS 43
Db 12 LREKLAEGSLTAGNKAEVLVSRLTAATESNDENTS 46

RESULT 4
T45644
hypothetical protein F13112.130 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000
C:Accession: T45644
R:Choisne, N.; Robert, C.; Brottier, P.; Wincker, P.; Cattolico, L.; Artiguenave, F.; Sanger
submitted to the Protein Sequence Database, November 1999
A:Reference number: 223010
A:Accession: T45644
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-515 <CHO>
A:Cross-references: EMBL:AL133292
A:Experimental source: cultivar Columbia; BAC clone F13112
C:Genetics:
A:Map position: 3
A:Introns: 434/2

A:Note: F13112.130

Query Match 24.9%; Score 59; DB 2; Length 515;
Best Local Similarity 35.9%; Pred. No. 5.1;
Matches 14; Conservative 8; Mismatches 17; Indels 0; Gaps 0;

Qy 5 DLWCVRKRYKSGFSCAGRYSENISROTSETADNDNAS 43
Db 112 EAFSVKMQELASQFRNAGDEEEENKQKSEAVDNDNDS 150

RESULT 5
S61155
hypothetical protein YDR359c - yeast (Saccharomyces cerevisiae)
N:Alternate names: hypothetical protein D9476.11
C:Species: Saccharomyces cerevisiae
C:Date: 23-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 29-Oct-1999
C:Accession: S61155
R:Du, Z.
submitted to the EMBL Data Library, June 1995
A:Description: The sequence of S. cerevisiae cosmid 9476.
A:Reference number: S61146
A:Accession: S61155
A:Molecule type: DNA
A:Residues: 1-959 <DUZ>
A:Cross-references: EMBL:U28372; NID:g849170; PID:g849181; GSPDB:GN00004; MIPS:YDR359
C:Genetics:
A:Gene: MIPS:YDR359c
A:Map position: 4R

Query Match 24.3%; Score 57.5; DB 2; Length 959;
Best Local Similarity 37.5%; Pred. No. 15;
Matches 18; Conservative 7; Mismatches 12; Indels 11; Gaps 3;

Qy 3 LKDLW-----CVRRKY-----KSSGFSCAGRYSENISROTSETADNDN 40
Db 391 IKDYWTYGTCCVKKRKTLLPGKENKLSDDGRISEK-SGRPSDTSRND 437

RESULT 6
GNFF42
retrovirus-related pol polyprotein - fruit fly (Drosophila melanogaster) retrotranspo
N:Contains: retropepsin (EC 3.4.23.16)
C:Species: Drosophila melanogaster
C:Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 16-Jun-2000
C:Accession: D29349
R:Yuki, S.; Inouye, S.; Ishimaru, S.; Saigo, K.
Eur. J. Biochem. 158, 403-410, 1986
A:Title: Nucleotide sequence characterization of a Drosophila retrotransposon, 412.
A:Reference number: A91171; MUID:86274717
A:Accession: D29349
A:Molecule type: DNA
A:Residues: 1-1237 <YUK>
A:Cross-references: GB:X04132; GB:X03733; NID:g8500; PIDN:CAA27750.1; PID:g1335652
A:Note: the authors translated the codon CAA for residue 21 as Lys
C:Genetics:
A:Gene: FlyBase:412
A:Cross-references: FlyBase:FBgn0000006
C:Superfamily: pol polyprotein
C:Keywords: aspartic proteinase; hydrolase; polypeptide; reverse transcriptase
F:39-133/Product: retropepsin #status predicted <RTP>
F:63/Active site: Asp (shared with dimeric partner) #status predicted

Query Match 23.6%; Score 56; DB 1; Length 1237;
Best Local Similarity 34.1%; Pred. No. 32;
Matches 15; Conservative 8; Mismatches 17; Indels 4; Gaps 1;

Qy 1 KILKD-----LWCVRKRYKSGFSCAGRYSENISROTSETADNDN 40
Db 738 KELKDITGNILKWTTRFQSRQKSCAGKQLDLQKQKTEASEPN 781

```
RESULT 7
A42210
alpha-1-macroglobulin precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 16-Jul-1999
C:Accession: A42210; A26124
R:Warmegard, B.; Martin, N.; Johansson, S.
Biochemistry 31, 2346-2352, 1992
A:Title: cDNA cloning and sequencing of rat alpha 1-macroglobulin.
A:Reference number: A42210; MUID:92172859
A:Accession: A42210
A:Molecule type: mRNA
A:Residues: 1-1500 <WAR>
A:Cross-references: GB:M84000; GB:J05359; NID:g205383; PIDN:AAA41591.1; PID:g205384
A:Experimental source: Strain Sprague-Dawley, liver
A:Note: sequence extracted from NCBI backbone (NCBIP:87164)
R:Lonberg-Holm, K.; Reed, D.L.; Roberts, R.C.; Hebert, R.R.; Hillman, M.C.; Kutney, R.M.
J. Biol. Chem. 262, 438-445, 1987
A:Title: Three high molecular weight protease inhibitors of rat plasma. Isolation, chara
A:Reference number: A26124; MUID:87083487
A:Accession: A26124
A:Molecule type: protein
A:Residues: 25-29,'F',31-44 <LON>
C:Superfamily: alpha-2-macroglobulin
C:Keywords: glycoprotein; plasma; proteinase inhibitor
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-1474/Product: alpha-1-macroglobin #status predicted <MAT>

Query Match 23.6%; Score 56; DB 2; Length 1500;
Best Local Similarity 41.4%; Pred. No. 39;
Matches 12; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

QY 9 VRRKYSKSGFSCAGRYSENISROTSETAD 37
| ||| | : | : | : | : | : | : | : | : |
Db 266 VCRKYTQSYNSCHGSHKSICEEFSKQAD 294

RESULT 8
T24088
hypothetical protein R09E10.5 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T24088
R:Matthews, L.
submitted to the EMBL Data Library, March 1996
A:Reference number: Z19839
A:Accession: T24088
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-1459 <WIL>
A:Cross-references: EMBL:Z70287; PIDN:CAA94300.1; GSPDB:GN00022; CESP:R09E10.5
A:Experimental source: clone R09E10
C:Genetics:
A:Gene: CESP:R09E10.5
A:Map position: 4
A:Introns: 86/1; 128/3; 392/1; 504/3; 723/3; 763/2; 819/3; 865/1; 1108/1; 1168/2; 1197/1

Query Match 23.0%; Score 54.5; DB 2; Length 1459;
Best Local Similarity 40.6%; Pred. No. 59;
Matches 13; Conservative 4; Mismatches 12; Indels 3; Gaps 2;

QY 7 WCVRRK--YKSSGFCAGRYSEN-ISRQTS 35
|||:| | : | : | | | | | | | |
Db 1370 WCIRKKLQESRNYSGTAAYSNNAFQNOTVET 1401

RESULT 9
A47527
transcription factor HNF-3 beta - zebra fish
N:Alternate names: axial protein; hepatocyte nuclear factor 3 beta
C:Species: Brachydanio rerio (zebra fish)
C:Date: 11-Nov-1994 #sequence_revision 19-Oct-1995 #text_change 18-Jun-1999
C:Accession: A47527; S36040
R:Strahle, U.; Blader, P.; Henrique, D.; Ingham, P.W.
Genes Dev. 7, 1436-1446, 1993
A:Title: Axial, a zebra fish gene expressed along the developing body axis, shows alt
A:Reference number: A47527; MUID:93321871
A:Accession: A47527
A:Molecule type: mRNA
A:Residues: 1-409 <STR>
A:Cross-references: EMBL:Z22762; NID:g311267; PIDN:CAA80443.1; PID:g311268
C:Function:
A:Description: required for induction of axial mesoderm and of ventral central ne
A:Note: expressed in all three layers of the developing embryonic axis and in adult 1
C:Superfamily: transcription factor HNF-3; fork head DNA-binding domain homology
C:Keywords: DNA binding; transcription factor
F:151-242/Domain: fork head DNA-binding domain homology <FHD>

Query Match 22.8%; Score 54; DB 1; Length 409;
Best Local Similarity 36.1%; Pred. No. 19;
Matches 13; Conservative 7; Mismatches 14; Indels 2; Gaps 1;

QY 8 CVRRKYKSGFSCAGRYSENISRQTSADNDNASS 43
| | : | | : | : | : | : | : | : | : |
Db 239 CYLRQKR--FKDKKLSKDPKRKTSEGGNSSES 272

RESULT 10
S71628
sensory transduction histidine kinase doka - slime mold (Dictyostelium discoideum)
C:Species: Dictyostelium discoideum
C:Date: 27-Nov-1997 #sequence_revision 12-Dec-1997 #text_change 29-Oct-1999
C:Accession: S71628; S78068
R:Schuster, S.C.; Noegel, A.A.; Oehme, F.; Gerisch, G.; Simon, M.I.
EMBO J. 15, 3880-3889, 1996
A:Title: The hybrid histidine kinase Doka is part of the osmotic response system of D.
A:Reference number: S71628; MUID:96324396
A:Accession: S71628
A>Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-1670 <SCH>
A:Cross-references: EMBL:X96869
A:Experimental source: strain AX2; substrain 214
R:Schuster, S.C.; Noegel, A.A.; Oehme, F.; Gerisch, G.; Simon, M.I.
submitted to the EMBL Data Library, March 1996
A:Description: The hybrid histidine kinase Doka is part of the osmotic response syste
A:Reference number: S78068
A:Accession: S78068
A:Molecule type: DNA
A:Residues: 1-149,'E',151-219,'TRVLKLIQSTNNWIYV',238-1671 <SCW>
A:Cross-references: EMBL:X96869; NID:g1237201; PIDN:CAA65612.1; PID:e233513; PID:g123
C:Genetics:
A:Gene: doka
C:Function:
A:Description: modulates cell response to changes in osmolarity; involved in spore fo
C:Superfamily: response regulator homology
C:Keywords: phosphoprotein; signal transduction
F:1520-1629/Domain: response regulator homology <RRH2>
F:1568/Binding site: phosphate (Asp) (covalent) #status predicted

Query Match 22.8%; Score 54; DB 2; Length 1671;
Best Local Similarity 32.1%; Pred. No. 80;
Matches 17; Conservative 8; Mismatches 18; Indels 10; Gaps 2;

QY 1 KILKDLWCVRKRYKS-----SGFSCAGRYSEN--SRQTSADNDNASS 43
| : | : | : | : | : | : | : | : | : | : |
Db 499 KVLNLLIRQYKSRATIKPDPGCGICIFEYIENINLNYQPPTSNDNRINS 551

RESULT 11
```

C:Superfamily: aspartate aminotransferase
C:Keywords: acetylated amino end; aminotransferase; phosphoprotein; pyridoxal phospho
F:2-412/Product: aspartate transaminase, cytosolic #status experimental <MAL>
F:2/Modified site: acetylated amino end (Ala) (in mature form) #status experimental
F:258/Binding site: pyridoxal phosphate (Lys) (covalent) #status experimental

Query Match 22.4%; Score 53; DB 1; Length 412;
Best Local Similarity 34.8%; Pred. No. 25;
Matches 16; Conservative 4; Mismatches 16; Indels 10; Gaps 3;

QY 4 KDLWCVRKRYKSSGFS-CA-----GRYSENISROTSETADNDN 40
||| | | : || | | | | : | | |
Db 235 KDAWAV-RYFVSEGFELFCAQSFKNFGLYNERVGNLSVVGKDEDN 279

RESULT 13
T13621
hypothetical protein F40G9.9 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C:Accession: T13621
R:Graves, T.; Sutterer, C.; Ozersky, P.
Submitted to the EMBL Data Library, October 1998
A:Description: The sequence of C. elegans cosmid F40G9.
A:Reference number: Z21378
A:Accession: T13621
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-933 <GRA>
A:Cross-references: EMBL:AF099919; PIDN:AA068801.1; GSPDB:GN00021; CESP:F40G9.9
A:Experimental source: strain Bristol N2; clone F40G9
C:Genetics:
A:Gene: CESP:F40G9.9
A:Map position: 3
A:Introns: 48/2; 151/2; 349/2; 449/2; 691/2; 889/2

Query Match 22.2%; Score 52.5; DB 2; Length 933;
Best Local Similarity 35.0%; Pred. No. 69;
Matches 14; Conservative 6; Mismatches 19; Indels 1; Gaps 1;

QY 6 LWCVRKRYKSSGFCAGRYSENISROTSETADNDNASFT 45
||| : || : | : | || | | : ||
Db 162 LWSINSSPTSHLADKRL-RSIHRPTSEIHLNINSKDET 200

RESULT 14
T10633
hypothetical protein T13K14.70 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 18-Aug-2000
C:Accession: T10633
R:Bevan, M.; Pohl, T.; Weizenegger, T.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X.; Lem
Submitted to the Protein Sequence Database, June 1999
A:Reference number: Z16991
A:Accession: T10633
A:Molecule type: DNA
A:Residues: 1-957 <BEV>
A:Cross-references: EMBL:AL080282; GSPDB:GN00062; ATSP:T13K14.70
A:Experimental source: cultivar Columbia; BAC clone T13K14
C:Genetics:
A:Gene: ATSP:T13K14.70
A:Map position: 4
A:Introns: 84/3; 115/2; 133/1; 280/2; 365/2; 682/1; 732/3; 771/3; 811/3
C:Superfamily: Arabidopsis thaliana hypothetical protein T13K14.70

Query Match 22.2%; Score 52.5; DB 2; Length 957;
Best Local Similarity 40.0%; Pred. No. 71;
Matches 14; Conservative 6; Mismatches 12; Indels 3; Gaps 1;

QY 1 KILKDLWCVRKRYKSSGFCAGRYSENISROTSET 35

```

Query Match      21.9%; Score 52; DB 2; Length 160;
Best Local Similarity 24.3%; Pred. NO. 13;
Matches 9; Conservative 12; Mismatches 16; Indels 0; Gaps 0;

OY 1 KILKDLWCVRKYKSGFGSCAGRYSENISROTSETAD 37
   :: : | : | : : : | : | : | : : | :
Db 81 RLARDGWIILQYRYRTFTFLTPAGKALAAASRGCHQYVE 117

```

Search completed: May 23, 2001, 15:32:04
Job time: 511 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 23, 2001, 15:36:21 ; Search time 62.39 seconds
(without alignments)

24.707 Million cell updates/sec

Title: US-08-887-977-10_COPY_320_364

Perfect score: 237

Sequence: 1 KILKDLWCVRKRRKSSGFSC.....ENISRQTSETADNDNASFT 45

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	237	100.0	374	1	CKR6_HUMAN
2	164.5	69.4	367	1	O54689 mus musculus
3	64	27.0	1025	1	P021 NASVI
4	56	23.6	720	1	NRG3_HUMAN
5	56	23.6	1237	1	P0L4 DROME
6	54.5	23.0	1459	1	YFIM CAEEL
7	54	22.8	409	1	AXIA BRARE
8	53.5	22.6	978	1	YSX7 CAEEL
9	53	22.4	411	1	AATC CHICK
10	52	21.9	369	1	OMPE XENNE
11	51.5	21.7	768	1	EF2K CAEEL
12	51.5	21.7	2222	1	DPOE YEAST
13	50	21.1	152	1	T200 SALTY
14	50	21.1	638	1	HS70 CERCA
15	50	21.1	713	1	NRG3 MOUSE
16	49	20.7	129	1	LYC ORTVE
17	49	20.7	835	1	AXN1 BRARE
18	48	20.3	282	1	OMPD SALTY
19	48	20.3	363	1	TOBI MOUSE
20	48	20.3	412	1	AATC MOUSE
21	48	20.3	442	1	UL17 HSV6U
22	48	20.3	826	1	CRAA BACUH
23	48	20.3	893	1	AXN1 RAT
24	48	20.3	992	1	AXN1 MOUSE
25	47.5	20.0	100	1	YD79 METJA
26	47.5	20.0	267	1	KORB ARCFU
27	47.5	20.0	477	1	YK9 YEAST
28	47.5	20.0	491	1	FIBE HUMAN
29	47.5	20.0	527	1	ESR2 SHEEP
30	47.5	20.0	1018	1	DPOG SCHPO
31	47	19.8	72	1	VF06 VARV
32	47	19.8	233	1	RNS4 ANTHI
33	47	19.8	296	1	CYCG RHOSH

34 47 19.8 345 1 TOB1_HUMAN
35 47 19.8 412 1 AATC_BOVIN
36 47 19.8 412 1 AATC_PIG
37 47 19.8 616 1 Y396_HELPJ
38 47 19.8 619 1 NBL4_BRARE
39 47 19.8 860 1 LDLR_HUMAN
40 46.5 19.6 415 1 B2AR_NACMU
41 46.5 19.6 615 1 YG10_METJA
42 46.5 19.6 804 1 CADD_STAAU
43 46.5 19.6 961 1 LIN2_CAEEL
44 46.5 19.6 1271 1 BCR_HUMAN
45 46 19.4 95 1 NCCY_ALCXX

ALIGNMENTS

RESULT 1
CKR6_HUMAN STANDARD; PRT; 374 AA.
AC PS1684; Q92846; P78553;
DT 01-OCT-1996 (Rel. 34, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE C-C CHEMOKINE RECEPTOR TYPE 6 (C-C CKR-6) (CCR-6) (LARC
DE RECEPTOR) (GPR-CY4) (GPCY4) (CHEMOKINE RECEPTOR-LIKE 3) (CKR-L3)
DE (DRY6).
GN CCR6 OR CMKBR6 OR STRL22 OR GPR29 OR CKRL3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID:9606;
RN [1]
RP SEQUENCE FROM N.A., AND FUNCTION.
RX MEDLINE=97313465; PubMed=9169459;
RA Baba M., Imai T., Nishimura M., Kakizaki M., Takagi S., Hieshima K.,
RA Nomiya H., Yoshie O.;
RT Identification of CCR6, the specific receptor for a novel
RT lymphocyte-directed CC chemokine LARC.*;
RL J. Biol. Chem. 272:14893-14898(1997).
RN [2]
RP SEQUENCE FROM N.A.
RA Lautens L.L., Modi W., Bonner T.I.;
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=97040707; PubMed=8886020;
RA Zaballo A., Varona R., Gutierrez J., Lind P., Marquez G.;
RT Molecular cloning and RNA expression of two new human chemokine
RT receptor-like genes.*;
RL Biochem. Biophys. Res. Commun. 227:846-853(1996).
RN [4]
RP SEQUENCE FROM N.A.
RA McCoy R., Perlmutter D.H.;
RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=97224503; PubMed=9070937;
RA Liao F., Lee H.-H., Farber J.M.;
RT Cloning of STRL22, a new human gene encoding a G-protein-coupled
RT receptor related to chemokine receptors and located on chromosome
RT 6q27.*;
RL Genomics 40:175-180(1997).
CC -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-3-
CC ALPHA/LARC AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE
CC INTRACELLULAR CALCIUM IONS LEVELS.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- TISSUE SPECIFICITY: SPLEEN, LYMPH NODES, APPENDIX, AND FETAL
CC LIVER. EXPRESSED IN LYMPHOCYTES, T CELLS AND B CELLS BUT NOT IN
CC NATURAL KILLER CELLS, MONOCYTES, OR GRANULOCYTES.
CC -!- INDUCTION: INTERLEUKIN-2.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -!- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-6 IS THE INITIATOR.


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RESULT 3
PO21_NASVI
ID PO21_NASVI STANDARD; PRT; 1025 AA.
AC Q03278;
DT 01-JUN-1994 (Rel. 29, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE RETROVIRUS-RELATED POLYPROTEIN FROM TYPE I RETROTRANSPOSABLE
DE ELEMENT R2 [CONTAINS: REVERSE TRANSCRIPTASE (EC 2.7.7.49);
DE ENDONUCLEASE] (FRAGMENT).
OS Nasonia vitripennis (Parasitic wasp).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita;
OC Chalcidoidea; Pteromalidae; Nasonia.
OX NCBI_TaxID=7425;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93196484; PubMed=8383793;
RA Burke W.D., Eickbush D.G., Xiong Y., Jakubczak J.L., Eickbush T.H.;
RT "Sequence relationship of retrotransposable elements R1 and R2 within
RT and between divergent insect species.";
RL Mol. Biol. Evol. 10:163-185(1993).
RN [2]
RP REVISIONS.
RA Burke W.D., Eickbush D.G., Xiong Y., Jakubczak J.L., Eickbush T.H.;
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: N DEOXYNUCLEOSIDE TRIPHOSPHATE =
CC N PYROPHOSPHATE + DNA(N).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: L00950; AAC34927.1; --
CC FIR: I44490; I44490.
CC InterPro: IP000477; -.
CC Pfam: PF00078; rvt; 1.
CC Pfam: PF00096; zf-C2H2; 1.
CC PROSITE: PS00028; ZINC_FINGER_C2H2_1; 1.
CC PROSITE: PS0157; ZINC_FINGER_C2H2_2; 1.
CC Transferase: RNA-directed DNA polymerase; Transposable element;
KW Hydrolase; Nuclease; Endonuclease.
FT NON_TER 1
FT DOMAIN <1 754 REVERSE TRANSCRIPTASE.
FT DOMAIN 755 1025 NUCLEIC ACID-BINDING ENDONUCLEASE.
FT ZN_FING 46 69 C2H2-TYPE.
FT ZN_FING 1025 AA; 115884 MW; 387BDE63BCF5C518 CRC64;
SQ SEQUENCE 1025 AA; 115884 MW; 387BDE63BCF5C518 CRC64;

Query Match 27.0%; Score 64; DB 1; Length 1025;
Best Local Similarity 43.9%; Pred. No. 1.1;
Matches 18; Conservative 6; Mismatches 11; Indels 6; Gaps 2;

QY 8 CVRR--KYKSGFGSCAGRYSENISRQTS-----ETADNDNAS 42
|:|: |||: | | :|: ||: |||: |||: |||: |||
Db 125 CLAKQKQYKTIKRRVRRNRARENARETELRLTETADDPAS 165

RESULT 4
NRG3_HUMAN
ID NRG3_HUMAN STANDARD; PRT; 720 AA.
AC P56975;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE PRO-NEUREGULIN-3 PRECURSOR (PRO-NRG3) [CONTAINS: NEUREGULIN-3 (NRG-
DE 3)].
CN NRG3.

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OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97420720; PubMed=9275162;
RA Zhang D., Sliwkowski M.X., Mark M., Frantz G., Akita R., Sun Y.,
RA Hillan K., Crowley C., Brush J., Godowski P.J.;
RT "Neuregulin-3 (NRG3): a novel neural tissue-enriched protein that
RT binds and activates ErbB4.";
RT Proc. Natl. Acad. Sci. U.S.A. 94:9562-9567(1997).
CC -1- FUNCTION: DIRECT LIGAND FOR THE ERBB4 TYROSINE KINASE RECEPTOR.
CC BINDING RESULTS IN LIGAND-STIMULATED TYROSINE PHOSPHORYLATION AND
CC ACTIVATION OF THE RECEPTOR. DOES NOT BIND TO THE EGF RECEPTOR,
CC ERBB2 OR ERBB3 RECEPTORS.
CC -1- SUBCELLULAR LOCATION: EXISTS AS AN TYPE I MEMBRANE PROTEIN AND AS
CC A PROTEOLYTICALLY RELEASED SOLUBLE GROWTH FACTOR FORM. THE
CC MEMBRANE-BOUND FORM DOES NOT SEEM TO BE ACTIVE (BY SIMILARITY).
CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN MOST REGIONS OF THE BRAIN
CC WITH THE EXCEPTION OF CORPUS CALLOSUM. EXPRESSED AT LOWER LEVEL IN
CC MUSCLE, KIDNEY, PANCREAS, SPLEEN, THYMUS, PROSTATE, OVARY, SMALL
CC INTESTINE, COLON AND PERIPHERAL BLOOD LEUKOCYTES.
CC -1- DOMAIN: THE CYTOPLASMIC DOMAIN MAY BE INVOLVED IN THE REGULATION
CC OF TRAFFICKING AND PROTEOLYTIC PROCESSING. REGULATION OF THE
CC PROTEOLYTIC PROCESSING INVOLVES INITIAL INTRACELLULAR DOMAIN
CC DIMERIZATION (BY SIMILARITY).
CC -1- DOMAIN: ERBB RECEPTOR BINDING IS ELICITED ENTIRELY BY THE EGF-LIKE
CC DOMAIN (BY SIMILARITY).
CC -1- PTM: PROTEOLYTIC CLEAVAGE CLOSE TO THE PLASMA MEMBRANE ON THE
CC EXTERNAL FACE LEADS TO THE RELEASE OF THE SOLUBLE GROWTH FACTOR
CC FORM (BY SIMILARITY).
CC -1- PTM: EXTENSIVE GLYCOSYLATION PRECEDES THE PROTEOLYTIC CLEAVAGE (BY
CC SIMILARITY).
CC -1- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE NEUREGULIN FAMILY.
CC InterPro: IPR000561; -.
CC Pfam: PF00008; EGF; 1.
CC PROSITE: PS00022; EGF_1; 1.
CC PROSITE: PS01186; EGF_2; 1.
KW Growth factor; EGF-like domain; Transmembrane; Multigene family.
FT CHAIN 1 720 PRO-NEUREGULIN-3, MEMBRANE-BOUND FORM.
FT CHAIN 1 359 NEUREGULIN-3.
FT DOMAIN 1 360 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 361 381 INTERNAL SIGNAL SEQUENCE (POTENTIAL).
FT DOMAIN 382 720 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 105 285 SER/THR-RICH.
FT DOMAIN 286 329 EGF-LIKE.
FT DOMAIN 5 8 POLY-ALA.
FT DOMAIN 13 21 POLY-ALA.
FT DOMAIN 26 34 POLY-THR.
FT DOMAIN 127 135 POLY-SER.
FT DOMAIN 252 260 POLY-THR.
FT DOMAIN 262 265 BY SIMILARITY.
FT DISULFID 290 304 BY SIMILARITY.
FT DISULFID 298 317 BY SIMILARITY.
FT DISULFID 319 328 BY SIMILARITY.
SQ SEQUENCE 720 AA; 77900 MW; A4D6F10DDB95A693 CRC64;

Query Match 23.6%; Score 56; DB 1; Length 720;
Best Local Similarity 41.2%; Pred. No. 8.7;
Matches 14; Conservative 2; Mismatches 14; Indels 4; Gaps 1;

QY 6 LWCVRR-----KYKSGFGSCAGRYSENISRQTSSET 35
| | | | | | | | | | | | | | | | | |
Db 542 LWCVERPLDLKYSYSSGLKTRNTSINQLPSRET 575

RESULT 5
POLA_DROME

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ID POL4_DROME STANDARD; PRT; 1237 AA.
AC P10394;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE RETROVIRUS-RELATED POL POLYPROTEIN FROM TRANSPOSON 412 [CONTAINS:
DE PROTEASE (EC 3.4.23.-); REVERSE TRANSCRIPTASE (EC 2.7.7.49);
DE ENONUCLEASE].
GN POL.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86274717; PubMed=2426108;
RA Yuki S., Inouye S., Ishimaru S., Saigo K.;
RT "Nucleotide sequence characterization of a Drosophila
retrotransposon, 412.";
RL Eur. J. Biochem. 158:403-410(1986).
CC -!- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY U22.
CC -----
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CC -----
CC EMBL; X04132; CAA27750.1; -
DR PIR; D29349; GNPF42.
DR HSSP; P03366; LHG.
DR FlyBase; FBgn000006; 412.
DR InterPro; IPR000477; -
DR InterPro; IPR001969; -
DR InterPro; IPR001995; -
DR Pfam; PF00077; tvp; 1.
DR Pfam; PF00078; tvt; 1.
DR PROSITE; PS00141; ASP_PROTEASE; 1.
DR PROSITE; PS01175; ASP_PROT_RETROV; 1.
KW Hydrolase; Aspartyl protease; RNA-directed DNA polymerase;
KW Endonuclease; Transferase; Polyprotein; Transposable element.
FT ACT_SITE 63
FT ACT_SITE 63 PROTEASE (BY SIMILARITY)
SQ SEQUENCE 1237 AA; 143041 MW; AC57F1C159D14B65 CRC64;

Query Match 23.6%; Score 56; DB 1; Length 1237;
Best Local Similarity 34.1%; Pred. No. 16;
Matches 15; Conservative 8; Mismatches 17; Indels 4; Gaps 1;

QY 1 KILKD- - - - LNCVRRKYSKSGFCAGRYSENISROTSETADNDN 40
Db 738 KELKDITNLIKVTTFOSQKSCAGKGLDLOKQKTEIASPN 781

RESULT 6
YELM_CAEEL
ID YELM_CAEEL STANDARD; PRT; 1459 AA.
AC Q21874;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE HYPOTHETICAL 166.0 KDA PROTEIN R09E10.5 IN CHROMOSOME IV.
GN R09E10.5.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;

Matthews L.;
RA Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
RL -!- SIMILARITY: STRONG, TO C.ELEGANS F54D1.6.
CC -----
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CC -----
CC EMBL; Z70287; CAA94300.1; -
DR WormPep; R09E10.5; CE06287.
KW Hypothetical protein; Transmembrane.
SQ SEQUENCE 1459 AA; 165994 MW; 769014C5599513C4 CRC64;

Query Match 23.0%; Score 54.5; DB 1; Length 1459;
Best Local Similarity 40.6%; Pred. No. 30;
Matches 13; Conservative 4; Mismatches 12; Indels 3; Gaps 2;

QY 7 WCVRRK- - YKSSGFCAGRYSEN-ISRQTSST 35
Db 1370 WCIRKKLQESRNYSGTAAYSNNAFQNTYET 1401

RESULT 7
AXIA_BRARE
ID AXIA_BRARE STANDARD; PRT; 409 AA.
AC Q07342;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE AXIAL PROTEIN.
GN AXIAL.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Rasbora; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=93321871; PubMed=7687227;
RA Straehle U., Blader P., Henrique D., Ingham P.W.;
RT "Axial, a zebrafish gene expressed along the developing body axis,
RT shows altered expression in cyclops mutant embryos.";
RL Genes Dev. 7:1436-1446(1993).
CC -!- FUNCTION: MAY PLAY A CRUCIAL ROLE IN SPECIFICATION OF BOTH THE
CC AXIAL MESENODERM AND THE VENTRAL NERVOUS SYSTEM.
CC -!- SUBCELLULAR LOCATION: NUCLEAR.
CC -!- DEVELOPMENTAL STAGE: EXPRESSED JUST BEFORE GASTRULATION IN A
CC NARROW REGION ON THE DORSAL SIDE OF THE EMBRYO. EXPRESSION CAN BE
CC DETECTED IN THE INVOLUTED CELLS COMPRISING THE MESENODERM OF THE
CC DEVELOPING AXIS. AT THE END OF GASTRULATION EXPRESSION IS TURNED
CC ON IN THE VENTRAL NEURAL PLATE IN CELLS ADJACENT TO THE AXIAL-
CC EXPRESSING MESENODERMAL CELLS.
CC -!- INDUCTION: BY MESENODERM-INDUCING FACTOR ACTIVIN A.
CC -!- SIMILARITY: CONTAINS 1 FORK-HEAD DOMAIN.
CC -----
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CC -----
CC EMBL; Z22762; CAA80443.1; -
DR ZFIN; ZDB-GENE-980526-404; axial.
DR InterPro; IPR001766; -
DR Pfam; PF00250; Fork_head; 1.

```

DR PRINTS; PR00053; FORKHEAD.
DR PROSITE; PS00657; FORK_HEAD_1; 1.
DR PROSITE; PS00658; FORK_HEAD_2; 1.
DR PROSITE; PS00039; FORK_HEAD_3; 1.
KW DNA-binding; Developmental protein; Nuclear protein.
FT DNA_BIND 150..241
SQ SEQUENCE 409 AA; 45075 MW; 3ABB5B1D7B37071A CRC64;

Query Match      22.8%; Score 54; DB 1; Length 409;
Best Local Similarity 36.1%; Pred. No. 8.6;
Matches 13; Conservative 7; Mismatches 14; Indels 2; Gaps 1;

QY 8 CVRRKYSKGFSCAGRYSENISROTSETADNDNASS 43
   | | | | | : | : | : | | | | | : | : |
Db 239 CYLRQKR--FKCDKKLSKDPKRKTSEGGSSNSES 272

RESULT 8
YSX7_CAEEL
ID YSX7_CAEEL STANDARD; PRT; 978 AA.
AC Q10025;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE HYPOTHETICAL 113.1 KDA PROTEIN T28D9.7 IN CHROMOSOME II.
GN T28D9.7.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Waterston R.;
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: SOME, TO THE AMILORIDE-SENSITIVE SODIUM CHANNELS
CC FAMILY
CC -----
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CC -----
DR EMBL; U28738; AAA68309.1; -.
DR WormPep; T28D9.7; CF02889.
DR InterPro; IPR001873; -.
DR Pfam; PF00858; ASC; 1.
DR Hypothetical protein; Transmembrane.
FT TRANSMEM 32..52 POTENTIAL.
SQ SEQUENCE 978 AA; 113116 MW; B3B5C48ABF2607B9 CRC64;

Query Match      22.6%; Score 53.5; DB 1; Length 978;
Best Local Similarity 32.7%; Pred. No. 26;
Matches 17; Conservative 9; Mismatches 13; Indels 13; Gaps 4;

QY 3 LKDLWCV-RRK-----YKSSGFSCAGRY-----SENISRQTS--ETADNDNA 41
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 819 VKLLWCLDRKSDRDIGWFKNCSQGVWRIFVNFENFEKNNDETEDSNS 870
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 9
AATC_CHICK
ID AATC_CHICK STANDARD; PRT; 411 AA.
AC P00504;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE ASPARTATE AMINOTRANSFERASE, CYTOPLASMIC (EC 2.6.1.1) (TRANSAMINASE A)

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DE (GLUTAMATE OXALOACETATE TRANSAMINASE-1).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=89335814; PubMed=2503046;
RA Mattes U., Jaussi R., Ziak M., Juretic N., Lindenmann J.-M.,
RA Christen P.;
RT "Structure of cDNA of cytosolic aspartate aminotransferase of chicken
RT and its expression in E. coli.";
RL Biochimie 71:411-416(1989).
RN [2]
RP SEQUENCE.
RC TISSUE=Heart;
RX MEDLINE=80047259; PubMed=499525;
RA Shlyapnikov S.V., Myasnikov A.N., Severin E.S., Myagkova M.A.,
RA Torchinsky Y.M., Braunstein A.E.;
RT "Primary structure of cytoplasmic aspartate aminotransferase from
RT chicken heart and its homology with pig heart isoenzymes.";
RL FEBS Lett. 106:385-388(1979).
RN [3]
RP SEQUENCE.
RC TISSUE=Heart;
RA Shlyapnikov S.V., Myasnikov A.N., Severin E.S., Myagkova M.A.,
RA Demidkina T.V., Torchinsky Y.M., Braunstein A.E.;
RT "Primary structure of cytoplasmic aspartate aminotransferase from
RT chicken heart IV. Structure of cyanogen bromide peptides and the
RT complete amino acid sequence of the protein.";
RL Bioorg. Khim. 6:876-884(1980).
RN [4]
RP GENE STRUCTURE.
RC STRAIN=WHITE LEGHORN;
RX MEDLINE=90382432; PubMed=2401287;
RA Juretic N., Mattes U., Ziak M., Christen P., Jaussi R.;
RT "Structure of the genes of two homologous intracellularly heterotopic
RT isoenzymes. Cytosolic and mitochondrial aspartate aminotransferase of
RT chicken.";
RL Eur. J. Biochem. 192:119-126(1990).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (3.2 ANGSTROMS).
RX MEDLINE=82165126; PubMed=7067826;
RA Harutyunyan E.G., Malashkevich V.N., Tersyan S.S., Kochkina V.M.,
RA Torchinsky Y.M., Braunstein A.E.;
RT "Three-dimensional structure at 3.2-A resolution of the complex of
RT cytosolic aspartate aminotransferase from chicken heart with 2-
RT oxoglutarate.";
RL FEBS Lett. 138:113-116(1982).
RN [6]
RP X-RAY CRYSTALLOGRAPHY (3.5 ANGSTROMS).
RX MEDLINE=80143195; PubMed=7360247;
RA Borisov V.V., Borisova S.N., Sosfenov N.I., Vainshtein B.K.;
RT "Electron density map of chicken heart cytosol aspartate transaminase
RT at 3.5-A resolution.";
RL Nature 284:189-190(1980).
RN [7]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX MEDLINE=95205406; PubMed=7897655;
RA Malashkevich V.N., Strokopytov B.V., Borisov V.V., Dauter Z.,
RA Wilson K.S., Torchinsky Y.M.;
RT "Crystal structure of the closed form of chicken cytosolic aspartate
RT aminotransferase at 1.9-A resolution.";
RL J. Mol. Biol. 247:111-124(1995).
CC -!- CATALYTIC ACTIVITY: L-ASPARTATE + 2-OXOGLUTARATE = OXALOACETATE +
CC L-GLUTAMATE.
CC -!- COFACTOR: PYRIDOXAL PHOSPHATE.
CC -!- SUBUNIT: HOMODIMER.
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -!- MISCELLANEOUS: IN EUKARYOTES THERE ARE TWO ISOZYMES: A CYTOPLASMIC
CC ONE AND A MITOCHONDRIAL ONE.
CC -!- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT

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Pfam: PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW ATP-binding; Heat shock
SQ SEQUENCE 638 AA; 70068 MW; EE86A60E861C36D7 CRC64;

Query Match 21.1%; Score 50; DB 1; Length 638;
Best Local Similarity 41.7%; Pred. No. 47;
Matches 10; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

QY 21 AGRYSENIISQTSSETADNDNASSF 44
||||:| ||::| :| :|
Db 520 AGRYAEEDQRNKIAARNLESY 543

RESULT 15
NRG3_MOUSE STANDARD; PRT; 713 AA.
ID NRG3_MOUSE AC C35181;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE PRO-NEUREGULIN-3 PRECURSOR (PRO-NRG3) [CONTAINS: NEUREGULIN-3 (NRG-3)].
DE 3)].
DE NRG3.
GN Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RZ TISSUE=Brain;
RX MEDLINE=97420720; PubMed=9275162;
RA Zhang D., Sliwkowski M.X., Mark M., Frantz G., Akita R., Sun Y.,
RA Hillan K., Crowley C., Brush J., Godowski P.J.;
RT "Neuregulin-3 (NRG3): a novel neural tissue-enriched protein that
RT binds and activates ErbB4.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:9562-9567(1997).
CC -!- FUNCTION: DIRECT LIGAND FOR THE ERBB4 TYROSINE KINASE RECEPTOR.
CC BINDING RESULTS IN LIGAND-STIMULATED TYROSINE PHOSPHORYLATION AND
CC ACTIVATION OF THE RECEPTOR. DOES NOT BIND TO THE EGF RECEPTOR,
CC ERBB2 OR ERBB3 RECEPTORS.
CC -!- SUBCELLULAR LOCATION: EXISTS AS AN TYPE I MEMBRANE PROTEIN AND AS
CC A PROTEOLYTICALLY RELEASED SOLUBLE GROWTH FACTOR FORM. THE
CC MEMBRANE-BOUND FORM DOES NOT SEEM TO BE ACTIVE (BY SIMILARITY).
CC -!- TISSUE SPECIFICITY: EXPRESSED IN SYMPATHETIC, MOTOR, AND SENSORY
CC NEURONS.
CC -!- DEVELOPMENTAL STAGE: DETECTED AS EARLY AS E11. IN E13 EMBRYOS,
CC DETECTED MAINLY IN THE NERVOUS SYSTEM. IN E16 EMBRYOS, DETECTED IN
CC THE BRAIN, SPINAL CORD, TRIGEMINAL, VESTIBULAR-COCHLEAR, AND
CC SPINAL GANGLIA. IN ADULTS, EXPRESSED IN SPINAL CORD, AND NUMEROUS
CC BRAIN REGIONS.
CC -!- DOMAIN: THE CYTOPLASMIC DOMAIN MAY BE INVOLVED IN THE REGULATION
CC OF TRAFFICKING AND PROTEOLYTIC PROCESSING. REGULATION OF THE
CC PROTEOLYTIC PROCESSING INVOLVES INITIAL INTRACELLULAR DOMAIN
CC DIMERIZATION (BY SIMILARITY).
CC -!- DOMAIN: ERBB RECEPTOR BINDING IS ELICITED ENTIRELY BY THE EGF-LIKE
CC DOMAIN (BY SIMILARITY).
CC -!- PTM: PROTEOLYTIC CLEAVAGE CLOSE TO THE PLASMA MEMBRANE ON THE
CC EXTERNAL FACE LEADS TO THE RELEASE OF THE SOLUBLE GROWTH FACTOR
CC FORM (BY SIMILARITY).
CC -!- PTM: EXTENSIVE GLYCOSYLATION PRECEDES THE PROTEOLYTIC CLEAVAGE (BY
CC SIMILARITY).
CC -!- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
CC -!- SIMILARITY: BELONGS TO THE NEUREGULIN FAMILY.

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 CC -----

DR EMBL; AF010130; AAB70914.1; -
 DR MGD; MGI:1097165; Nf93.
 DR InterPro; IPR000561; -
 DR Pfam; PF00008; EGF; 1.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS01186; EGF_2; 1.
 KW Growth factor; EGF-like domain; Transmembrane; Multigene family.
 FT CHAIN 1 713
 FT CHAIN 1 361
 FT CHAIN 1 362
 FT DOMAIN 1 362
 FT TRANSMEM 363 383
 FT DOMAIN 384 713
 FT DOMAIN 105 287
 FT DOMAIN 288 331
 FT DOMAIN 13 21
 FT DOMAIN 26 34
 FT DOMAIN 127 135
 FT DOMAIN 250 253
 FT DOMAIN 254 263
 FT DOMAIN 264 267
 FT DISULFID 292 306
 FT DISULFID 300 319
 FT DISULFID 321 330
 SQ SEQUENCE 713 AA: 77369 MW: 9F/DID5E7FC8DCF0 CRC64;

Query Match 21.1%; Score 50; DB 1; Length 713;
 Best Local Similarity 38.2%; Pred No. 53;
 Matches 13; Conservative 3; Mismatches 14; Indels 4; Gaps 1;

OY 6 LWCVR-----KYKSSGFSCAGRYSENISQTSET 35
 ||||| ||| ||| : ||
 Db 535 LWCVERPLDKYVNSNGLRTQQNASINMQLPSRET 568

Search completed: May 23, 2001, 15:36:22
 Job time: 653 sec

Result No.	Score	Query %		DB	ID	Description
		Match	Length			
1	164.5	69.4	367	11	Q9rlv0	mus musculus
2	63	26.6	92	3	Q92381	schizosach
3	63	26.6	245	3	Q74871	schizosach
4	59	24.9	515	10	Q9SD65	arabidopsis
5	58.5	24.7	113	14	Q9J841	spodoptera
6	57.5	24.3	959	3	Q06337	saccharomyc
7	56	23.6	240	10	Q9ZTE0	arabidopsis
8	56	23.6	1500	11	Q63041	rattus norv
9	56	23.6	1500	11	Q63332	rattus norv
10	55	23.2	251	9	Q9MCD4	bacterioph
11	54	22.8	1670	5	Q23901	dictyosteli
12	53.5	22.6	170	14	Q91WR9	human immu
13	53.5	22.6	1482	5	Q9V4Y0	drosophila
14	53	22.4	152	2	Q9X9G7	yersinia en
15	53	22.4	224	10	Q38746	atriplex nu
16	52.5	22.2	933	5	Q9T877	caenorhabd
17	52.5	22.2	942	10	Q65309	arabidopsis
18	52.5	22.2	957	10	Q9SUC2	arabidopsis
19	52	21.9	160	2	Q9PEL5	xylella fas

RESULT 2

DT	01-MAY-2000	(TEMBLrel. 13, Created)
DT	01-MAY-2000	(TEMBLrel. 13, Last sequence update)
DT	01-JUN-2000	(TEMBLrel. 14, Last annotation update)
DE	HYPOTHETICAL 58.2 KDA PROTEIN.	
GN	F3I12.130.	
OS	Arabidopsis thaliana (Mouse-ear cress).	
OC	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;	
OC	Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;	
OC	Brassicales; Brassicaceae; Arabidopsiis.	
OX	NCBI_TaxID=3702;	
RN	[1]	
RN	SEQUENCE FROM N.A.	
RP	Choise N., Robert C., Brottier P., Wincker P., Cattolico L.,	
RA	Artiguenave F., Saurin W., Weissenbach J., Mewes H.W., Lemcke K.,	
RA	Mayer K.F.X., Quetier F., Salanoubat M.;	
RL	Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.	
[2]		
RP	SEQUENCE FROM N.A.	
RA	EU Arabidopsis sequencing project:	
RL	Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.	
DR	EMBL; ALI33292; CAB61954.1; -	
DR	INTERPRO; IPR001440; -	
KW	Hypothetical protein.	
SQ	SEQUENCE 515 AA; 58190 MW; 7C9638ED679362C3 CRC64;	
Query Match 24.9%; Score 59; DB 10; Length 515;		
Best Local Similarity 35.9%; Pred. No. 5.9;		
Matches 14; Conservative 8; Mismatches 17; Indels 0; Gap		
Qy	5 DLWCVRKRYKSSGFCAGRYSENISQTSETADNDNAS 43	
Db	: : : : : : : : : : :	
Db	112 EAFSVKMQLASQFRNAGDEEEENKQKSEAVDNDNSN 150	
RESULT	5	
O9JB41		
ID	O9JB41 PRELIMINARY; PRT; 113 AA.	
AC	O9JB41;	
DT	01-OCT-2000 (TEMBLrel. 15, Created)	
DT	01-OCT-2000 (TEMBLrel. 15, Last sequence update)	
DT	01-OCT-2000 (TEMBLrel. 15, Last annotation update)	
DE	ORF96.	
OS	Spodoptera exigua nucleopolyhedrovirus.	
OC	Viruses; dsDNA viruses, no RNA stage; Baculoviridae;	
OC	Nucleopolyhedrovirus.	
OX	NCBI_TaxID=10454;	
RN	[1]	
RN	SEQUENCE FROM N.A.	
RX	MEDLINE-20036646; PubMed-10567663;	
RA	Ijkel W.F., van Strien E.A., Heldens J.G., Broer R., Zuidema D.,	
RA	Goldbach R.W., Vlak J.M.;	
RT	"Sequence and organization of the spodoptera exigua multicapsid	
RT	nucleopolyhedrovirus genome."	
RL	J. Gen. Virol. 80:3289-3304(1999).	
RN	[2]	
RN	SEQUENCE FROM N.A.	
RA	Ijkel W.F.J., van Strien E.A., Heldens J.G.M., Broer R., Zuidema D.	
RA	Goldbach R.W., Vlak J.M.;	
RL	Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.	
DR	EMBL; AF169823; AAF3625.1; -	
SQ	SEQUENCE 113 AA; 12673 MW; 74C916B8080B075 CRC64;	
Query Match 24.7%; Score 58.5; DB 14; Length 113;		
Best Local Similarity 46.4%; Pred. No. 1.5;		
Matches 13; Conservative 5; Mismatches 9; Indels 1; Gap		
Qy	18 FSCAGRYSENISRQTSETADNDNASFT 45	
Db	: : : :	
Db	20 YFCAGRCNNN-SSSGGSGDNDNSLFT 46	

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RESULT 6
Q06337 ID Q06337 PRELIMINARY: PRT; 959 AA.
AC Q06337;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE CHROMOSOME IV COSMID 9476.
GN D9476.11.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
OC Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C (AB972);
RA Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Du Z.,
RA Favello A., Fulton L., Gattung S., Greco T., Kirsten J., Kucaba T.,
RA Hallsworth K., Hawkins J., Hillier L., Jier M., Johnson D.,
RA Johnston L., Langston Y., Latreille P., Le T., Mardis E., Menezes S.,
RA Miller N., Nhan M., Pauley A., Peluso D., Rifken L., Riles L.,
RA Taich A., Trevasakis E., Vignati D., Wilcox L., Wohlman P., Vaudin M.,
RA Wilson R., Waterston R.;
RA Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C (AB972);
RA Du Z.;
RA Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C (AB972);
RA Waterston R.;
RA Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C (AB972);
RA Jia Y., Cherry J.M.;
RA Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
RN [5]
DE EMBL; 028372; AAB64794.1; -
DR INTERPRO: IPR001005; -
SQ SEQUENCE 959 AA; 110040 MW; AF6D8B7BF5589C2F CRC64;

Query Match 24.3%; Score 57.5; DB 3; Length 959;
Best Local Similarity 37.5%; Pred. No. 18;
Matches 18; Conservative 7; Mismatches 12; Indels 11; Gaps 3;

QY 3 LKDLW-----CVRKY-----KSGFSCAGRYSENISRQTSETADNDN 40
Db 391 INDYWTYGEICCVKRRLLPGKENKLSDDGRISEK-SGRPSDTSRND 437

RESULT 7
Q9ZTE0 ID Q9ZTE0 PRELIMINARY: PRT; 240 AA.
AC Q9ZTE0;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE PUTATIVE TRANSCRIPTION FACTOR (FRAGMENT).
GN MYB50.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
OC Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RX MEDLINE=99056848; PubMed=9839469;
RA Kranz H.D., Denekamp M., Greco R., Jin H.-L., Leyva A., Meissner R.,
RA Petroni K., Urzainqui A., Bevan M., Martin C., Smeekens S.,

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RA Tonelli C., Paz-Ares J., Weisshaar B.;
RT "Towards functional characterisation of the members of the R2R3-MYB
RT gene family from Arabidopsis thaliana.";
RL Plant J. 16:263-276(1998).
DR EMBL; AF062886; AAC83608.1; -
DR HSSP; P01103; IPOM.
DR INTERPRO: IPR001005; -
DR PFAM; PF00249; myb_DNA-binding; 1.
DR PROSITE; PS00334; MYB_2; 1.
FT NON_TER 1
SQ SEQUENCE 240 AA; 26684 MW; 9B789F7CC61AB823 CRC64;

Query Match 23.6%; Score 56; DB 10; Length 240;
Best Local Similarity 26.1%; Pred. No. 6.9;
Matches 12; Conservative 15; Mismatches 15; Indels 4; Gaps 3;

QY 3 LKDLW--CVRKYSKSGFS-CAGRYSENISRQTSETADNDNASSFT 45
Db 30 IKNLWNSCIKKLKKMGIDPTTHKPLSEVGKRETNR-SDNNNSTSFS 74

RESULT 8
Q63041 ID Q63041 PRELIMINARY: PRT; 1500 AA.
AC Q63041;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE ALPHA-1-MACROGLOBULIN.
GN ALPHA1 M.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Eggertsen G., Hudson G., Shields B., Reed D., Lonberg-Holm K.,
RA Fey G.H.;
RA Mol. Biol. Med. 0:0-0(0).
DR EMBL; M77183; AAA40723.1; -
DR HSSP; P01023; 1BV8
DR INTERPRO: IPR001599; -
DR INTERPRO: IPR002890; -
DR PFAM; PF00207; A2M; 1.
DR PFAM; PF01835; A2M_N; 1.
DR PROSITE; PS00477; ALPHA_2_MACROGLOBULIN; 1.
SQ SEQUENCE 1500 AA; 167124 MW; 8ABB810985795AB2 CRC64;

Query Match 23.6%; Score 56; DB 11; Length 1500;
Best Local Similarity 41.4%; Pred. No. 45;
Matches 12; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

QY 9 VRRKYKSGFSCAGRYSENISRQTSETAD 37
Db 266 VCRKYTSYNSCHGQHSKICEEFSKQAD 294

RESULT 9
Q63332 ID Q63332 PRELIMINARY: PRT; 1500 AA.
AC Q63332;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE ALPHA-1-MACROGLOBULIN PRECURSOR.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.

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RC STRAIN-SPRAGUE-DAWLEY; TISSUE=LIVER;
 RA MEDLINE=92172859; PubMed=1371696;
 RT "DNA cloning and sequencing of rat alpha 1-macroglobulin.";
 RL Biochemistry 31:2346-2352(1992).
 DR EMBL: M84000; AAA41591.1; -;
 DR HSP: P01023; 1BV8.
 DR INTERPRO: IPR001599; -;
 DR INTERPRO: IPR002890; -;
 DR PFAM: PF00207; A2M; 1.
 DR PFAM: PF01835; A2M_N; 1.
 DR PROSITE: PS00477; ALPHA_2_MACROGLOBULIN; 1.
 KW Signal.
 FT CHAIN 1 24 POTENTIAL.
 FT CHAIN 25 1500 ALPHA-1-MACROGLOBULIN.
 SQ SEQUENCE 1500 AA; 167158 MW; 2FCDD66CF3A617C6 CRC64;

Query Match 23.6%; Score 56; DB 11; Length 1500;
 Best Local Similarity 41.4%; Pred. No. 45;
 Matches 12; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

Qy 9 VRRYKSSGFSCAGRYSENISROTSETAD 37
 Db 266 VCRYTOSYNCHGQHSKICEEFSKOAD 294

RESULT 10
 Q9MQU4 ID Q9MQU4 PRELIMINARY; PRT; 251 AA.
 AC Q9MQU4
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE GP18.
 OS Bacteriophage HK022.
 OC Viruses; dsDNA viruses, no RNA stage; Tailed phages; Siphoviridae;
 OC Lambda phage group.
 OX NCBI_TaxID=10742;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Juhala R., Ford M.E., Duda R.L., Youlton A., Hatfull G.F.,
 RA Hendrix R.W.;
 RT "Genomic sequences of bacteriophages HK97 and HK022: pervasive genetic mosaicism in the lambdaoid bacteriophages.";
 RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF069308; AAF30369.1; -;
 SQ SEQUENCE 251 AA; 27535 MW; 5116519A0998FFFF CRC64;

Query Match 23.2%; Score 55; DB 9; Length 251;
 Best Local Similarity 40.0%; Pred. No. 9.9;
 Matches 12; Conservative 6; Mismatches 10; Indels 2; Gaps 2;

Qy 7 WCVRRKYS-SGFSCAG-RYSENISROTSE 34
 Db 186 WCIRNKYRTGDCDYAGTRYFDKNNQVSD 215

RESULT 11
 Q23901 ID Q23901 PRELIMINARY; PRT; 1670 AA.
 AC Q23901
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
 DE HISTIDINE KINASE.
 GN DOKA.
 OS Dictyostelium discoideum (Slime mold).
 OC Eukaryota; Dictyostellida; Dictyostelium.

OX NCBI_TaxID=44689;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN-AX2;
 RA MEDLINE=96324396; PubMed=8670893;
 RX Schuster S.C., Noegel A.A., Oehme F., Gerisch G., Simon M.I.;
 RT "The hybrid histidine kinase Doka is part of the osmotic response system of Dictyostelium.";
 RL EMBO J. 15:3880-3889(1996).
 DR EMBL: X96869; CAA65612.1; -;
 DR INTERPRO: IPR000410; -;
 DR INTERPRO: IPR001789; -;
 DR PFAM: PF00072; response_reg; 1.
 DR PFAM: PF00512; signal; 1.
 SQ SEQUENCE 1670 AA; 186391 MW; 85C76DEB847276B5 CRC64;

Query Match 22.8%; Score 54; DB 5; Length 1670;
 Best Local Similarity 32.1%; Pred. No. 94;
 Matches 17; Conservative 8; Mismatches 18; Indels 10; Gaps 2;

Qy 1 KILKDLWCVRKYS-----SGFSCAGRYSENI--SRQTSATADNDNASS 43
 Db 498 KVLNLFIRQYKSRATIKPFDPGICIFEYIENILNLYQPPSTLNDIRNS 550

RESULT 12
 Q9IWR9 ID Q9IWR9 PRELIMINARY; PRT; 170 AA.
 AC Q9IWR9;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE ENV GLYCOPROTEIN (FRAGMENT).
 GN ENV.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=85CD334;
 RA Yang C., Dash B., Hanna S.L., Frances H.S., Nzilambi N.,
 RA Colebunders R.C., St Louis M., Quinn T.C., Folks T.M., Lal R.B.;
 RT "Predominance of HIV-1 subtype Q among commercial sex-workers from Kinshasa, Democratic Republic of Congo.";
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF260457; AAF1605.1; -;
 FT NON_TER 1 170
 FT NON_TER 170 170
 SQ SEQUENCE 170 AA; 19430 MW; 3E068F04B1A71F12 CRC64;

Query Match 22.6%; Score 53.5; DB 14; Length 170;
 Best Local Similarity 32.8%; Pred. No. 11;
 Matches 19; Conservative 4; Mismatches 10; Indels 25; Gaps 3;

Qy 11 RKY-----KSSG-----FSCAGRYSE-----NISROTSETADNDNASS 43
 Db 86 RKYFQNKTFNTKSSGGDLITHTSFNCAGFEFFCYNTSLFNSSWTENDTASNDTVSS 143

RESULT 13
 Q9V4Y0 ID Q9V4Y0 PRELIMINARY; PRT; 1482 AA.
 AC Q9V4Y0; Q9V4Y1; Q9V4Y2; Q9V4Y3; Q9V4Y4; Q9V4Y5; Q9V4Y6;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE SNS PROTEIN.
 GN SNS.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Eukaryota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]

RP SEQUENCE FROM N.A.
RX MEDLINE-20317033; PubMed-10859168;
RA Bour B.A., Chakravarti M., West J.M., Abmayr S.M.;
RT "Drosophila SNS, a member of the immunoglobulin superfamily that is
RL essential for myoblast fusion.";
RN Genes Dev. 14:1498-1511(2000).
[2]
RP SEQUENCE OF 1-224; 334-477; 491-1061 AND 1274-1482 FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE-2019606; PubMed-10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton R.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers J.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Bertram B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Posler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K.A., Nusskern D.R., Pacieb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster";
RL Science 287:2185-2195(2000).
DR EMBL; AF254867; AAF77184.1; ALT_SEQ.
DR EMBL; AF254867; AAF59037.1; ALT_SEQ.
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